

Running Head: GALLIFORM BARAMINOLOGY

A Baraminological Analysis of the Land Fowl (Class Aves, Order Galliformes)

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Abstract

This study investigates the number of galliform bird holobaramins. Criteria used to determine the members of any given holobaramin included a biblical word analysis, statistical baraminology, and hybridization. The biblical search yielded limited biosystematic information; however, since it is a necessary and useful part of baraminology research it is both included and discussed. Baraminic distance and multidimensional scaling suggest four holobaramins (cracids, megapodes, guineafowl, and all other galliforms), while a review of hybridization records implies only two (megapodes and all other galliforms). All analyses for statistical methods were based on a dataset obtained from Dyke *et al.* (2003). I suggest that the Order Galliformes contains a megapode holobaramin and a cracid + phasianoid holobaramin, based on analyses of morphological and hybridization data.

A Baraminological Analysis of the Land Fowl (Class Aves, Order Galliformes)

Introduction

*An Introduction to Baraminology*

Today, scientists and others are interested in the science of classifying living organisms. As intuitive beings, humans see the need to organize creatures into an orderly system that can be easily understood. The science of classifying living organisms is called taxonomy. Charles Darwin, the father of evolutionary theory, certainly influenced the course of present-day taxonomy, which heavily incorporates the theory of evolution. According to Darwin (1859), simpler organisms evolved gradually into more complex organisms. Detailed taxonomic cladograms and “evolutionary trees” have been developed using the underlying assumption of evolution. However, most times there is not enough data to affirm complete accuracy of these diagrams, making them only theory at best. Consequently, what is desired is the creation of a system of taxonomy that accurately portrays the variation of species since the beginning of history. Baraminology, the study of created kinds (from the Hebrew words “bara” and “min”), is a classification method that relies on natural data and on information found directly in Scripture, especially that relating to the Creation account (Wise, 1990). Since the Creation model dictates that the various kinds of organisms were created during the span of the Creation week, it undoubtedly takes a very different approach to taxonomy.

One of the advantages of baraminology is that it does not necessitate that every living thing must somehow be related to every other living thing, as taxonomy that incorporates Darwinian evolution does. Additionally, the fact that there are many gaps within evolutionary depictions of the “tree of life,” lends support for the need of a new

method of classification. Baraminology does not dictate that all forms of evolution do not occur, nor does it reject the use of hierarchy in its analysis. However, the criteria that divide the data into categories do not imply that they are in any way ranked.

Baraminology simply seeks to use criteria to organize species or taxa; subsequently, it uses this data to form groups of organisms by joining them on the basis of their similarities and (unlike modern taxonomy) separating them on the basis of their dissimilarities (Cummins, 1996; Baraminology Study Group, 2006).

The goal of baraminology is to join organisms that share common ancestry while also taking another important step: identifying the boundaries that separate organisms. Baraminology is very new and much work lies ahead in developing it. Only a few studies have been done to date, and most species still have to be investigated to determine where they belong taxonomically. As these species are analyzed by methods such as hybridization, statistics, molecular studies, and morphological analysis (Wood *et al.*, 2003), their true relationship to other organisms will become more and more defined. Subsequently, the history of the variation and diversification of species characteristics, as well as the species themselves, will become increasingly clear. As thousands of years are traced from the beginning of the post-Flood period, groups of created organisms that form today's families, orders, etc., come into view. This reveals a proper understanding of ancestor-descendant relationships, and the taxonomy is valuable as it can help reveal a grand picture of the diversity occurring among all species.

#### *History and Development of Baraminology*

Baraminology began with Frank Marsh (Marsh, 1944). Marsh believed when the Bible specified that the first-created living things were reproducing "after their kind"

(Genesis 1:21, for example), this indicated a special separation between the creatures, i.e., their ability to reproduce with each other was bounded within each created “kind.”

Marsh designated these kinds “baramins,” from the Hebrew words for “created” (“bara”) and “kind” (min) (Marsh, 1944; Wood and Murray, 2003). Each baramin, therefore, includes its own parental population and all of their descendants. Marsh (1944) furthermore concluded that since only organisms of the same baramin can interbreed, then successful hybridization indicates that two interbreeding organisms are part of the same baramin. This idea is fundamental to baraminology. To define a true baramin more specifically, Marsh (1944) stated that two living things were of the same kind if true fertilization occurred; he did not, however, state that the fertilized embryo had to develop to full term. Marsh also considered morphology to be a useful criterion in separating baramins, but did not consider it to be as definitive as hybridization. Instead, he suggested that morphology reflects reproductive ability only to a certain extent (Marsh, 1944). Marsh’s fundamental description of the created kinds based on their ability to reproduce or not reproduce is still maintained. However, because he never gave a complete definition for the baramin, some problems began to arise (Wood *et al.*, 2003).

In 1993, German creationists joined together to publish *Typen des Lebens*, translated *Basic Types of Life*. The idea of a basic type as given by Siegfried Scherer is comparable to Marsh’s baramin. Scherer (1993) maintained that two organisms were from the same basic type if they could hybridize with each other or if they could both hybridize with the same third organism. Scherer (1993), unlike Marsh (1944), required that the embryo produced from the two organisms be viable, expressing characteristics of both parents (in order for the parents to have been of the same basic type). One

advantage of this definition includes the ability for researchers to determine the basic type by hybridization experiments. If breeding results in viable offspring, then by Scherer's definition, the two paired adults are of the same basic type. Determining the different types or kinds of organisms on the basis of these sorts of hybridization experiments is key to baraminology. However, like almost any defined system, Scherer's basic type definition has its limitations. For instance, Scherer's requirement that the basic types be able to reproduce and form viable offspring is a consideration applying only to organisms that reproduce sexually. Thus, a basic type cannot be described for organisms that do not reproduce in this way. Additionally, the failure to hybridize is not itself determinative that two organisms are of different basic types. Furthermore, the line between successful and unsuccessful hybridization can be vague in some cases, making it difficult to establish the basic type. These limitations, however, do not cancel the importance of hybridization in determining basic types, and hybridization provides powerful evidence that two organisms are of the same basic type. The basic type system as described by Scherer is undoubtedly a helpful system to use for categorizing the different groups of life forms. However, it does not predict absolutely which types of organisms are derived from which others.

Walter ReMine (1990) revolutionized baraminology with his discussion of discontinuity systematics. Discontinuity, which is now basic to baraminology, is important because it develops the idea that classification no longer needs to be thought of as a strictly continuous system, but in terms of discontinuity. Introducing discontinuity into systematics allowed ReMine to create a new model entirely separate from evolutionary taxonomy (which he thought was blind to discontinuity) (ReMine, 1990).

ReMine created terms to accommodate his new system: holobaramin, monobaramin, apobaramin, and polybaramin. These terms are still being used, and are essential to understanding and using baraminology. ReMine describes the holobaramin as “a complete set of organisms related by common descent” (ReMine, 1990, p. 208). A monobaramin includes organisms that are related by origin, but not necessarily all of them. Thus, a monobaramin may be a holobaramin, but many times it is just a part of the holobaramin. An apobaramin is a group that includes every descendant or ancestor for each individual contained inside of it. An apobaramin may be divided into subgroups that are not related to each other. Part of ReMine’s definition is that an apobaramin contains either one or more than one separate holobaramin (ReMine, 1990). An apobaramin, then, is either broader than a holobaramin, or else by definition it is a holobaramin. Lastly, ReMine introduces the term polybaramin. Within a polybaramin are organisms that do not all share the same ancestor (ReMine, 1990). There is always more than one baramin represented in a polybaramin.

One of ReMine’s (1990) thoughts about these terms is that they could be used by evolutionists and creationists to communicate their points of view. According to ReMine, evolutionists should be very interested in this new idea, because it seeks to recognize those events (such as rapid forming of creatures that have no documentation or description within evolutionary theory) that have not been successfully portrayed by evolution alone. Baraminology is in fact an area of study that can be used by evolutionists as well as creationists for discovering the history of species.

Ultimately, discontinuity systematics is designed to break down large groups into smaller groups for the purpose of eventually describing the many separate

holobaramins—the created kinds at the beginning of their existence and all of their known descendants. Discontinuity systematics uses membership criteria, which are the methods used to determine whether or not an organism should be included within a given group (ReMine, 1990). These criteria are extremely important because they are what allow holobaramins to be defined. Membership criteria can be used to create holobaramins by either adding to a monobaramin or subtracting from an apobaramin. The idea is to separate the holobaramin as an individual entity. Baraminology seeks to isolate as many holobaramins as possible, because this sheds light on the true relationship that different organisms share in relation to each other. Practically, it is important that more than one criterion be used to determine holobaramins. A good criterion that is very reliable in most cases is what ReMine calls the reproductive viability criteria (ReMine, 1990). This is similar to the hybridization principles laid out earlier with Scherer's (1993) basic type and Marsh's (1944) baramin methods (the reproductive viability criteria was the only criterion used by both). Basically, it states that two organisms that are able to hybridize must be a part of the same monobaramin. ReMine gave examples of many criteria to use when trying to isolate organisms into their respective holobaramins, and it is important not to limit research to one area. Other criteria may also be used as they are further developed and understood, such as genetics and molecular biology, for example (Wood *et al.*, 2003).

Paleontologist Kurt Wise, whose ideas are a continuation of Walter ReMine's discontinuity systematics, was the first to actually give the name "baraminology" to his method of biosystematics (Wise, 1990). Much of what makes up baraminology today is the compilation of definitions and concepts of Marsh, Scherer, ReMine, Wise, and others.

The contributions of Wise (1990, 2002) have separated baraminology from other methods of systematics. Wise included Scripture as a reliable source for approximating holobaramins (Wood *et al.*, 2003), and it is now common in biosystematics for biologists to use the Bible as a reliable source of data. Additionally, Wise introduced a new term to baraminology: archaebaramin. While he still retained Marsh's expression "baramin," archaebaramin is used to define the very first organisms that ever existed. By defining such, Wise solved the dilemma of Marsh's baramin that did not include the first ancestors (Wood *et al.*, 2003). According to Wise, members of one archaebaramin were (in agreement with Marsh's methodology) not able to reproduce with members of other archaebaramins. Since Wise's definitions for holobaramin, monobaramin, polybaramin, and apobaramin were described in much the same way as ReMine's definitions, the problems arising from ReMine's definitions apply to Wise's as well (Wood *et al.*, 2003). However, his introduction of the archaebaramin term does at least solve one problem. Even so, Wise did not give a formal definition for the archaebaramin (Wood *et al.*, 2003). Nevertheless, baraminology has come a long way since Marsh, and will most likely prove to be a widely-used method among creationists for deducing relationships between organisms.

