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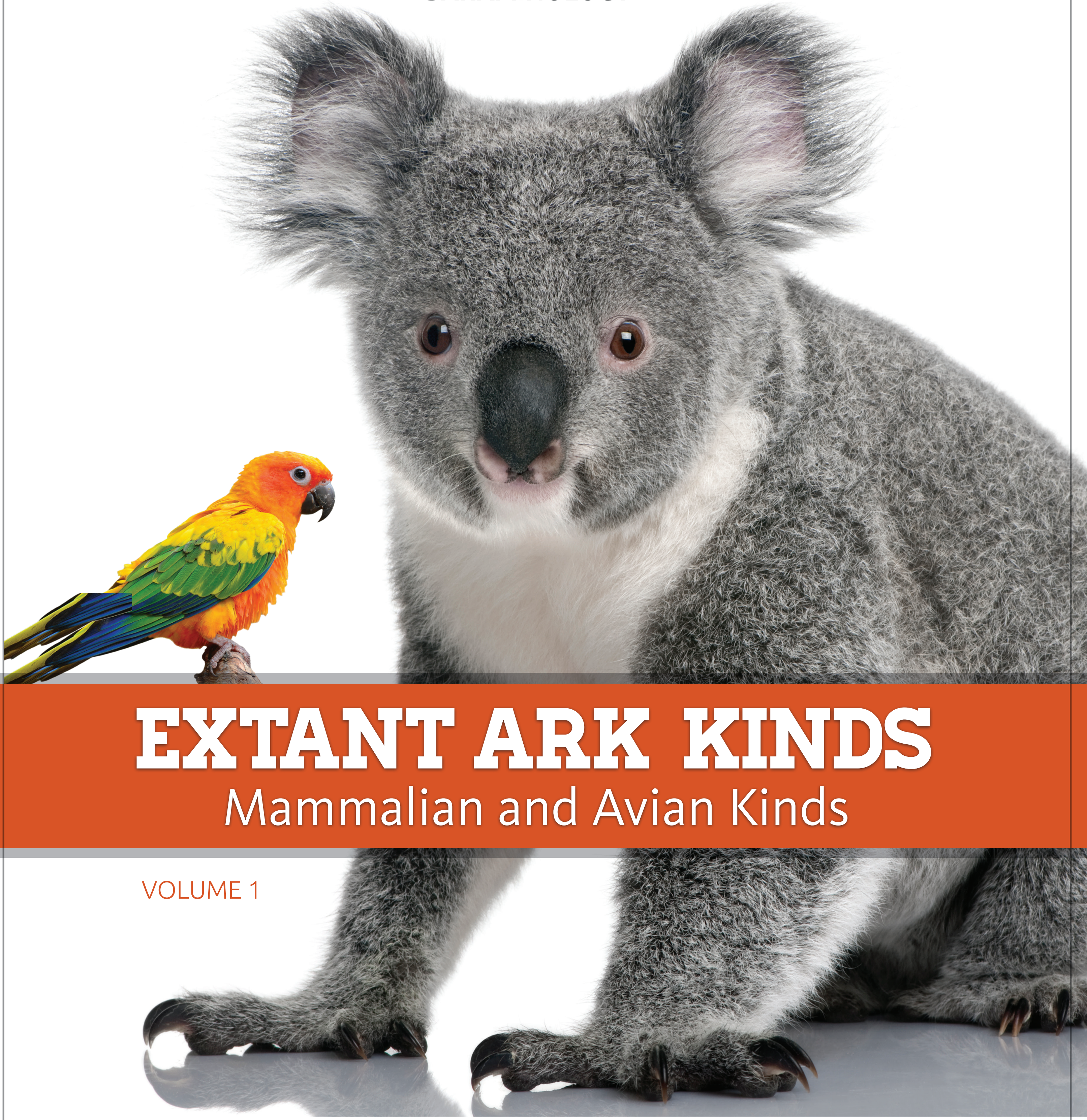
BARAMINOLOGY



