

Determining the Ark Kinds

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Abstract

As part of the Ark Encounter Project at Answers in Genesis, a research effort has been initiated to provide information necessary for the best possible reconstruction of the animal kinds preserved on the Ark. This initial paper outlines the basic rationale that will be used and the underlying justification for it. The biblical text provides strong evidence for each kind being a reproductive unit. Based on this and biological evidence that reproduction requires significant compatibility, hybridization will be considered the most valuable evidence for inclusion within an “Ark kind.” The cognitum and statistical baraminology are discussed as they are relevant to this venture. Where hybrid data is lacking, we have chosen to use a cognitum method. Using current taxonomic placement as a guide, pictures and/or personal experience with the animals will be used to find obvious groupings. If the grouping seems excessively high taxonomically, the family level may be used as the default level to avoid underestimating the number of kinds on the Ark. Results from statistical baraminology studies and other information will be used where appropriate. It is hoped the result will be a valuable resource for future studies in baraminology.

Keywords: Ark, Flood, created kinds, baraminology, cognitum

Introduction

Long before the Ark Encounter project was announced by Answers in Genesis, it was realized that a considerable amount of research would be necessary to allow for a high quality exhibit. How many kinds were there on the Ark? What might they have looked like? How can we even begin to answer these questions? This paper is the first in a series that will attempt to address these questions.

At a time when the world was filled with violence, God chose to destroy all land-dwelling, air-breathing life on it by a global Flood (Genesis 7:21–23). Noah, a righteous man, was instructed to build an Ark that would protect him, his family, and pairs of animals and birds from this coming destruction (Genesis 6: 9–22). God told Noah:

Of the birds after their kind, of animals after their kind, and of every creeping thing of the earth after its kind, two of every *kind*¹ will come to you to keep *them* alive. (Genesis 6:20)

This designation of flying and terrestrial creatures preserved on the Ark “after their kind” is repeated in Genesis 7:14 and is reminiscent of how these creatures were created (Genesis 1:21, 24–25).² Since the Bible does not mention specifically how many kinds there were, nor give us specific physical descriptions of them, any attempt to discern what they were will necessarily include a significant amount of conjecture.

Nevertheless, there is information that can be used to make educated guesses about these animals preserved on the Ark. While it is important to recognize that these are informed guesses, and therefore not to be accepted with the level of certainty of Scripture, they can help us gain a general appreciation for what things may have been like on the Ark.

Biblical Evidence

A comprehensive understanding of biology should necessarily include the origin of life. While the secular world ignores the Bible and speculates naturalistic origins for life, a Christian should recognize that reliable eyewitnesses are invaluable for establishing historical facts (Numbers 35:30, Deuteronomy 17:6; 19:15, Isaiah 8:2; 43:9–12; 44:6–8, Jeremiah 6: 16–18, 32:12, Matthew 18:16, Acts 2:32, 2 Corinthians 13:1, 1 Timothy 5:19). Clearly, in the first few chapters of Genesis, we have a historical account of the creation of the world and life on it from the most reliable eyewitness, God himself. So this is where we will begin.

During Creation Week God created plants (Day 3), sea creatures and flying creatures (Day 5), and land animals (Day 6) each “according to its kind” (Genesis 1:11–13, 20–25). This phrase is used of all animal life except humans, who were created in the image of God (Genesis 1:26, 27). So it is important to understand what is being conveyed.

¹ Italicized words are not in the Hebrew, but are necessary for the sentence to make sense in English.

² “after its kind” and “according to its kind” are two different ways to translate the same underlying Hebrew phrase, which appears in Genesis 1, 6, and 7.

The underlying Hebrew word for *kind* here is מין, *mîn*. It, along with the Hebrew word for *create* (ברא, *bārā*), was used to coin the word *baramin*, a creationist term for created kind. While the word *baramin* has strong taxonomic connotations to most creationists, Hebrew scholars have warned against assuming that מין is a technical term (Turner 2009; Williams 1997). Both Williams (1997) and Turner (2009) suggest that מין can be understood to refer to subdivisions within a larger group much like the meaning of the English word *kind*. So caution needs to be exercised in this area.