### *Modern Baraminology*

Combining the previously discussed ideas, authors Wood, Wise, Sanders, and Doran (2003) have produced *A Refined Baramin Concept*, a product of the Baraminology Study Group (BSG). The paper conveniently compiles the information explained above and gives an overall summary of how baraminology started. Baraminology is a young science, and so any study done is basically new research. However, before getting started

into such an undertaking, it is vitally important that the researcher have a thorough understanding of modern baraminology. Wood *et al.* (2003) conveniently give a few of their own definitions to make baraminological concepts more clear. The authors define continuity to illustrate a “significant, holistic similarity between two different organisms,” whereas discontinuity is described as “a significant, holistic difference between two organisms” (Wood *et al.*, 2003, p. 7). Significant implies statistical verifiability; holistic means that the similarities involve the full spectrum of biological characteristics (Wood *et al.*, 2003, p. 7). Their paper also explains two other important terms. The first, biological character space, defines the boundaries of the characteristics of the organisms. The space is unique to individual plots of organisms, and is multidimensional in form. Furthermore, a potentiality region is a region where certain individuals’ expressions may be found within the biological character space. The baramin or baramins within the potentiality region may not fill the entire space initially, which shows the possibility for expansion (variability).

With these new terms explained, it is finally possible to introduce what the refined baramin is. The authors of the paper describe a baramin as the “actualization of a potentiality region at any point or period in history (including but not limited to all of history)” (Wood *et al.*, 2003, p. 8). The authors point out that this definition of a baramin includes every extant individual in the potentiality region, all of their possible descendants, and even their ancestors up to that time (which would include the archaebaramin). Since this is true, all members of the baramin may not be concretely knowable. This definition gives a strong foundation to begin building research. Wood *et al.* (2003) chose to recognize the original definitions for holobaramin, monobaramin,

polybaramin, and apobaramin (ReMine, 1990; Wise, 1990) because of their value, but for ease of use redefine them in their paper using their own terms of continuity and discontinuity, as described above. For example, a holobaramin is “a group of known organisms that share continuity (i.e. each member is continuous with at least one other member) and are bounded by discontinuity” (Wood *et al.*, 2003, p. 8).

*A Refined Baramin Concept* (2003) describes briefly some advantages of the new baraminology system over the older systems, such as using many criteria for its purposes (not hybridization only). The refined baramin concept will be most helpful for future researchers to use and forms the basis for this thesis. It employs methods such as biblical searches and also includes theological issues (Wood *et al.*, 2003).

### *The Galliform Birds*

The galliform birds consist of over 250 species throughout the world (Howard, 2004). They are the chicken-like order of birds and many are game fowl including some familiar birds such as chickens, pheasants, grouse, quails, and guineafowl. The species are quite diverse and cover a broad range of different habitats. Most galliform birds dwell on land (Howard, 2004), and have short, oval-shaped wings, a distinguishable keel, and stocky legs to strut about with. All have four toes which may be covered with tufts of feathers, and in some species the back toe is raised higher on the leg and does not touch the ground level as do the other toes (Gill, 1995). Spurs are also found on the tarsi of certain species of the Phasianidae family (del Hoyo *et al.*, 1994). The beaks of the galliforms are usually short and sometimes curved, convenient for picking small seeds and grains; their large gizzards serve as powerful aids for digesting food (Gill, 1995). Some galliforms are adorned with bland feather patterns, and many are adorned with

spots or stripes in beautiful detail. Others display striking feather patterns, like those seen in the feathers of a peacock tail. The size of the galliform birds ranges from medium to large; from small quails to the larger birds such as the peacock. Galliform birds will usually lay large clutches, and the hatchlings, for the most part, are independent, mobile, and equipped with a soft layer of down (del Hoyo *et al.*, 1994; Gill, 1995; Howard, 2004).

Galliforms are also sometimes referred to as fowl, or the fowl-like birds.

Commonly stated families of the Order Galliformes include Cracidae (curassows, guans, chachalacas); Megapodiidae (moundbuilders); Numididae (guineafowl); Phasianidae (pheasants, Old World quails); and Odontophoridae (New World quails). del Hoyo *et al.* (1994) and Dyke *et al.* (2003) list seven families in the galliform order: Megapodiidae, Cracidae, Numididae, Odontophoridae, Meleagrididae (turkeys), Tetraonidae (grouse), and Phasianidae. A total of 281 species are included in del Hoyo *et al.* (1994), with Phasianidae claiming 153 species, Cracidae 50 species, Odontophoridae 32 species, Megapodiidae 19 species, Tetraonidae 17 species, Numididae 6 species, and Meleagrididae 2 species.

One cause of potential confusion for taxonomists is the hoatzin. While some have placed this odd bird with the galliform bird order, some evidence suggests that it is more closely associated with the Order Cuculiformes (cuckoos) (Sibley and Monroe, 1990; Roberson, 2005). Taxonomically, the Order Anseriformes has been included basally with Galliformes in the Class Aves and the taxon that results is referred to as either Galloanserae or Galloanserimorphae (Dyke *et al.*, 2003). The Order Anseriformes includes screamers, the magpie-goose, and true ducks (Dyke *et al.*, 2003).

Galliformes is a large taxon, and although previous studies have been performed on Galliformes (e.g. Sibley and Ahlquist, 1990; Dyke *et al.*, 2003), there are still many aspects that must be considered. As more data are collected, the decision as to where a certain group of birds should be placed taxonomically becomes clearer. Therefore, research of any sort that utilizes the methods of modern baraminology will help modern taxonomists deduce the relationships that exist among organisms (Wood *et al.*, 2003).

Dyke *et al.* (2003) was the first publication that dealt with osteological considerations for this entire order of birds. Research like this is much needed to give a more comprehensive overview of the many characteristics of the galliform birds and to accurately deal with them from a taxonomic standpoint. Because baraminology is a relatively new science, there is great opportunity for new research, and most organisms have not yet been studied from this perspective.

#### *The Focus of This Study*

The goal of this project is to perform a baraminological study of the galliform birds (commonly known as the landfowl) using the following four methods of analyses: 1) a biblical word search; 2) a baraminic distance correlation analysis; 3) classical multidimensional scaling; and, 4) hybridization. These methods used are exemplified by Wood's (2002) tutorial paper for the grasses, and Wood's (2005a) monograph on the Galápagos Islands. Ideally, the data will reveal the number of holobaramins that exist in this bird order. Wood encourages other researchers to use his example as a template for future baraminological research (Wood, 2002).

This study is based on the assumptions given by baraminology, including the Creation model. A literal six-day Creation of the earth, animals, and man is assumed.

Organisms acceptable for baraminological analysis include both those presently existing, and those that are extinct. This project furthermore assumes the complete infallibility and accuracy of the Bible. Consequently, the study begins with a biblical word search as the first method of analysis for studying the galliform birds. Finally, all statistical analyses performed employ the morphological dataset from Dyke *et al.* (2003).

## Materials and Methods

### *Biblical Word Search*

A biblical word search was the first method used to determine the limits of potential holobaramins within the Order Galliformes. The Bible reveals a wealth of recorded history, including the Creation account in Genesis and further early history recorded in ancient books such as Job. Referencing such material gives potential for revealing the state of creatures at an ancient period of time, specifically early in history immediately following the Flood (Wood, 2002). Indeed, the very core of baraminology is derived from suppositions based on Scripture. Therefore, birds mentioned in the Bible that refer to modern-day galliform birds could be significant to this study.

Because the original text of the Bible is Hebrew, Aramaic, and Greek, a careful word study needs to be carried out in order to gain a complete knowledge of the inferences made in the text. To begin, a list of English words was composed that relate to the galliform birds (Klemm, 1993; Gill, 1995; Dyke *et al.*, 2003; UMMZ Animal Diversity Web, 2006; Tree of Life Web Project, 2006). Key words searched included: fowl, guineafowl, pheasant, quail, chicken, hen, rooster, cock, turkey, grouse, ptarmigan, partridge, junglefowl, landfowl, curassow, guan, chachalaca, moundbuilder, hoatzin,

capercaillie, peacock, tragopan, francolin, bobwhite, argus, monal, snowcock, maleo, hokkos, koklas, and paraka. Each word was searched in five different versions of the English Bible: the King James Version (KJV), the New King James Version (NKJV), the New American Standard Bible (NASB), the New International Version (NIV), and the Revised Standard Version (RSV). BibleGateway.com (2006) was employed for searches within the first four versions mentioned, and the University of Virginia's Electronic Text Center (2006) for the Revised Standard Version. Key words that were found in any of the five English translations searched were investigated for their original meaning as suggested by the Hebrew or Greek words from which they were derived. *The New Strong's Exhaustive Concordance of the Bible* (1990), BibleWorks 6.0 (2003), and the *New International Dictionary of Theology and Exegesis* (NIDOTTE) (VanGemeren, 1997) were all referenced for this purpose. These resources helped to reveal the originally inferred meaning of these words found in the biblical text. An online version of *Strong's Concordance* (Strong, 2006) was also accessed for each of the key words searched.

#### *Baraminic Distance*

Since this study is heavily based on the work of Dyke *et al.* (2003), the original taxonomy assumed in their paper (Johnsgard, 1986; Monroe and Sibley, 1990; del Hoyo *et al.*, 1994) will also be used here. The recognized galliform families will include the megapodes (Megapodiidae), cracids (Cracidae), guineafowl (Numididae), pheasants and their relatives (Phasianidae), New World quail (Odontophoridae), turkeys (Meleagrididae), and grouse (Tetraonidae). Additionally, the superfamily Phasianoidea includes the families Numididae, Phasianidae, Odontophoridae, Meleagrididae, and

Tetraonidae, and its members are many times referred to as the “phasianoids” (Dyke *et al.*, 2003).

Baraminic distance (Robinson and Cavanaugh, 1998) was the first statistical method used to analyze the relationships among species. Baraminic distance as a criterion makes use of character analysis. In character analysis, specimens are coded for a particular set of characters, and these may be morphological characteristics, behavioral characteristics, or molecular characteristics (Wood, 2002; Dyke *et al.*, 2003). Usually, a number is associated that corresponds with a given character state (for example, genus A has an elevated toe and is coded as 1 for the character of toe positioning; genera B does not have an elevated toe and is coded as 0). Once coded, taxa may be compared statistically. By use of this sort of character coding, baraminic distance analyzes relationships between, and within, the holobaramins of interest. The usefulness of baraminic distance over hybridization is that it includes both additive and subtractive evidence, meaning that it can add organisms to expand a monobaramin while also giving evidence that allows for the dividing of an apobaramin (eliminating organisms that do not belong).