EXTANT ARK KINDS

Mammalian and Avian Kinds

VOLUME 1

Dr. Andrew A. Snelling | Editor

Extant Ark Kinds

ARMS

Answers Research Monograph Series 1

Baraminology

Volume 1

EXTANT ARK KINDS
MAMMALIAN AND AVIAN KINDS

ANDREW A. SNELLING, *Editor*

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Answers
IN GENESIS®

Petersburg, Kentucky, USA

Answers Research Monograph Series
1. Baraminology
Volume 1. Extant Ark Kinds: Mammalian and Avian Kinds

First Printing: March 2018

Published by Answers in Genesis
P.O. Box 510 Hebron, KY 41048
www.answersingenesis.org

ISBN: 978-1-9844-0079-6
Library of Congress Control Number: 2018934782

Cover Design by Brandie Lucas

Cover Images:
Young koala, 14 months old, (*Phascolarctos cinereus*)
GlobalP/iStock/Getty Images

Sun conure parrot bird (*Aratinga solstitialis*)
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Printed in United States of America

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Editor's Foreword

Since its initial publication in January 2008, the *Answers Research Journal* has existed as one of the premier professional, peer-reviewed technical journals for the publication of interdisciplinary scientific and other relevant research from the perspective of the recent Creation and the global Flood within a biblical framework. As an increasing number of quality papers have been submitted to the *Answers Research Journal* over the last several years, one of our desires has been to arrange and publish collections of many of those papers in topical formats, with the aim of providing creationists with in-depth resources on given subjects all in one place. The *Answers Research Monograph Series* represents the result of that desire.

Like the *Answers Research Journal*, the *Answers Research Monograph Series* serves to address the need to disseminate the latest original research conducted by creationist experts in the vast fields of theology, history, archaeology, anthropology, biology, geology, astronomy, and other disciplines of science, and to provide scientists and students the results of cutting-edge research that demonstrates the validity of the young-earth model, the global Flood, the non-evolutionary origin of "created kinds," and other evidences that are consistent with the biblical account of origins. Most of the papers contained in the *Answers Research Monograph Series* began as contributions to the *Answers Research Journal*, though some of the articles to be published are original to this series.

It is our sincere hope that the *Answers Research Monograph Series*, like the *Answers Research Journal*, proves a blessing to creationists as they endeavor to defend the literal account of the early chapters of Genesis and as they seek to uphold biblical authority on every issue with which they engage.

Dr. Andrew A. Snelling
Petersburg, Kentucky
February, 2018

CONTRIBUTORS

Dr. Jean K. Lightner

Dr. Jean K. Lightner studied animal science and veterinary medicine at The Ohio State University. She received a BS in Agriculture (1978), a doctorate in veterinary medicine (DVM; 1985), and an MS in veterinary preventive medicine (1987).

Currently Jean is an adjunct instructor with Liberty University Online, teaching biology and creation studies. She also serves as a board member of the Creation Research Society (CRS), an organization that averages over 600 voting members who have advanced science degrees and hold to a young earth perspective on origins. CRS also has many more lay members who help support scientific research that advances the creation model. Jean is married with four adult children, six grandchildren, and currently lives in Northeast Ohio.

Since high school, Jean has had a strong interest in the subject of origins, and has recognized the importance of believing the Bible for living a consistent Christian life. When her children were older, she began to devote considerable time to research and writing. As a result, she has contributed numerous articles to creation journals, magazines, and websites based on intensive review of the scientific literature.

Tom Hennigan

Tom Hennigan has an AAS degree in forest technology (Forest Ranger School at Wanakena, New York); a BS in Natural Resources Management (University of Alaska, Fairbanks); an MS in Education (Syracuse University); and an MPS in Environmental and Forest Biology (SUNY College of Environmental Science and Forestry). For fifteen years Tom had been trained that today's amazing biodiversity is a product of universal common descent via random natural processes. In 1980, he became involved in a series of conversations centered on viewing biodiversity as a product of Intelligent Agency and that the God of the Bible created this world. Over time, he realized that he had rejected Christ's gift of salvation because of his trust in a worldview that rejected God. Once the stumbling block of this worldview was removed, he was ripe for the Gospel of Christ and life transformation by the Spirit of God. Tom is currently an associate professor of ecology and organism biology at Truett McConnell University. Other topics of interest include herpetology, forest ecology, stream ecology, and black bear biology. Tom has been married to his wife Jennifer for over 30 years and has four grown children and five grandchildren

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 would 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 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). 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 6:6–18, 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) all "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.