Plants are described as being created according to their kinds with seed (זרע, *zera*), implying they were to reproduce (Genesis 1:11–12). Aquatic and flying creatures, after being created according to their kinds, were blessed and told to reproduce to fill the earth (Genesis 1:22). A similar blessing was pronounced on humans (Genesis 1:28) along with a command for them to rule the earth. Since life was created “according to their kinds” and told to reproduce, it is often assumed that life reproduces according to its kind. While Scripture does not emphatically state that life reproduces only after its own kind, there is a very strong inference given both the biblical text and observations made in the world today.

The account of the Flood seems to reinforce this understanding. God told Noah:

And of every living thing of all flesh you shall bring two of every *sort* into the ark, to keep *them* alive with you; they shall be male and female. Of the birds after their kind, of animals after their kind, and of every creeping thing of the earth after its kind, two of every *kind* will come to you to keep *them* alive. (Genesis 6:19–20).

Notice verse 19 mentions two of all living things, a male and a female, are to come on the Ark. The obvious purpose is for reproduction (cf. Genesis 7:2, 3, and 9). This is adjacent to a verse mentioning the preservation of animals according to their kinds, again specifying two of each. A very similar situation is found in the next chapter.

they [Noah and family] and every beast after its kind, all cattle after their kind, every creeping thing that creeps on the earth after its kind, and every bird after its kind, every bird of every sort. And they went into the ark to Noah, two by two, of all flesh in which is the breath of life. So those that entered, male and female of all flesh, went in as God had commanded him; and the LORD shut him in. (Genesis 7:14–16)

These pairs of animals were brought on the Ark for the purpose of preserving their seed (Genesis 7:3; זרע, *zera*). Word-for-word translations render זרע as offspring (for example New American Standard Bible,

English Standard Version, New English Translation), clarifying things since the modern English word “seed” has a narrower semantic range than the Hebrew word. The New International Version, which is more of a dynamic equivalence translation, renders the encompassing phrase: “to keep their various kinds alive throughout the earth.” Thus, where מין is used in the Creation or Flood accounts, it seems to be referring to distinct groups of animals and strongly implying that reproduction occurs within these groups (Table 1).

Methods for Ascertaining Baramins (Created Kinds) Hybridization

Based on the concept that living things reproduce according to their kinds, hybrids between different species of animals has long been considered conclusive evidence that both species belong to the same created kind (*baramin*). For example, crosses between dogs and wolves, wolves and coyotes, and coyotes and jackals are interpreted to mean that all these species of animals belong to a single *baramin*.

Reproduction is a complex process and sometimes barriers arise that make it more difficult. This can be seen in attempts to form hybrids between different species. When cattle are crossed with bison, live hybrids are formed. However, the males are sterile. The females can generally reproduce and can be crossed with either parent species. For this reason, cattle and bison are considered to belong to the same *baramin*, but are not the same species because they cannot consistently produce fertile offspring. Crosses between horses and donkeys produce a mule, which is rarely fertile in either sex.

More serious barriers to reproduction can be apparent within a *baramin*. Sheep and goats were identified as belonging to the same *baramin* because several live hybrids have been produced between them. However, a live hybrid is not the most common result when these species mate with each other. In one study, when rams were mated with does (female goats) fertilization was fairly common, although not as high as matings within the respective species. The hybrid embryos died within 5 to 10 weeks. When the cross was made the other direction, bucks (male goats) mated with ewes, fertilization did not occur (Kelk et al. 1997).

So how much development is necessary for hybridization to be considered successful? Is fertilization enough? The answer to the latter question is clearly no, as human sperm can fertilize hamster eggs in the laboratory.³ Even the first few divisions are under maternal control. For this reason Scherer (1993) stated that embryogenesis must continue until

³ It should be noted that just because we report on the results of certain laboratory findings does not necessarily imply we believe a specific procedure is ethical.

Table 1. Passages discussing reproduction in kinds at Creation and the Flood.