The baraminic distance between two taxa is defined as the percentage of characters that are different between those taxa (Wood, 2002). As described originally by Robinson and Cavanaugh (1998), the coefficient of baraminic distance is the ratio of dissimilar characters between two organisms over the total number of characters compared. Species with many characteristics being the same or nearly the same will have a small baraminic distance in relation to each other. Species whose characteristics

are very different will have large baraminic distances showing that the species are not very similar (Robinson and Cavanaugh, 1998; Wood 2002).

In 2006, Todd Wood developed a computer program called BDISTMDS (v. 1.0), which takes a set of characters and calculates the baraminic distances for those characters. BDISTMDS first sorts through the data to calculate character relevance, which is the percentage of taxa whose character states are known for any given character (Wood, 2002). Next, BDISTMDS removes characters that do not meet the minimum relevance. BDISTMDS then calculates baraminic distances and outputs them as a matrix (Wood, 2002). In addition to a baraminic distance matrix, the Pearson correlation coefficient ( $r$ ) is calculated for each pair of taxa. The final step uses these  $r$ -values to determine whether there is significant positive or negative correlation between each of the pairs of taxa. Significant positive correlation can be viewed as similarity in baraminological relationship, while significant negative correlation indicates dissimilarity, or discontinuity (Robinson and Cavanaugh, 1998; Wood, 2002). The graphical output given by BDISTMDS is a combination of the correlations and probabilities between the pairs of taxa.

A baraminic distance correlation analysis was performed on a morphological dataset compiled by Dyke *et al.* (2003) which consists of sixty-five galliform and outgroup taxa. The dataset consists of five genera belonging to the Order Anseriformes, the outgroup (used for comparison). The remaining sixty specimens belong to the Order Galliformes and include three megapodes, five cracids, four guineafowl, seven New World quail, six grouse, two turkeys, twelve Old World quail and partridges, three francolins, two junglefowl, four pavonines, and twelve other phasianid taxa. The

majority of characters (89 of 102) chosen for analysis by Dyke *et al.* (2003) are based on osteological data. For a listing of the names of all genera used in the dataset, and the families they belong to, see Appendix.

Using BDISTMDS (Wood, 2006), the coded characters were inputted from the complete dataset and the baraminic distances were calculated. All datasets employed in this study were sorted for 95% character relevance as recommended by Robinson and Cavanaugh (1998). Ninety-eight of the original 102 characters in Dyke *et al.*'s (2003) original dataset were found to have character relevance of 95% or above and were used to calculate baraminic distances. In some cases, results prompted further baraminic distance analyses for subsets of the complete dataset. The outputs of these analyses were also viewed for consideration. Both text outputs and baraminic distance correlation matrices from BDISTMDS were viewed.

#### *Classical Multidimensional Scaling*

Classical multidimensional scaling (MDS) was introduced by Wood (2005b) for use in baraminology. MDS converts the baraminic distances into a set of k-dimensional coordinates (Wood, 2005a). These coordinates may then be plotted by MAGE (<http://kinemage.biochem.duke.edu/software/mage.php>) to create kinemages (3D clusters of data points). Kinemages are extremely useful for visualizing MDS results in three-dimensional space. When data points are arranged in three-dimensional space they form clusters which can be interpreted to represent monobaraminic and holobaraminic groups. Stress is a measure of the “goodness of fit” between the scaled data and the baraminic distances. BDISTMDS calculates stress at multiple dimensions and produces a stress graph that displays how well the scaled data is being represented at each of these

dimensions. Both baraminic distance and classical multidimensional scaling are used because they have yielded significant results in previous studies (Wood, 2002; Wood, 2005b).

MDS was performed on the uncorrected baraminic distance matrix (Wood, 2005a, b) using BDISTMDS, v. 1.0 (Wood, 2006). The baraminic distance matrix was also made by adding the maximum distance in the matrix, which was 0.673 between *Anhima* and *Dendragapus*. Next, the minimal stress and the stress at three dimensions were calculated for these procedures. Finally, all three-dimensional scaling results were converted into Kinemages for display using MAGE (<http://kinemage.biochem.duke.edu/software/mage.php>).

### *Hybridization*

As mentioned earlier, hybridization has long proved to be a very valuable tool for determination of similarity between species. Successful hybridization is an additive criterion, and is used to add organisms with similar characteristics into the same monobaramin.

No direct hybridization experiments were performed in this study. Not all crosses are easy to perform, but since the galliform birds are raised worldwide for meat and decorative plumage (Klemm, 1993), records of natural hybridization (and the results of hybridization experiments) are available for many of the galliform birds. The most recent and comprehensive compilation of hybridization data comes from McCarthy's *Handbook of Avian Hybrids of the World* (2006). Data from this source were compiled and assessed. To summarize the data, two hybridograms were constructed following Wood (2002).

## Results and Discussion

*Biblical Word Search*

Table 1 summarizes the findings of the key words searched and includes their corresponding numbers as designated by *The New Strong's Exhaustive Concordance* (1990). The table includes the Hebrew, Greek, or Aramaic word used in the biblical text and also the Scriptural reference for each word. Most of the information gathered was extracted from the online version of Strong's Concordance (Strong, 2006) and from *The New International Dictionary of Old Testament Theology and Exegesis* (VanGemeren, 1997). *The New International Dictionary of Old Testament Theology and Exegesis* (NIDOTTE) numbers its entries in a manner similar to Strong (1990), and these numbers are also included in Table 1.

For the sake of completeness, both Old and New Testament Scriptures were searched for relevant words. Since the Old Testament words are those carrying greater potential biosystematic value, they are discussed here, with all transliterations written as given by *NIDOTTE* (1997). The most common relevant word is the Hebrew word 'ôp (found 60 times), and is translated "bird" in most cases within the NKJV, NASB, RSV, and NIV. The KJV translates the same word as "fowl." Furthermore, 'ôp (number 5775) is rendered by Strong (2006) as a bird or something with wings or feathers that flies; fowl. Since bird and fowl are general terms in the English language, no specific kind of bird can be assumed. Additionally, in *NIDOTTE* 'ôp (number 6416) is rendered "flying creatures," including birds and even insects, as in Deuteronomy 14:19 (Kiuchi, 1997b). This indicates that 'ôp is more general than even its English translation of "bird," so it

Table 1: The occurrences of relevant galliform words as searched in five different versions of the Bible. Hebrew, Aramaic or Greek words are in the first column followed by Scriptural references where they are found, English transliterations of the word by each version, and numbering for the words as given by Strong's (Strong, 1990) and NIDOTTE (VanGemenen, 1997). All Hebrew transliterations are written as given in NIDOTTE (VanGemenen, 1997).

Original Biblical Word	Scriptural References	KJV	NKJV	NASB	RSV	NIV	Strong's	NIDOTTE	
'ôp (Hebrew)	Genesis 1:20, 21, 22, 26, 28, 30; 2:19, 20; 6:7, 20; 7:3, 8, 14a, 21, 23; 8:17, 19, 20; 9:2, 10	fowl(s)	bird(s)	bird(s)	bird(s)	bird(s)	bird(s)	5775	6416
	Leviticus 1:14	fowl(s)	bird(s)	bird(s)	bird(s)	bird(s)			
	Leviticus 7:26	fowl	bird	bird	fowl	bird			
	Leviticus 11:13	fowls	birds	birds	birds	birds			
	Leviticus 11:20	fowls	flying insects	insects	insects	insects			
	Leviticus 11:46	fowl	birds	bird	bird	birds			
	Leviticus 17:13	fowl	bird	bird	bird	bird			
	Leviticus 20:25a	fowls	birds	bird	bird	birds			
	Leviticus 20:25b	fowl	bird	bird	bird	bird			
	Deuteronomy 14:19	creeping thing that flieth	creeping thing that flies	teeming life with wings	winged insects	flying insects			
	Deuteronomy 14:20	fowls	birds	bird	winged things	winged creature			
	Deuteronomy 28:26	fowls	birds	birds	birds	birds			
	I Samuel 17:44, 46	fowls	birds	birds	birds	birds			
	I Kings 4:33; 14:11; 16:4; 21:24	fowls	birds	birds	birds	birds			
	Job 12:7; 28:21; 35:11; Psalm 50:11	fowls	birds	bird	birds	bird			

Original Biblical Word	Scriptural References	KJV	NKJV	NASB	RSV	NIV	Strong's	NIDOTTE
'ôp (Hebrew)	Psalms 78:27 79:2; 104:12 Jeremiah 7:33; 9:10; 15:3; 16:4; 19:7; 34:20 Ezekiel 29:5; 31:6, 13; 32:4; 38:20; 44:31 Hosea 2:18; 4:3; 7:12 Zephaniah 1:3	fowls fowls fowls fowl(s) fowls fowls	fowl birds birds birds birds birds	fowl birds birds birds birds birds	birds birds birds bird birds birds	birds birds birds birds birds birds	5775	6416
šippôr (Hebrew)	Genesis 7:14b  Deuteronomy 4:17 Nehemiah 5:18 Psalm 8:8  Psalm 148:10 Ezekiel 17:23  Ezekiel 39:17	bird  winged fowl fowls fowl  flying fowl fowl feathered fowl	bird  winged bird fowl birds  flying fowl birds  every	birds  winged bird birds birds  winged fowl birds  bird	bird winged bird fowls birds flying birds birds  birds	everything with wings  bird poultry birds  flying birds birds  bird	6833	7606
'ayiṭ (Hebrew)	Genesis 15:11 Job 28:7  Isaiah 18:6 (x2)	fowls fowl  fowls	vultures bird  birds of prey	birds of prey bird  birds of prey	birds of prey bird birds of prey	birds of prey bird birds of prey	5861	6514
śēlāw (Hebrew)	Exodus 16:13 Numbers 11:31, 32 Psalm 105: 40	quails quails quails	quails quail quail	quails quail quail	quails quails quails	quail quail quail	7958	8513
tinšemet (Hebrew)	Leviticus 11:18  Deuteronomy 14:16	swan  swan	white owl  white owl	white owl  white owl	water hen water hen	white owl  white owl	8580	9491, 9492
qōrē' (Hebrew)	I Samuel 26:20 Jeremiah 17:11	partridge partridge	partridge partridge	partridge partridge	partridge partridge	partridge partridge	7124	7926