Originally published in the Answers Research Journal 4 (2011):195–201.
www.answersingenesis.org/contents/379/arj/v4/Ark_kinds_Flood_baraminology_cognitum.pdf

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 five to ten 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.[1] Even the first few divisions are under maternal control. For this reason Scherer

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[1] 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

(1993) stated that embryogenesis must continue until 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 eight 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 (e.g., mammals), below the level of the baramin (e.g., 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 (Suidae).

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 test 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.[2] These advantages have allowed for numerous datasets to be analyzed, adding useful information to the field of baraminology (Wood

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[2] 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.

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, 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, 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, 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 under estimating 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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Mammalian Ark Kinds

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Abstract

Based on the methods outlined in "Determining the Ark Kinds" (Lightner et al. 2011), information on the class Mammalia was evaluated in an attempt to get a realistic estimate of what mammalian kinds would have been represented on the Ark. Examining information on extant species (those alive today), it was estimated that they represent 138 created kinds. Given the number of extinct mammalian families known from the fossil record, the actual number on the Ark could easily have been well over 300. This estimate is very low compared with those in the past. In evaluating the information, a number of important creationist research questions have been discussed. As further research is undertaken to address these, our knowledge of created kinds will be significantly advanced.

Keywords: Ark, baraminology, kinds, mammals

Introduction

Mammals belong to the taxonomic class Mammalia. Nowak (1999) lists them in 28 orders that include 146 families and over 4800 species. They are distinctive in several traits. They possess mammary glands that enable the female to suckle her young. They possess hair, though in cetaceans this is generally confined to early stages of development. Circulating red blood cells lack a nucleus. Additionally, the lower jaw is a single bone on each side that attaches directly to the skull. Like birds, mammals are homeothermic (warm-blooded) and have a four-chambered heart with complete double circulation.

In school I was taught that taxonomy is a scientific discipline that, among other things, gave each animal species in the world a unique binomial name. Unlike common names which can vary from region to region, scientific names were to remain constant so any scientist in any country could use the name and it would be easily recognized by any other scientist anywhere else. Unfortunately, taxonomy has fallen short of this ideal. It is not uncommon to find species for which the genus name has changed over time and according to author. Many times subspecies are elevated to the rank of species; other times the reverse situation occurs. Further, at higher levels taxonomy is in flux. This is because, driven by the secular worldview, taxonomists are interested in classifying life according to its supposed evolutionary history. Often similarity based on morphology doesn't correlate with genetic similarity, causing some rather surprising associations (Nishihara, Hasegawa, and Okada 2006). For the purpose of this analysis, the taxonomic structure used in Wilson and Reeder's (2005) *Mammal Species of the World* is used.

To further complicate matters, many species classified as mammals are known only from the fossil record. It is impossible to identify in such specimens many of the important features that have historically defined mammals, as soft tissue is nearly always absent. Even the skeletal remains can be fragmentary, making their placement difficult and severely limiting our understanding of how they appeared in life (McKenna and Bell 1997). For this reason, fossil data will only be addressed to a limited degree in this paper.

Since hybrid information is so important to help identify biblical kinds, *Mammalian Hybrids* (Gray 1972) was used extensively. However, any hybrids she listed as "presumed" or "alleged" are generally disregarded. Since her work is far from complete, considerable effort was made to identify other hybrids in the literature. Where possible, papers summarizing findings were referenced, from which someone can trace the information back to its original source if they desire. Tables summarizing hybrid data are included at the end of this paper in the appendices.

What follows is an initial attempt, using currently available information, to identify all the created kinds of mammals that would have been represented on the Ark. Since cetaceans (whales, dolphins, porpoises) and sirenians (dugongs and manatees) spend their entire lives in the water, these two orders of mammals are not considered. Previous creationist work is helpful in some taxa. A discussion of the strategy for identifying kinds as well as relevant terminology used in creationist work was outlined in a previous paper (Lightner et al. 2011). It is hoped that this work will provide a strong basis for future creation research that will bring even greater clarity to our understanding of created kinds.