Subject	Passage	Reproduction Mentioned— Genesis 1?	Reproduction Mentioned— Genesis 6–9?
Vegetation	Genesis 1:12 And the earth brought forth grass, the herb that yields seed according to its kind, and the tree that yields fruit, whose seed is in itself according to its kind. And God saw that it was good.	Yes, seeds	
Sea creatures	Genesis 1:21–22 So God created great sea creatures and every living thing that moves, with which the waters abounded, according to their kind, and every winged bird according to its kind. And God saw that it was good. And God blessed them, saying, “Be fruitful and multiply, and fill the waters in the seas, and let birds multiply on the earth.”	Yes: be fruitful and multiply	
Flying creatures	Genesis 1:21–22 So God created great sea creatures and every living thing that moves, with which the waters abounded, according to their kind, and every winged bird according to its kind. And God saw that it was good. And God blessed them, saying, “Be fruitful and multiply, and fill the waters in the seas, and let birds multiply on the earth.” Genesis 8:17 Bring out with you every living thing of all flesh that is with you: birds and cattle and every creeping thing that creeps on the earth, so that they may abound on the earth, and be fruitful and multiply on the earth.	Yes: be fruitful and multiply	Yes: be fruitful and multiply
Land animals (on Ark)	Genesis 6:19–20 And of every living thing of all flesh you shall bring two of every sort into the ark, to keep them alive with you; they shall be male and female. Of the birds after their kind, of animals after their kind, and of every creeping thing of the earth after its kind, two of every kind will come to you to keep them alive. Genesis 8:17 Bring out with you every living thing of all flesh that is with you: birds and cattle and every creeping thing that creeps on the earth, so that they may abound on the earth, and be fruitful and multiply on the earth.		Yes: a kind is represented on the Ark by a male and its mate; be fruitful and multiply

there is coordinated expression of both maternal and paternal morphogenetic genes. Lightner (2007) suggested that the advanced blastocyst stage may be sufficient. This was partially based on a study by Patil and Totey (2003) which showed failure of embryos around the 8 cell stage was associated with a lack of mRNA transcripts. Thus it seemed significant coordinated expression was necessary to advance past this stage, through the morula stage, to a late blastocyst.

This brings us to some limitations of hybridization in determining kinds. While well documented hybrids can confirm that two species belong to the same baramin, lack of hybridization data is inconclusive.

There are several reasons why hybrid data may

be lacking between individuals within the same baramin. First, it is relatively difficult to gather good hybrid data in the wild, and often the opportunity for hybridization is lacking when animals live in different parts of the world. As a result, hybrid data is more complete for animals that are domesticated or held in captivity (for example, in zoos).

Second, as described earlier with sheep and goats, even for animals that have produced hybrids, many attempts may be unsuccessful. This may be the result of genetic changes (mutations) that have accumulated in one or both species since the Fall, that causes a loss of ability to interbreed. Finally, if an animal is only known from the fossil record there is no opportunity for it to hybridize with animals alive today.

Cognitum

A cognitum is a group of organisms that are naturally grouped together through human cognitive senses. A cognitum can be above the level of the baramin (for example, mammals), below the level of the baramin (for example, foxes), or at the level of the baramin. This perception-based concept was proposed by Sanders and Wise (2003) as a separate tool in baraminology. Though not originally proposed as a means to identify baramins, the basic concept could prove useful for our purposes here. Use of this method assumes that created kinds have retained their distinctiveness even as they have diversified.

Human cognitive senses influence where animals are placed taxonomically. To some degree a cognitum approach is used in baraminologic studies, though not always consciously acknowledged. Lightner (2006) used it when proposing that all members of the genera *Ovis* and *Capra* belonged to the same baramin. Hybrid data had connected most members across these genera, and the members who had no hybrid data naturally fit in the group based on their physical appearance. They also happened to fit in the same group taxonomically.

The cognitum has played a role in determining what is accepted as true hybridization. As discussed previously, fertilization is clearly insufficient evidence of hybridization. When Lightner (2007) found documented evidence that domestic cattle (*Bos taurus*) had been crossed *in vitro* with water buffalo (*Bubalus bubalis*) and a few fertilized eggs survived to the well-developed blastocyst stage, it seemed sufficient coordinated expression of genes had been demonstrated. The fact that water buffalo naturally group with cattle based on anatomy, physiology, and the husbandry practices used with them was an important part of why it was accepted. If a blastocyst could be formed between domestic cattle and a skunk, this criterion would no doubt be reconsidered.