<b>Original Biblical Word</b>	<b>Scriptural References</b>	<b>KJV</b>	<b>NKJV</b>	<b>NASB</b>	<b>RSV</b>	<b>NIV</b>	<b>Strong's</b>	<b>NIDOTTE</b>
tukkiyyîm (Hebrew)	I Kings 10:22 II Chronicles 9:21	peacocks peacocks	monkeys monkeys	peacocks peacocks	peacocks peacocks	baboons baboons	8500	9415
'ls (Hebrew)	Job 39:13	peacocks	wave proudly	flap joyously	wave proudly	flap joyfully	5965	6632
barbur (Hebrew)	I Kings 4:23	fowl	fowl	fowl	fowl	fowl	1257	1350
motnayim + zarzîr (Hebrew)	Proverbs 30:31	greyhound	greyhound	strutting rooster	strutting cock	strutting rooster	4975 + 2223	5516 + 2435
tsephar (Aramaic)	Daniel 4:12, 14, 21	fowls	birds	birds	birds	birds	6853	10616
'owph (Aramaic)	Daniel 2:38; 7:6	fowl(s)	bird(s)	bird(s)	bird(s)	bird(s)	5776	10533
peteinon (Greek)	Matthew 6:26; 13:4 Mark 4:4, 32 Luke 8:5; 12:24; 13:19 Acts 10:12; 11:6	fowls fowls fowls fowls	birds birds birds birds	birds birds birds birds	birds birds birds birds	birds birds birds birds	4071	4509
alektor (Greek)	Matthew 26:34, 74, 75 Mark 14:30, 72 (x2) Mark 14:68 Luke 22:34, 60, 61 John 13:38; 18:27	cock cock rooster cock cock	rooster rooster rooster rooster rooster	rooster rooster rooster rooster rooster	cock cock -- cock cock	rooster rooster -- rooster rooster	220	774
ornis (Greek)	Matthew 23:37 Luke 13:34	hen hen	hen hen	hen hen	hen hen	hen hen	3733	4119, 4120, 4121
nossion (Greek)	Matthew 23:37	chickens	chicks	chicks	brood	chicks	3556	3919
nossia (Greek)	Luke 13:34	brood	brood	brood	brood	chicks	3555	3918
orneon (Greek)	Revelation 19:17, 21	fowls	birds	birds	birds	birds	3732	4118

certainly cannot be taken as strictly a galliform bird, nor can specific conclusions about the galliform bird baramin be deduced.

Strong (2006) describes the second word from Table 1, *šippôr* (number 6833), as a little hopping bird such as a sparrow or another bird or fowl. The word is mentioned seven times throughout the Old Testament, and one of these times *šippôr* appears in the same verse as *‘ôp* (Genesis 7:14). According to *NIDOTTE* (Kiuchi, 1997e), this word (number 7606) is used as a subject or symbol of a biblical covenant or ritual and is often referred to metaphorically. The word occurs extensively in the fourteenth chapter of Leviticus, where purification is discussed (Kiuchi, 1997e). However, the use of *šippôr* does not point to a category containing galliform birds. *Tsephar* is the Aramaic word that corresponds to the Hebrew word *šippôr*, and simply refers to a bird (Strong, 2006).

*‘Ayit* (Strong’s number 5861) is translated “birds of prey” in most cases, but it is rendered as “vulture” in the New King James Version of the Bible and simply as “fowl” in the King James Version. Strong (2006) suggests either a hawk or another bird of prey. *NIDOTTE* (Kiuchi, 1997a) gives an interesting perspective on the term (number 6514), noting that the nominative is used eight times, mainly as a reference to an enemy or adversary. Galliform birds are typically game species, and *‘ayit* does not likely refer to a bird of this sort. *Barbur* (Strong’s 1257; *NIDOTTE* 1350) is found only in I Kings 4:23. Although there is no firm agreement on what the Hebrew word *barbur* refers to, both *Strong’s Concordance* (2006) and *NIDOTTE* (O’Connell, 1997) note that it is probably a domesticated, or grain-fattened, fowl. There is a possibility of this being a type of galliform bird such as a hen or chicken, but it could also refer to a goose, swan, capon,

cuckoo or another similar bird (O'Connell, 1997). These words did not yield any useful biosystematic information.

The Hebrew word *s<sup>e</sup>lāw* (Strong's 7958; *NIDOTTE* 8513) is undoubtedly translated "quail" in all five English translations. This is consistent with both Strong (2006) and *NIDOTTE* (Kiuchi, 1997d) translations. Within the Old Testament, Numbers 11:31-32, Exodus 16:13, and Psalm 105:40 all mention the quail. Quail are traditionally classified within the Order Galliformes, and their mere mention during the Old Testament era indicates their existence at this period of time, i.e., during the Exodus circa the 15<sup>th</sup> or 13<sup>th</sup> century B.C. (Bright, 1981). As in the case of any of the words being investigated, additional Scriptures describing the quail's behavior, characteristics, surroundings, and even habits would be of much value to this study. These subjects could lead to possible distinguishing features or physical qualities that are only observed in similar birds of the same baramin. However, there are no detailed passages like this describing the behavior or morphology of the quail. Nevertheless, these few passages of interest are discussed here.

Numbers 11:31-32 is a passage describing God's provision of meat for Israel when He sent a wind bringing scores of quail across the sea and onto land where the Israelites were camping. The phenomenon described here by the Bible is precisely what happens during modern-day quail migrations. Quail (*Coturnix coturnix*) make their journey to the Sinai Peninsula (where the Israelites were camping in Numbers 11:31-32), but by the time they reach their destination, they wearily settle on the ground—exhausted (Stratton-Porter, 1915; Klemm, 1993). Even though they use the wind to help carry them across, after heavy feeding they become very large and fat, which may explain why their

name means, literally, “to be fat” (Stratton-Porter, 1915). Also, taking into consideration the method by which the quail arrived at the Israelites’ camp (by the wind sent of the Lord), it could be assumed that quail were migratory birds at that time, just as they are today. What is virtually certain, however, is that the birds which the Israelites were finding and eating were quail, and can be classified as galliform birds. Although interesting and important, this information does not add any biosystematic value.

Apart from the above-mentioned, another Hebrew word is mentioned that without question pertains to the galliform birds: *qōrē’*, which is translated “partridge” in all cases. *Qōrē’* is found in I Samuel 26:20 (which mentions the hunting of a partridge in the mountains) and in Jeremiah 17:11. *NIDOTTE* gives two views of the translation from Jeremiah 17:11, one of which suggests deceptiveness, and the other the vulnerability, of the partridge (Kiuchi, 1997c). The lack of certainty in translating this verse limits the details of the partridge’s habits, despite the clear meaning of *qōrē’*.

The remainder of the key words found within one or more of the five Bible versions are problematic because of unclear translations. For example, the Hebrew word *tukkiyyîm* (*NIDOTTE* number 9415) is translated “peacock” in the King James Version (I Kings 10:22 and II Chronicles 9:21), and this could be a relevant word since peacocks are galliform birds. However, a look at some other translations of the same two passages shows that the same Hebrew word is translated as “baboon” (NIV; see also Kiuchi, 1997f) or “monkey” (NKJV). Likewise, *tinšemet*, *motnayim* (used with *zarzîr*), and *’ls* have more than one possible meaning. *Tinšemet* is translated “swan” in the King James Version, but “water hen” in the Revised Standard Version and “white owl” (as suggested in *NIDOTTE*, number 9492; see also Kiuchi 1997e) in the remaining three versions.

*Motnayim* (Strong, 1990: “to be slender”) along with *zarzâr* (Strong, 1990: “tightly girt”) are together translated variously as “greyhound,” “strutting rooster,” or “strutting cock.” *NIDOTTE* lists *zarzâr* (number 2435) as “rooster,” and it is mentioned with *motnayim* (Hamilton, 1997: “loins, hips, and small of the back”) in Proverbs 30:31 to refer to a stately and majestic animal (see also Kiuchi, 1997b). Lastly, *’ls* (Strong’s 5965; *NIDOTTE* 6632) can be rendered “peacock” (KJV), but four of the five translations used “wave proudly,” “flap joyously,” or “flap joyfully” instead. Both translations coincide with Strong (2006). *NIDOTTE* translates the term as “enjoy,” or “appear glad” (Grisanti, 1997). The uncertainty of translation among potentially important words like these disqualifies their usefulness for baraminological study. The opposite case is also seen with words that secure a clear translation, but are meaningless to the study because they do not relate strongly to the galliform baramin.

This completes the checklist of Old Testament biblical terms relevant to the galliforms. Although the above research does not give sufficient information to include or exclude any species from the galliform bird baramin, it is an extremely important and necessary consideration, and many times important taxonomical information is derived from the biblical text.

#### *Baraminic Distance*

The baraminic distance correlation graph for the complete dataset reveals two separate square groupings that suggest two holobaramins (Figure 1). The first consists of the families Numididae, Meleagrididae, Tetraonidae, Odontophoridae, and Phasianidae; the second contains Anseriformes (the outgroup), Megapodiidae, and Cracidae. Due to results from Classical Multidimensional Scaling which show more than two distinct