Originally published in the Answers Research Journal 5 (2012):151–204.
www.answersingenesis.org/contents/379/arj/v4/Ark_kinds_Flood_baraminology_cognitum.pdf

Order Monotremata

Monotremes are unusual mammals that lay eggs instead of giving birth to live young. They have a number of other unusual features as well. The structure of the eye and the presence of certain bones in the skull resemble anatomic features of reptiles. Additionally, they have distinct coracoid bones and an interclavicle in their pectoral (shoulder) girdle, resembling that of reptiles. Some features of their ribs and vertebrae are also considered more reptile-like.

Monotremes have three body systems, the digestive, urinary, and reproductive, that all end in a common chamber called the cloaca. This is the basis for the name of this order, which literally means "one hole." In the male, the penis is in the ventral wall of the cloaca and is divided at the tip into paired canals that are only for conveying sperm. In the female, each oviduct opens separately into the cloaca. After fertilization in the oviduct, the egg is covered with albumin and a flexible, sticky, leathery shell before it is laid (Nowak 1999).

Monotremes suckle their young after they hatch. Like marsupials, monotremes have eupubic (marsupium) bones associated with the pelvis. Monotremes maintain a lower body temperature than most mammals (30–32°C; 86–90°F). There is evidence that they have electroreceptors in their snout that aid in acquiring food (Nowak 1999; Pasitschniak-Arts and Marinelli 1998). Young monotremes have teeth, but they don't cut through the gums and true functional teeth are not present in the adults of extant species. Adult males possess horny spurs on their ankles (Nowak 1999).

Tachyglossidae (Echnida kind)

Size: *smaller adult around 40–45 cm (15.7–17.7 in) long (nose to rump; male larger than female). Eats bugs and worms, likes to dig; might hibernate.*[1]

Echidnas are also known as spiny anteaters. In addition to their fur, they are covered on the back and sides by barbless spines. They have broad feet with three to five strong, curved claws which they effectively use for digging. They are divided into two genera: *Tachyglossus* is the short-nosed echidna; *Zaglossus* is the long-nosed echidna. Some authors list multiple species, particularly in the latter genus. Though there is no hybrid data available, the whole family forms a strong cognitum. *Tachyglossus* is smaller, has longer spines, and generally lays only one egg which it incubates in the temporary pouch that forms at the appropriate time. In contrast, *Zaglossus* is larger with shorter spines, and may incubate and suckle four to six young at a time in its temporary pouch.

Fig. 1. Short-beaked echidna (*Tachyglossus aculeatus*). Fir0002/Flagstaffotos, "Wild Shortbeak Echidna," https://commons.wikimedia.org/wiki/File:Wild_shortbeak_echidna.jpg, http://www.gnu.org/licenses/old-licenses/fdl-1.2.html.

Fig. 2. Long-beaked echidna (*Zaglossus bruijnii*). User: Jaganath, "Long-Beaked Echidna," https://commons.wikimedia.org/wiki/File:Long-beakedEchidna.jpg, CC BY-SA 3.0.

Echidnas have been reported to become torpid if food supply dwindles and, in some instances, may hibernate through the winter (Nowak 1999). This leaves open the possibility that the pair on the Ark may have slept through much of the voyage, thus reducing their need for food. Interestingly, in those cases where hibernation has been documented, the females are ready to mate at the end of this period (Nowak 1999).

Ornithorhynchidae (Platypus kind)

Size: *head and body 30 cm (11.8 in); tail 10 cm (3.9 in); male larger than female. Caging requirements: Male has venomous spurs on hind feet; cage separate from other species.*

Fig. 3. Duck-billed platypus (*Ornithorhynchus anatinus*). Klaus, "Wild Platypus 4," https://commons.wikimedia.org/wiki/File:Wild_Platypus_4.jpg, CC BY-SA 2.0.

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[1] This is an estimate of the size for the individuals on the Ark using the range reported in the Nowak (1999) source.