From previous work in baraminology, researchers have suggested that the level of the baramin tends to fall at or near the taxonomic level of family (Wood 2006). There is often a strong cognitum at the family level. This suggests that the family is a good initial approximation of the level of the baramin. In some instances a strong cognitum may be above or below this level. For example, pigs (Suidae) and peccaries (Tayassuidae) form a strong cognitum even though they are in separate families. From looking at these animals or pictures of them, they are easily grouped together by human cognitive senses. Their division into separate families is based on more subtle details,

and most people would not naturally split them into these groupings unless they were familiar with the taxonomy of these animals. So in this case the baramin appears to be at the level of the superfamily (Suoidea).

Statistical baraminology

Although developed separately, statistical baraminology has similarities to the cognitum in some ways. It takes a collection of characteristics (character traits) and using several statistical tests attempts to discern significant holistic continuity (similarity) or discontinuity between species (Wood et al. 2003). Like the cognitum, it assumes that baramins retain their distinctiveness today. However, in contrast to the cognitum, it assumes that the baramin is the level where statistical tests will consistently point when a set of character traits are analyzed.

Following the introduction of statistical baraminology the definition of the term holobaramin was changed. Essentially, a holobaramin can be thought of as all members of a specific created kind; in other words, the whole baramin. Now, a holobaramin is defined as a group of organisms that share continuity, but are bounded by discontinuity. Continuity is defined as significant, holistic similarity between two different organisms (Wood et al. 2003). A precise definition of *holistic* and *significant* has been somewhat elusive, so Wood (2007) has pointed out the importance of drawing tentative conclusions based on these statistical tests.

Previously, a holobaramin was only identified after considerable detailed study involving multiple lines of evidence. This meant the term carried a definitive connotation. A group was not called a holobaramin until a substantial amount of supporting evidence was amassed. This is not the case when a holobaramin is identified based on statistical tests from a single dataset, even though a dataset may include many character traits. This dramatic shift in the level of certainty associated with the term holobaramin is often not appreciated by creationists who don't use these statistical methods.

There are some clear advantages of statistical baraminology. A suitable matrix of characters is often available together with published cladistic analyses of taxonomic groups. Since someone else has done the work of compiling the data, the baraminologist can enter it into a spreadsheet and run it through the software package available at the Center for Origins Research (CORE) website.⁴ These advantages have allowed for numerous datasets to be analyzed, adding

⁴ Available online at <http://www.bryancore.org/resources.html>. The BDISTMDS software package does not need to be downloaded; the data is entered directly from the spreadsheet. It allows for calculation of baraminic distance correlation and bootstrapping, for determining the robustness of these correlations. It also performs multidimensional scaling which can be viewed in 3D via a downloadable program called MAGE.

useful information to the field of baraminology (Wood 2008). Another potential advantage is that statistical baraminology may help identify the placement of animals known only from the fossil record.

These methods have not been without their critics. The strongest reactions seem to be when the conclusions are at odds with how other creationists feel creatures naturally group. A dramatic example was when an analysis of craniodental characters placed *Australopithecus sediba* in the human holobaramin (Wood 2010). This led to numerous articles expressing disagreement about these specific results and the techniques in general (Line 2010; Lubenow 2010; Menton, Habermehl, and DeWitt 2010; Wilson 2010). Important points in the discussion included the significance of specific anatomic features, the inclusion of inference in certain character states of the dataset, and the possibility that statistical analysis may not consistently point to the level of the holobaramin.

At the opposite end of the spectrum, there are times where the statistical tests have shown discontinuity between animals connected by hybrid data (Brophy and Kramer 2007; Wood 2008, pp.57–60). In one case (McConnachie and Brophy 2008) a dataset of 102 mostly osteologic characters was used to evaluate landfowl. Three of the putative holobaramins were connected by hybrid data. Hybrid data is considered more conclusive than the statistical tests because it requires considerable continuity at the genetic, metabolic, developmental, and immunologic levels. This discrepancy between the hybrid data and statistical results is a concern because datasets involving fossils are generally limited to osteologic characters.

The majority of holobaramins identified by statistical tests are not controversial, but they still need confirmation from further study (Wood 2008, p.230). Given the limitations of other methods, it seems that statistical baraminology is an important tool for creationists to use and to continue to develop. As Wood (2007, p.9) has stated

[a]s long as baraminologists recognize the flaws and remember to draw tentative conclusions, baraminology research with these methods will give a good starting place for future generations of creationists.