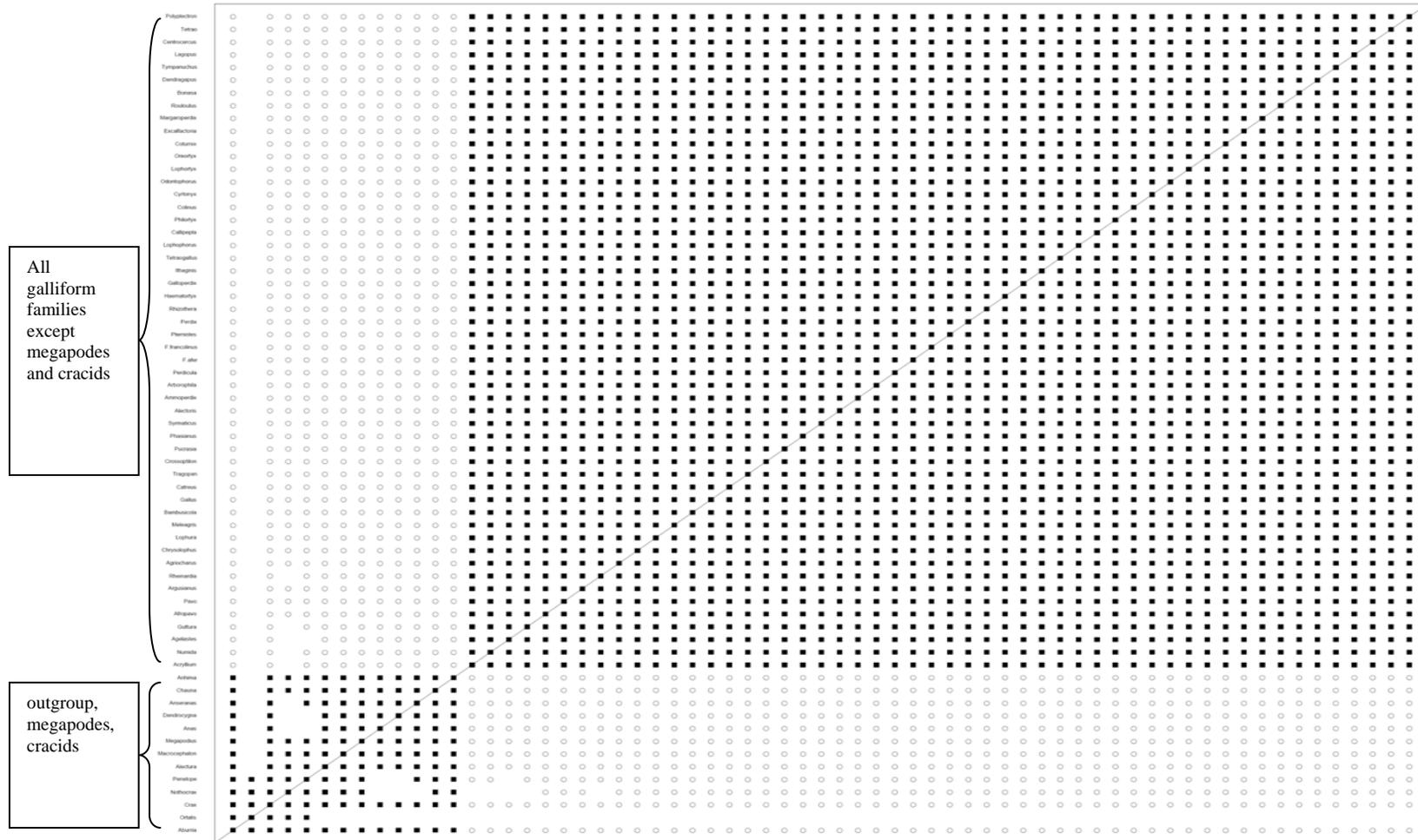


Figure 1. Baraminic distance correlation for the complete (entire) Dyke *et al.* (2003) data set, with a relevance cutoff value of 0.95. Taxa with significant positive correlation are indicated with dark squares, whereas taxa with significant negative correlation are indicated with open circles (where  $p < 0.05$  is significant). 98 of the original 102 characters were used to calculate baraminic distances for the complete dataset.

clusters, both the large and small square groupings from the correlation graph were analyzed separately (see Wood, 2005a). This is a justified procedure since the layout of the data in the matrices (i.e. in two dimensions only) often hides the true representation of the multivariate results (Robinson and Cavanaugh, 1998; Wood, 2005a). Performing the separate analysis for the larger dataset revealed that a considerable amount of continuity within the guineafowl (Numididae) and a considerable amount of discontinuity between the guineafowl (Numididae) and the remaining galliforms (Figure 2). When the smaller of the two groups was analyzed, continuity was seen within the cracids and megapodes, in addition to a clear separation of Anseriformes with respect to the cracids (family Cracidae) (Figure 3). To verify discontinuity between the groups, further analyses on subsets within both the large and small groups were carried out. These analyses included a baraminic distance correlation analysis of the megapodes and cracids only (Figure 4), the megapodes and the outgroup only (Figure 5), the cracids and the outgroup only (Figure 6), and every other genus of the initial large group with Numididae (Figure 7). In the last analysis, every other genus of the initial large group was included instead of every genus in order to reduce the number of phasianoid genera which were potentially overwhelming the analysis when analyzed with Numididae.

Baraminic distance showed a good amount of significant negative correlation (discontinuity) between the megapodes and cracids (Figure 4). Both megapodes, and to an even more drastic extent, the cracids, showed significant discontinuity with the outgroup. Specifically, two out of the three megapode genera show significant negative correlation with respect to the outgroup (Figure 5), and there is complete significant negative correlation between all cracid genera and the outgroup (Figure 6). Finally,

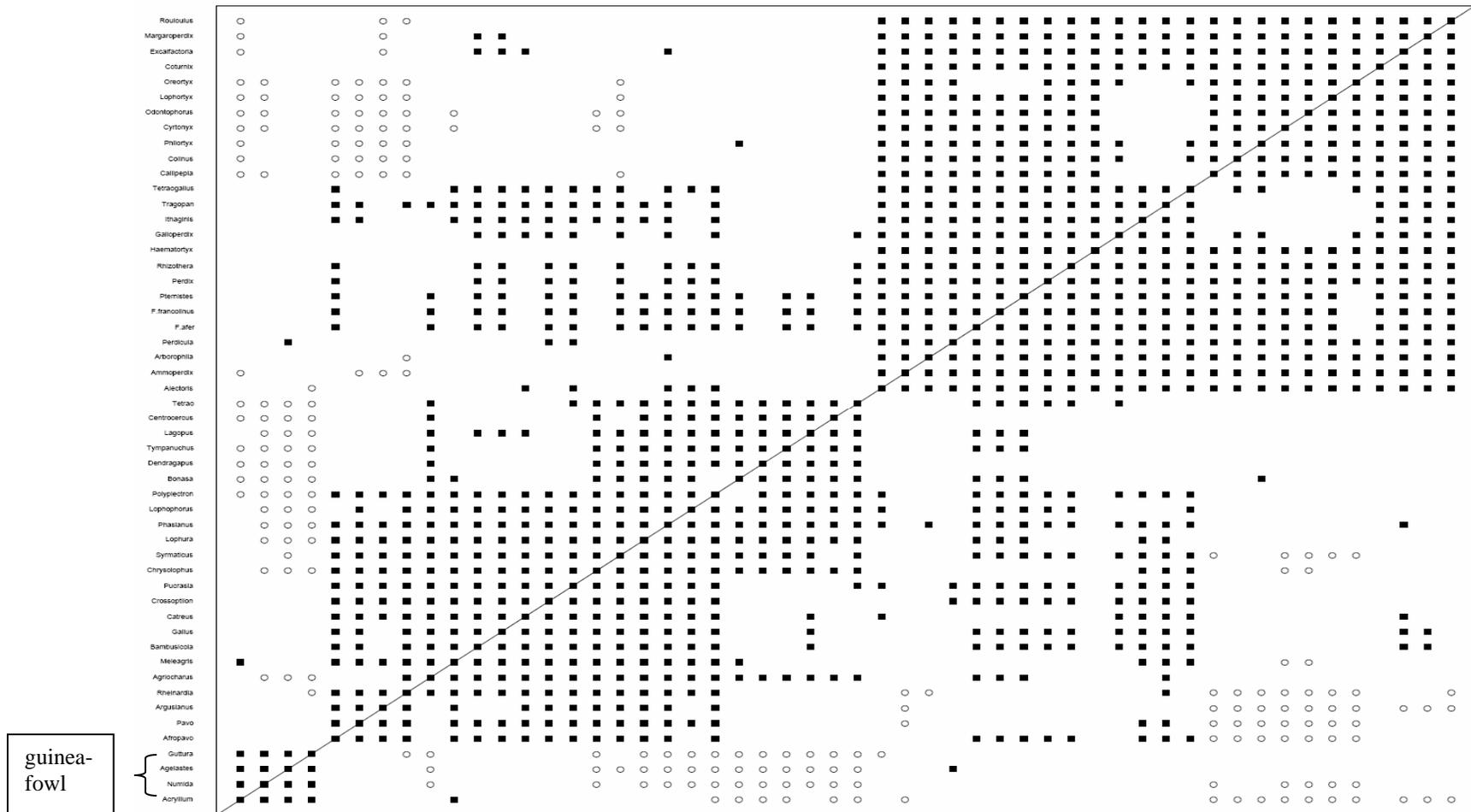


Figure 2 (Partial Large). Baraminic distance correlation for members of the large square group of the Dyke *et al.* (2003) data set of Figure 1, with a relevance cutoff value of 0.95. Taxa with significant positive correlation are indicated with dark squares whereas taxa with significant negative correlation are indicated with open circles (where  $p < 0.05$  is significant). 100 (out of the original 102) characters were used to calculate baraminic distances for the partial large data set.

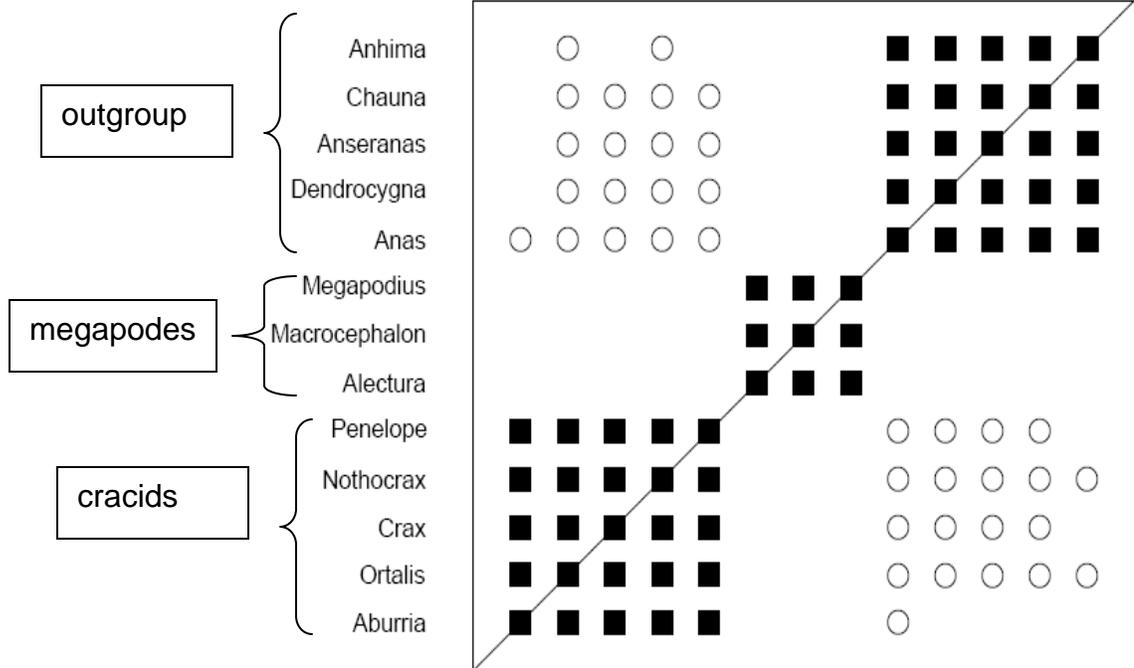


Figure 3 (Partial Small). Baraminic distance correlation for the Dyke *et al.* (2003) data set, with a relevance cutoff value of 0.95. Correlations are calculated for the Megapodiidae and Cracidae families in addition to the outgroup (Anseriformes Order). Taxa with significant positive correlation are indicated with dark squares whereas taxa with significant negative correlation are indicated with open circles (where  $p < 0.05$  is significant). 99 (out of 102) characters were used to calculate baraminic distances.