The only extant member of this family is the duck-billed platypus, *Ornithorhynchus anatinus*. Its bill, though superficially similar to a duck's, is covered with soft, hairless skin. The body is streamlined as in other semi-aquatic mammals (for example, otters and beavers) and it has webbing on the feet. The tail is somewhat like a beaver's, but is covered with fur; it is used in fat storage. The spurs on the hind feet of the males are connected with venom glands and can be used for defense if necessary (Nowak 1999; Pasitschniak-Arts and Marinelli 1998).

There are several fossil specimens that have been placed in this family. They are quite fragmentary, but one is of particular interest. *Obdurodon dicksoni* exhibits well-developed functional teeth. In *O. anatinus*, teeth are only found in juveniles; flattened horny plates are present in adults and used in mastication. This suggests that originally this kind may have had teeth, but this trait is largely lost in the present-day platypus.

Some may question the need of putting a semi-aquatic creature on the Ark. Who really wants to bring a creature with venomous spurs on the Ark? Besides, extant platypuses aren't exactly known for doing particularly well in captivity (Pasitschniak-Arts and Marinelli 1998). While a platypus may spend half its day in the water, it lives in a burrow. Times of resting on land appear essential to its well being. It seems unlikely that months of swimming in Flood waters would be conducive to the survival of this created kind. Therefore we will assume it was on the Ark.

Marsupials

At one time marsupials were considered an order. However, currently extant marsupials are usually placed in seven different orders which include about 20 families. There are five more orders of marsupial or marsupial-like animals known only from the fossil record, which comprise 37 families (Nowak 2005a). Only orders that include at least one extant species will be considered here. Currently, there are still areas of marsupial taxonomy where considerable controversy exists.

Although the kangaroo is probably the most familiar marsupial, several orders of marsupials have a rodent-like to ferret-like appearance. In fact, even some marsupials in the same order as kangaroos exhibit a very rodent-like face (for example, *Potorous longipes*, long-footed Potoroo). This, along with the fact that marsupials are generally less familiar, makes it more difficult to identify cognita in many cases. Further, only the family Macropodidae, which includes kangaroos and wallabies, has significant hybrid data (Close and Lowry 1990). For these reasons the kinds identified here should be considered only a rough estimate and more research in this group is highly encouraged.

Order Didelphimorphia

Didelphidae (Opossum kind)

Size: *head and body 16–20 cm (6.2–7.8 in); tail 19–33 cm (7.4–12.9 in)*

Opossums are marsupials that live in the Americas. Generally, they comprise a single family with two subfamilies (Wilson and Reeder 2005), though it has been suggested that they should be divided into four distinct families (Nowak 2005a). The main difference noted between the two subfamilies involves specific details of the ankle bones. Several other details differ as well, but none that obviously affect the overall cognitum.

Most opossums have a long, scaly, nearly naked prehensile tail. However, some forms have a shorter tail and/or one that is hairier. Hair is most likely to be abundant at the base of the tail and/or along its dorsal surface (Nowak 1999).

It is interesting to note that the bushy-tailed Opossum (*Glironia venusta*) was at one time placed in one subfamily (Didelphinae). Later, based on some dental and supposed basicranial similarities, it was placed, along with several other genera (*Caluromys*, *Caluromysiops*), in what is now a separate order (Microbiotheriidae, which contains *Dromiciops*). Later, the basicranial similarities were disputed and the dental similarities were considered to be from convergent evolution. Now the bushy-tailed Opossum is in the other subfamily (Caluromyinae) of Didelphidae (Marshall 1978).

Fig 4. North American opossum (*Didelphis virginiana*). Cody Pope, "Opossum 2," https://commons.wikimedia.org/wiki/File:Opossum_2.jpg, CC BY-SA 2.5.

Order Paucituberculata

Caenolestidae (Shrew opossum kind)

Size*: total body length female 17 cm (6.6 in); male 20 cm (7.8 in); tail about 40% of total length*

Though fossil evidence suggests this order was once more widespread with seven recognized families, extant species are confined to a single family. These marsupials are small and shrew-like in appearance with a long conical head and small eyes. They have a limited range in South America. This order is diagnosed by some finer details of the molars and wrist bones, which do not significantly affect the overall cognitum. They lack a pouch, a trait shared by some opossums as well as some members of other marsupial orders (Nowak 2005a).