Approach to Determining Ark Kinds

As we embark on the Ark Kinds research, we have outlined basic principles that will be used to determine probable Ark kinds. We unanimously agree that hybrid data, for both biblical and biological reasons, is the best way to definitively demonstrate that creatures are descendants of the same Ark kind. Due to the high value placed on such hybrid data, our research will include a literature search

to identify documented hybrids. Emphasis will be placed on hybrids across higher taxonomic levels (for example, between genera, like the coyote, *Canis latrans*, and the red fox, *Vulpes vulpes*) since they are more informative than crosses within a genus. When a hybrid is found that crosses two taxa, all species in both taxa will be considered to be from the same created kind (for example, all *Canis* species and all *Vulpes* species).

Unfortunately, hybrid data is lacking for many creatures. In these cases, a cognitum approach will be used. More specifically, using the context of where taxonomists place the creatures, morphology will be examined to find where they most naturally group together. In addition to drawing on personal experience and training, published works describing and illustrating various taxa will be used. A valuable resource for this will be the University of Michigan Museum of Zoology's Animal Diversity Web website (ADW 2008), which contains numerous photographs covering many animal species. When the cognitum is unclear or seems excessively high taxonomically, the family level may be used as the default level for the kind. This should help guard against seriously underestimating the number of kinds represented on the Ark.

One reason the cognitum is the preferred method after hybridization is that Adam would have recognized created kinds by sight. Presumably the same would have been true in Noah's time. Humans are designed to be able to visually detect patterns and have a natural tendency to group according to those patterns. Therefore, when the cognitum is used, emphasis will be placed on traits that affect the overall appearance of the animal over those that represent more obscure anatomical or physiological details.

Other data, including results of statistical baraminology analyses as well as protein and DNA sequence data, will be evaluated where it seems appropriate. However, none of these will be given as high a priority as hybrid data or the cognitum. This may seem counterintuitive to some. Sequence data is considered hard, objective data. The cognitum seems so subjective. Certainly, it would seem that it is more scientific to use hard data than the subjective cognitum. Besides, these other methods use such interesting mathematical analyses that they must be better, right?

In reality, the really good math masks the fact that conclusions based on these other data have a highly subjective component. Statistical baraminology analyses are based on certain selected character traits, and character selection is not an unbiased process. Brophy (2008), in explaining why hybrid data and statistical baraminology results were in conflict, proposed that purpose for which the dataset

was gathered could bias the results. In the case of landfowl (Galliformes), the dataset was intended to divide the birds up for taxonomic purposes. This seems a reasonable explanation for why the statistical tests based on that dataset divided birds that were connected by hybrid data.

To some, using sequence data may seem more objective. Certainly identifying sequences is objective. It is the interpretation that is not. How does one distinguish between sequences that are the same because two creatures are from the same kind and sequences that are the same because God created them the same in two different kinds? Why do differences exist? Are they simply variability God placed in one created kind at Creation? Are they differences that have arisen within a kind since Creation? Are they created differences between different kinds? Are they differences that have arisen between two different created kinds that originally had identical or very similar sequences in a particular region? The bottom line is that we don't have enough understanding of genetics to understand the significance of most sequence data.

Once the modern descendants of the Ark kinds are determined, we need to use this information to infer what the actual pair on the Ark may have looked like. One thing that is evident when looking at animals in the world today, many have specialized to live in specific niches. There are hares that live in the arctic, others that live in the desert, and others in intermediate climates. There are cattle (for example, the yak) that can withstand high altitudes and cold climates; there are other cattle (for example, zebu) that are adapted to live in hot, arid climates. We also see specialization in domestic animals, where some cattle have been bred for milk production and others have been bred for beef production. Given these trends, the Ark kinds would be relatively unspecialized animals that fit nicely into the cognitum of the created kind.

Just as building the Ark was a monumental task, so our task to determine the Ark kinds is monumental as well. We clearly recognize that in many ways God has prepared us for this task. Yet we are also keenly aware that to do this task well we need power, strength, wisdom, insight and perseverance that only our awesome, sovereign God can give us. For this, your prayers would be much appreciated.

When we are done, we will not have all the answers regarding created kinds, but we hope to have made a substantial contribution to creation research that can serve as a strong resource for future research on created kinds. Beyond this we pray that this information will be used to help people understand that God's Word is trustworthy. May it be used to play a role in many coming to know Christ and living fully for His honor and glory.

Soli Deo Gloria!

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