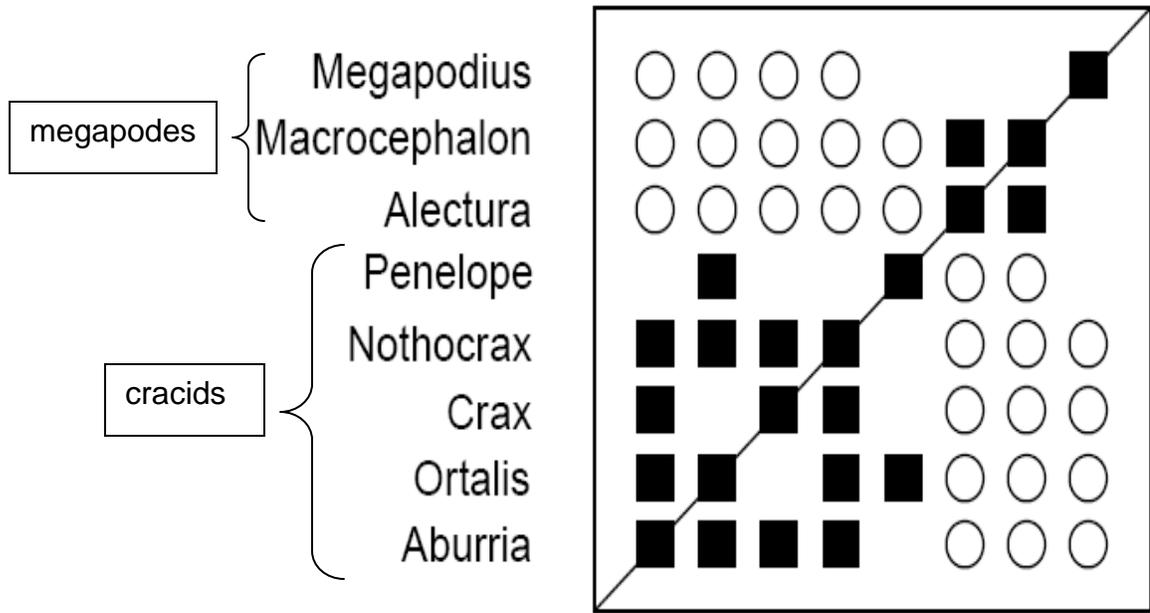


Figure 4. Baraminic distance correlation for a subset of the Partial Small dataset. Correlations are calculated for megapodes and cracids only.

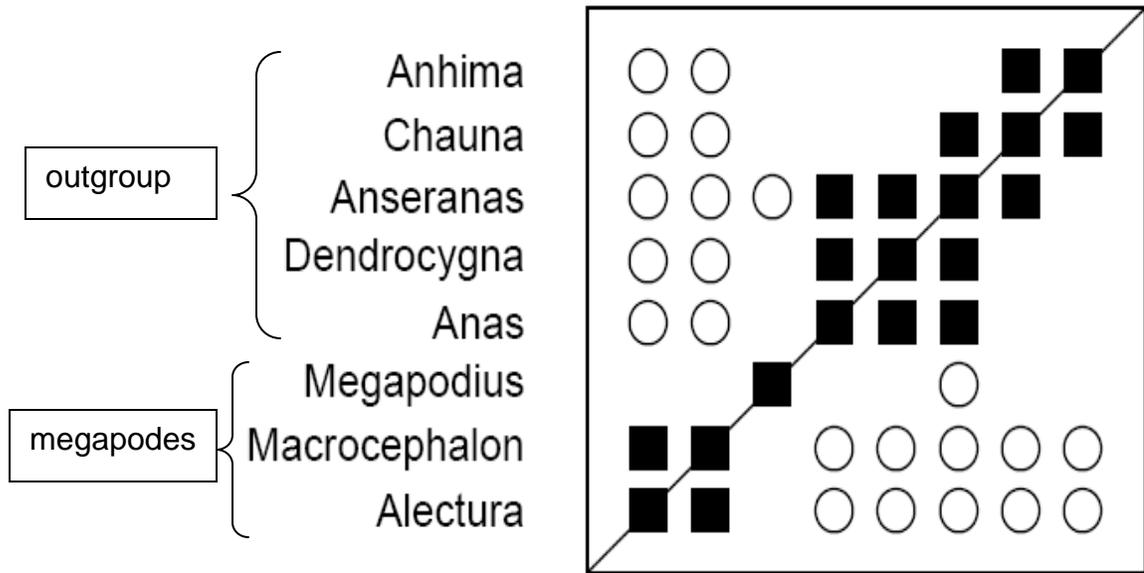


Figure 5. Baraminic distance correlation for a subset of the Partial Small dataset. Correlations are calculated for megapodes and the outgroup only.

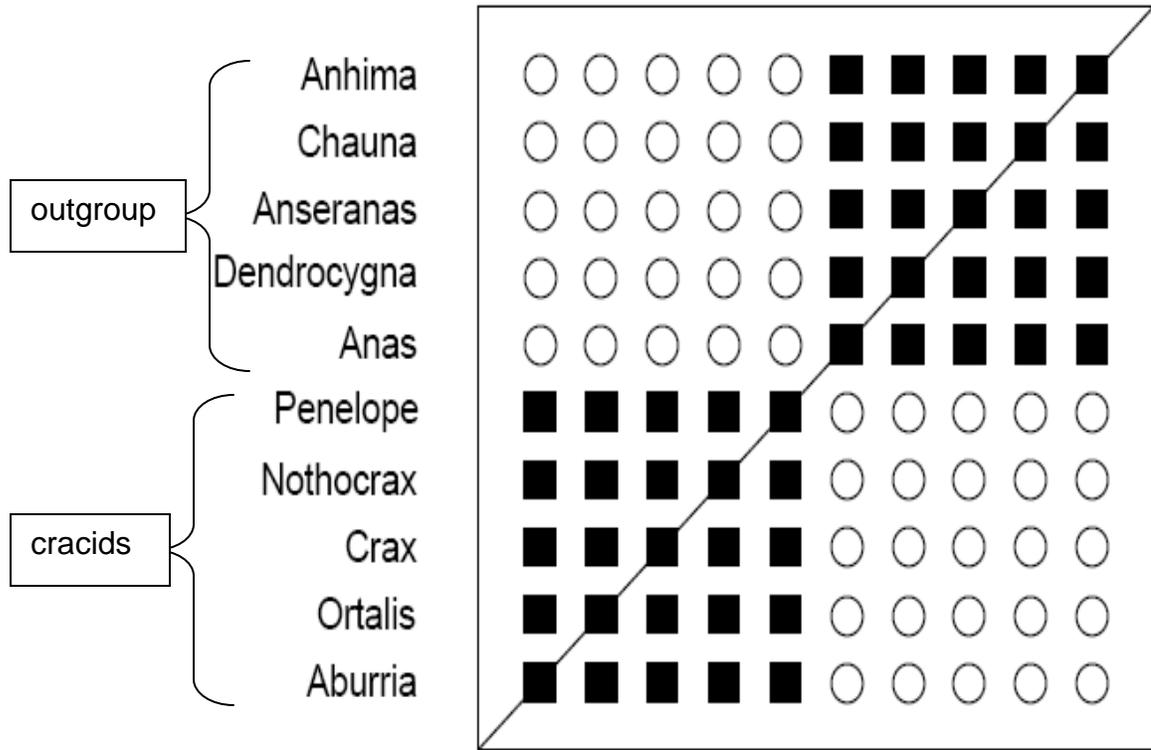


Figure 6. Baraminic distance correlation for a subset of the Partial Small dataset. Correlations are calculated for cracids and the outgroup only.



significant negative correlation between the phasianoids (every other genus) and the guineafowl (Numididae) was found (Figure 7).

#### *Classical Multidimensional Scaling*

The kinemage output generated from MDS of the complete dataset gives a representation of the scaled baraminic distances in three-dimensional space (Figure 8). It shows 4, possibly 5, separate clusters of genera that are separated by a considerable distance. One distinct cluster consists of the five genera of the Anseriformes outgroup. A second cluster contains the three genera representing the Megapodiidae, and a third consists of those genera representing the family Cracidae. The fourth cluster has all four members representing the Numididae. Compared to the other three clusters, this fourth cluster lies close to the remaining group of genera, which is rest of the superfamily Phasianoidea (includes families Numididae, Phasianidae, Odontophoridae, Meleagrididae, and Tetraonidae).

The stress graph (Figure 9) gives the stress of k-dimensional MDS plotted as a function of the number of dimensions (Wood, 2005a) and includes the stress at all dimensions k that are less than or equal to 31. For the uncorrected matrix, the minimum stress is 0.063 at 12 dimensions, and the three-dimensional stress was over four times that: 0.279. Stress values for the corrected distance matrix were much higher. Because of the lower stress values, the uncorrected matrix was the one used in all analyses mentioned above.