Shrew opossums are considered here as a separate kind for several reasons. Available pictures of extant species can be distinguished from opossums by head shape and eye size. Since these features are variable within many of the rodent-like marsupials, these criteria could reasonably be challenged. A second reason is that combining them would involve combining two groups that currently occupy the status of order (though previously they had been placed below this). To avoid underestimating Ark kinds, it was decided to list the shrew opossum as a separate kind.

The Chilean shrew opossum (*Rhyncholestes raphanurus*) differs from others in this family in that it seasonally stores fat in its tail. This trait appears in some species from other marsupial orders and is associated in several small mammals with extended torpor (Patterson and Gallardo 1987). It is interesting to note that the Flood began on the seventeenth day of the second month (Genesis 7:11), which would correspond to about the beginning of November.[2] If we assume that seasons prior to the Flood were similar to those today (Genesis 1:14–15; 8:21–22), then animals prone to hibernate in the Northern Hemisphere could have easily built up the body reserves for this prior to entering the Ark. Further, some animals are able to enter shorter periods of torpor which is not necessarily related to winter hibernation. Such abilities would not only reduce their food requirement, it would likely reduce the stress of the voyage on them significantly.

Fig. 5. Andean shrew opossum (*Caenolestes condorensis*). Photograph courtesy of mammalsrus.com. http://www.mammalsrus.com/metatheria/paucituberculata/paucituberculata.html.

Order Microbiotheria

Microbiotheriidae (Little-monkey opossum kind)

Size: *total length 19.5 cm (7.6 in); head and body 8.5+cm (3.3+in); tail 9+cm(3.5+in)*

This family is represented by a single living species known as monito del monte (little monkey of the mountain), *Dromiciops australis*, which lives in a limited range in South America. It is a good climber, rodent-like in appearance and was previously classified in the family Didelphidae with other American opossums. It was reclassified into the otherwise extinct family Microbiotheriidae, which for a while was retained under the same order (Didelphimorphia). Later work suggested this order was more closely related to Australian marsupials. Based on limb bone analysis, one researcher placed them as a suborder next to Dasyuromorphia, which includes some rodent-like Australian marsupials. Another argued that they are separate from all other marsupials. They are unique among extant marsupials in that they have a basicaudal cloaca like monotremes and several cranial/dental traits found in some placental mammals (Nowak 2005a).

El monito del monte also stores fat in the basal portion of its tail in preparation for hibernation. It is known to be able to double its body weight in a week in this way. It has also been observed to enter periods of torpor on a daily basis, even when food is readily available (Nowak 2005a). As previously mentioned, these traits could have been useful on the Ark as this decreased metabolic activity would have reduced the required food intake and likely reduced the stress on the animal during its year on the Ark.

Fig. 6. Monito del Monte opossum (*Dromiciops gliroides*). Lin linao, "Monito Del Monte En Estado De Sopor Invernal," "https://commons.wikimedia.org/wiki/File:Monito_del_monte_en_estado_de_sopor_invernal._(36391982075).jpg, Public Domain.

Order Notoryctemorphia

Notoryctemorphia (Marsupial mole kind)

Size: *head and body 9+cm (3.5+in); tail (short cylindrical, stumpy, hard, leathery, terminates in horny knob) 1.2 cm (0.47 in)*

The marsupial mole consists of one extant species, *Notoryctes typhlops*. Its appearance is different from other marsupials, but it bears a striking resemblance to golden moles (Afrosoricida; Chrysochloridae) in overall morphology, burrowing habits, fur textures,

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[2] Originally, Tishri was the first month of the year. It was at the time of the Exodus, many years after the Flood, that the first month changed to the spring month of Abib (Nisan), (Exodus 12:1).

and external features of the brain. Not only is its appearance unique compared to other marsupials, but studies involving serology, karyotype, and DNA data have failed to show significant similarity with other marsupials (Nowak 2005a).

Since there are a number of marsupials that bear an uncanny resemblance to placental animals, some have suggested that perhaps they belong to the same kind as their placental counterparts. If this were so, these mammals would have been created with the ability to switch between two modes of reproduction. This would be analogous to some reptiles that can vary between egg laying and live birth (Adams et al. 2007; Arrayago, Bea, and Heulin 1996).