To restate the conclusions, baraminic distance showed continuity within the guineafowl but discontinuity between the guineafowl and the remaining galliforms. The MDS cluster in Figure 8 representing the four guineafowl genera can be viewed as its

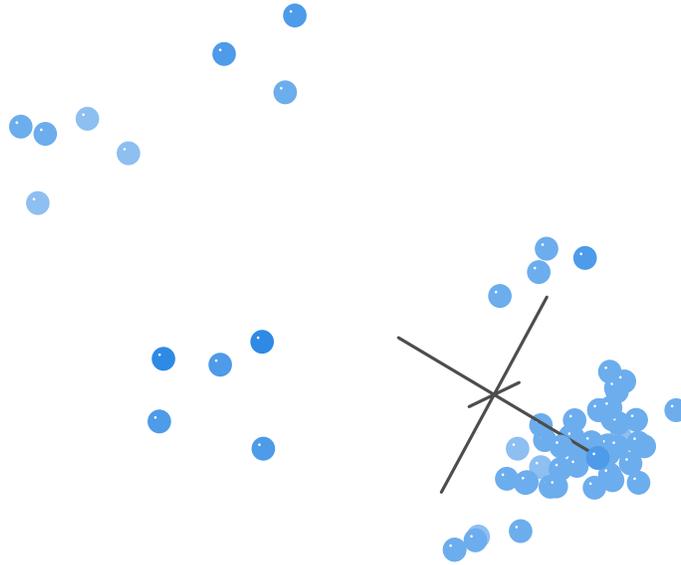


Figure 8. Three-dimensional classical MDS applied to uncorrected baraminic distances calculated from the complete dataset of Dyke *et al.* (2003).

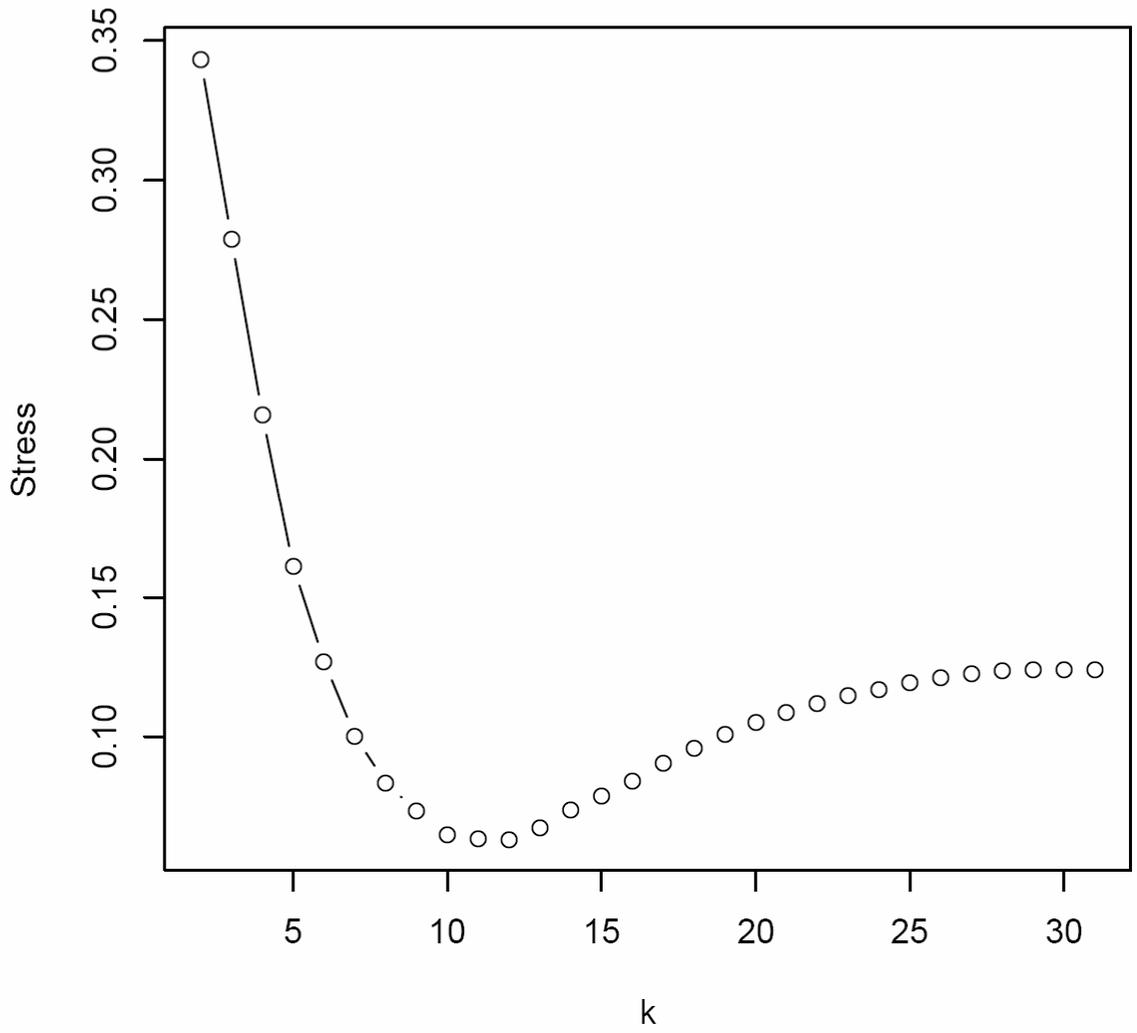


Figure 9. Stress graph of complete data set for dimensions, k, where  $k \leq 31$ .

own group. The outgroup is significantly continuous within, and significantly discontinuous with all galliform genera. The cracids and megapodes, when analyzed together showed significant negative correlation (discontinuity) and therefore can be viewed as separate groups, which is also seen in Figure 8. The rest of the galliforms are contained in the superfamily Phasianioidea, which show some discontinuity with respect to the Numididae. Based on these analyses, it may be hypothesized that four galliform holobaramins exist, besides the outgroup: Megapodiidae, Cracidae, Numididae, and the remaining members of the superfamily Phasianioidea (Figure 10).

### *Hybridization*

The two hybridograms created from McCarthy's (2006) data indicate that hybridization connects, either directly or indirectly, all but one of the families of galliform birds, the Megapodiidae. Since there are records of megapodes interbreeding with each, but no records of megapodes interbreeding with any other galliform genera, a separate hybridogram was created for the Megapodiidae.

Within the megapode family, no intergeneric hybrids are reported: there are only records for crosses within the same genus (Figure 11). Klemm (1993) reports similar results. Of all the crosses included in the Megapodiidae hybridogram, two reports are questionable. One is between *Megapodius affinis* and *Megapodius reinwardt*, and the other is between *Talegalla fuscirostris* and *Talegalla jobiensis* (Figure 11).

Among the other galliforms, hybridization connects sixty-six genera with good fidelity (Figure 12). Sixteen other intragenetic crosses are also recorded (Gray, 1958; McCarthy, 2006), but are questionable. Seventeen crosses connect one or more families, and nine additional interfamilial crosses are reported, but are speculative. A large portion

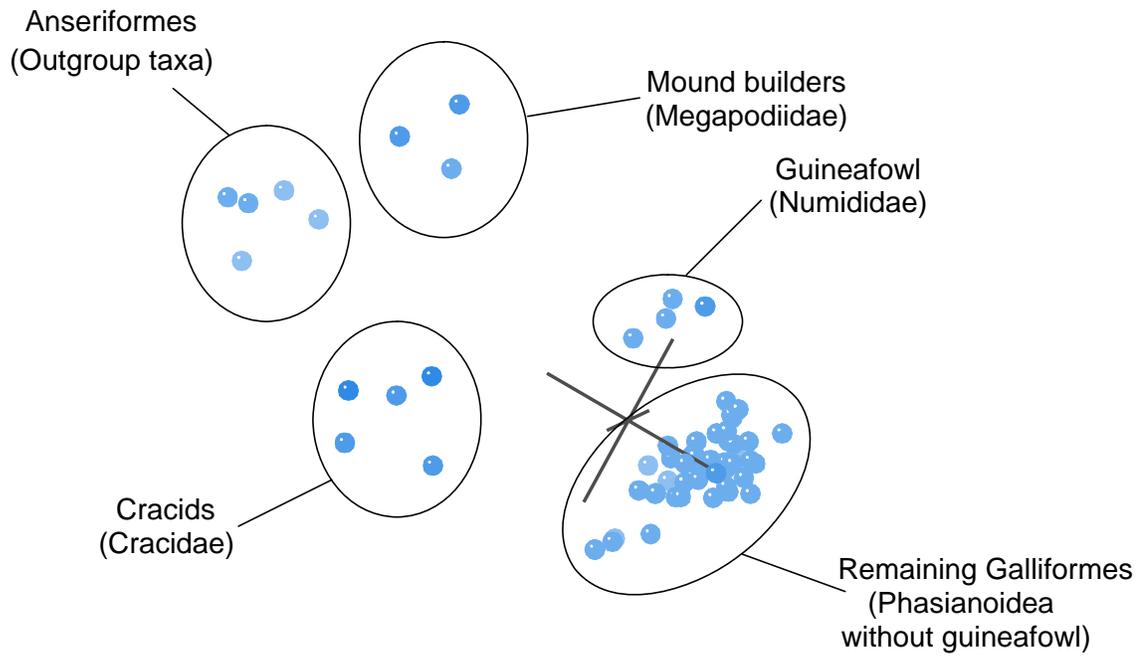


Figure 10. MDS indicating possible holobaramins as indicated by statistical analysis alone.

		1	2	3	4	5	6	7	8	9	10	11	12	13
<i>Alectura l. lathamii</i>	1	■	■											
<i>Alectura l. purpureicollis</i>	2	■	■											
<i>Megapodius affinis</i>	3			■	■	■					■			
<i>M. geelvinkianus</i>	4			■	■	■								
<i>M. reinwardt</i>	5			■		■				■	■			
<i>M. c. cumingii</i>	6						■	■						
<i>M. c. pusillus</i>	7						■	■						
<i>M. forstenii</i>	8								■	■				
<i>M. freycinet</i>	9					■			■	■				
<i>M. eremita</i>	10			■		■					■			
<i>Talegalla cuvieri</i>	11											■	■	
<i>T. fuscirostris</i>	12											■	■	■
<i>T. jobiensis</i>	13												■	■

Figure 11. Megapode species x species hybridogram. Black squares reveal successful crosses between species, gray squares indicate questionable reports. Open squares indicate no reported hybrids. Column numbers across the top correspond to each taxon numbered on the rows.

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33					
CRACIDAE	<i>Pipile</i>	1	█	█	█														█																				
	<i>Ortalis</i>	2	█	█	█														█																				
	<i>Penelope</i>	3	█	█	█	█			█										█																				
	<i>Mitu</i>	4	█	█	█	█													█																				
	<i>Crax</i>	5	█	█	█	█													█																				
NUMIDIDAE	<i>Acryllium</i>	6					█	█											█																				
	<i>Numida</i>	7		█			█	█											█									█		█									
TETRAONIDAE	<i>Dendragapus</i>	8						█	█	█	█	█																											
	<i>Centrocerus</i>	9						█	█	█	█	█																											
	<i>Tympanuchus</i>	10							█	█	█	█																											
	<i>Bonasa</i>	11							█	█	█	█																											
	<i>Tetrao</i>	12							█	█	█	█								█			█																
MELEAGRIDAE	<i>Lagopus</i>	13							█	█	█	█																											
	<i>Meleagris</i>	14							█																														
PHASIANIDAE	<i>Coturnix</i>	15																																					
	<i>Alectoris</i>	16																																					
	<i>Perdix</i>	17																																					
	<i>Gallus</i>	18	█	█	█	█								█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	█	
	<i>Pavo</i>	19																																					
	<i>Catreus</i>	20																																					
	<i>Lophura</i>	21																																					
	<i>Crossoptilon</i>	22																																					
	<i>Chrysolophus</i>	23																																					
	<i>Pucrasia</i>	24																																					
<i>Lophophorus</i>	25																																						
<i>Tragopan</i>	26																																						
<i>Symaticus</i>	27																																						
<i>Phasianus</i>	28																																						
<i>Ammoperdix</i>	29																																						
ODONTOPHORIDAE	<i>Callipepla</i>	30																																					
	<i>Oreortyx</i>	31																																					
	<i>Colinus</i>	32																																					
	<i>Philortyx</i>	33																																					

Figure 12. Inter-generic hybridogram of six putative galliform families (Megapodiidae are excluded from this hybridogram because of their lack of hybridization with other galliforms). Black squares reveal successful crosses between genera. Gray squares specify questionable crosses between genera. Open squares indicate no reported hybrids. Column numbers across the top correspond to each taxon numbered on the rows.

of intergeneric breeding that occurs is due to the enormous crossing potential of *Gallus* and *Phasianus*. These two genera alone are involved in 28 of the crosses (including questionable reports).

Considering solely hybridization records, it may be hypothesized that there are two galliform monobaramins. Data from the two hybridograms undoubtedly show that all galliform families, except the megapodes, are connected by hybridization, either directly or indirectly (directly if they hybridize with each other and indirectly if they both hybridize with the same third genus; Klemm, 1993).

### Conclusions

The Order Galliformes itself is considered separate from other birds (i.e. it is apobaraminic). First, they are morphologically distinct. Klemm (1993) notes that Heinroth and Heinroth (1966) delineated galliform birds by the unique development of their beginning feathers and also their wings. Second, Klemm (1993) notes that no hybridization reports between galliforms and other birds exist, except for a few questionable reports that are given by Gray (1958), which are inconclusive.

Baraminic distance correlation analysis and multidimensional scaling suggest that there are four galliform holobaramins: Megapodiidae, Cracidae, Numididae, and the remaining galliforms of the superfamily Phasianoidea. Hybridization, which traditionally has been used as a major criterion justifying an organism's inclusion within a certain baramin, joins three of these holobaramins: Cracidae, Numididae, and the remaining phasianoids. Based on evidence from both statistics and hybridization, the megapodes

make up a holobaramin separate from the rest of the galliform birds (Sibley and Ahlquist, 1990; McCarthy, 2006).

Hybridization among the cracids was examined carefully since the statistical data seems to allow for the separation of the cracids into a separate holobaramin. According to Klemm (1993), the Cracidae should at this point be regarded as a separate basic type, noting that many of the crosses between the cracids and the phasianoids (Gray, 1958) are questionable. Hybridization records from McCarthy (2006), however, do not allow for a separation of the Cracidae. McCarthy (2006) lists four unquestioned interfamilial crosses linking the cracids with the phasianoids, including a captive breeding between *Crax blumenbachii*, a red-billed curassow (Family Cracidae) and a female domestic fowl *Gallus gallus* (Family Phasianidae).

When combined, statistics and hybridization suggest two galliform holobaramins (Megapodiidae alone and Cracidae + Phasianoidea). Significant continuity exists within each of these groups (as suggested by statistics and hybridization) and significant discontinuity exists between them (as suggested by statistics). Figure 13, using the 3D-MDS results, gives a visual representation of these two holobaramins (also included is the outgroup holobaramin).

At first it may seem unconventional to join Cracidae with Phasianoidea to produce one holobaramin, since previous authors (Price, 1924 and 1938; Woodmorappe, 1996; Jones, 2002; Wood 2007) have suggested that a family-level grouping is an approximation of a baramin. However, many of the current families within the superfamily Phasianoidea were, until recently, subfamilies in a more broadly conceived Family Phasianidae. For example, both Johnsgard (1986) and Wolters (1975-1982) give

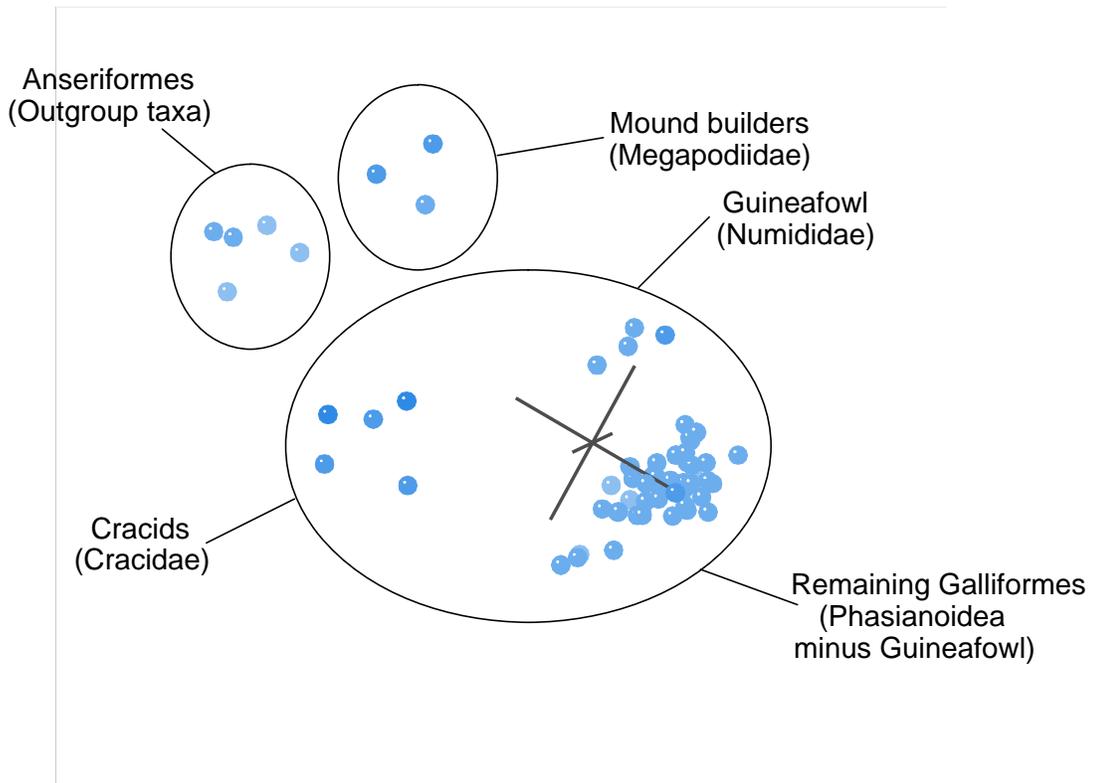


Figure 13. MDS indicating possible holobaramins as indicated by statistical analyses and hybridization data.

the following taxonomic arrangement:

Order Galliformes

Family Megapodiidae

Family Cracidae

Family Phasianidae

Subfamily Meleagridinae

Subfamily Tetraoninae

Subfamily Odontophorinae

Subfamily Numidinae

Subfamily Phasianinae

It is not surprising then, even from a creationist perspective, that many of the families in the currently recognized Superfamily Phasianoidea (del Hoyo *et al.*, 1994; Dyke *et al.*, 2003) are members of the same holobaramin.

The most surprising result of this study is the inclusion of the cracids in the phasianoid holobaramin. The cracids are thought to form a basal, monophyletic clade that is sister to the more derived phasianoids (Dyke *et al.*, 2003). In my analyses, the cracids form a distinct cluster in the 3D-MDS and group with the megapode and waterfowl taxa in the initial baraminic correlation analysis. Hybridization data, however, links the cracids with the phasianoids. This study emphasizes the continued value of hybridization data in baraminological research, illustrates the importance of using multiple lines of evidence when delimiting holobaramins, and is suggestive of the potential uses and limitations of statistical baraminology.

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## Appendix

The following appendix lists the genera used in the dataset of Dyke *et al.* (2003).

Taxonomy follows del Hoyo *et al.* (1994).

## Order Anseriformes (outgroup)

Family Anhimidae: *Chauna*, *Anhima*

Family Anseranatidae: *Anseranas*

Family Anatidae: *Dendrocygna*, *Anas*

## Order Galliformes

Family Megapodiidae: *Macrocephalon*, *Megapodius*, *Alectura*

Family Cracidae: *Aburria*, *Nothocrax*, *Crax*, *Penelope*, *Ortalis*

Family Numididae: *Acryllium*, *Numida*, *Guttera*, *Agelastes*

Family Odontophoridae: *Odontophorus*, *Cyrtonyx*, *Colinus*, *Lophortyx*, *Philortyx*,  
*Oreortyx*, *Callipepla*

Family Meleagrididae: *Agriocharus*, *Meleagris*

Family Tetraonidae: *Dendrogapus*, *Lagopus*, *Tetrao*, *Bonasa*, *Centrocercus*,  
*Tympanuchus*

Family Phasianidae: *Pternistis*, *Francolinus* (*F. francolinus*; *F. afer*), *Perdix*,  
*Galloperdix*, *Haematortyx*, *Perdicula*, *Crossoptilon*, *Catreus*, *Alectoris*,  
*Magaroperdix*, *Pavo*, *Gallus*, *Afropavo*, *Rollulus*, *Bambusicola*, *Ithaginis*,  
*Phasianus*, *Polyplectron*, *Lophophorus*, *Tetraogallus*, *Syrmaticus*,  
*Lophura*, *Excalfactoria*, *Pucrasia*, *Tragopan*, *Argusianus*, *Rheinardia*,  
*Chrysolophus*, *Ammoperdix*, *Arborophila*, *Coturnix*, *Rhizothera*