Similar to placentals, marsupials have an early forming yolk sac placenta through which nourishment is absorbed from the mother's uterus. In some marsupials (Phascolarctidae; Vombatidae; Peramelemorphia) a second chorioallantoic placenta forms and allows more intimate exchange between mother and developing embryo (Nowak 2005a). These factors would seem to suggest that switching mode of reproduction might be possible in mammals.

To evaluate this possibility further, a Blastn test was performed on the mitochondrial DNA (mtDNA) sequence for this species[3] and two species of golden moles (*Chrysochloris asiatica*[4] and *Eremitalpa granti*[5]) whose mtDNA sequences are found in the NCBI nucleotide database. The mtDNA of other marsupials showed the highest percent identity to the marsupial mole sequence; the sequences to the golden moles were not listed among the hits. When the golden mole sequences were queried, the other golden mole sequences were at the top of the list, followed by sequences from the pig (*Sus scrofa*); the marsupial mole was not on the list of hits for the golden mole sequences. These results do not support the conjecture that marsupial moles and golden moles are members of the same created kind.

Fig. 7. Southern marsupial mole (*Notoryctes typhlops*). Photograph courtesy of Alice Springs Desert Park, "Southern Marsupial Mole," http://www.alicespringsdesertpark.com.au/kids/nature/mammals/images/marsupialmole.jpg.

Order Dasyuromorphia

The members of this order had been placed in a single family, Dasyuridae, until around 1960. Since then, several species have been placed in separate families within this order. The many species that remain in Dasyuridae are mostly rodent-like, bearing a strong superficial resemblance to the American marsupials of Didelphimorphia. However, they differ in the number of upper and lower incisors. Members of Dasyuromorphia also lack a cecum and never have a prehensile tail (Nowak 2005a).

Thylacinidae

Thylacinus cynocephalus (Tasmanian wolf kind)

Size: *head and body length 85 cm (33.4 in); tail 38 cm (14.9 in); shoulder height 35 cm (13.7 in)*

The Tasmanian wolf, *Thylacinus cynocephalus*, is the most unique appearing member of its order, bearing a striking superficial resemblance to a dog. However, its mtDNA is similar to other marsupials, especially those in Dasyuromorphia, but is not similar to the mtDNA of any canids. Analysis of its skeletal proportions indicates that it is very much like a large dasyurid. It does not have specialized pursuit adaptations like those found in wolves (Nowak 2005a). This single species, which became extinct in the last century, naturally falls into a class by itself using the cognitum.

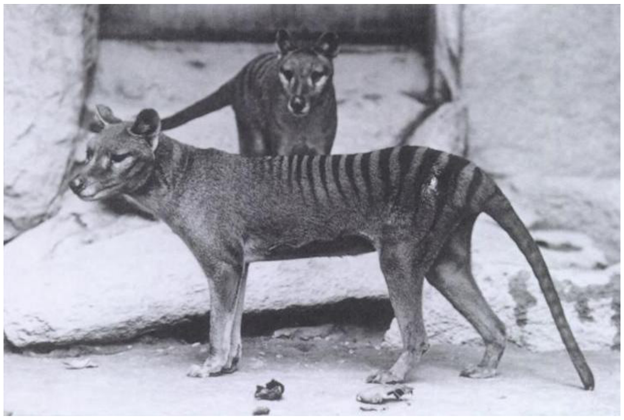

Fig. 8. Tasmanian wolves (*Thylacinus cynocephalus*). Baker; E. J. Keller, "Thylacinus," https://commons.wikimedia.org/wiki/File:Thylacinus.jpg, Public Domain.

Myrmecobiidae (Banded anteater kind)

Size: *body length 17.5 cm (6.8 in); tail length 13 cm (5.1 in)*

The banded anteater (*Myrmecobius fasciatus*), also known as the numbat, is unique among marsupials in that it is diurnal and uses its long tongue to eat termites. It was once classed as a

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[3] http://www.ncbi.nlm.nih.gov/nuccore/NC_006522.1

[4] http://www.ncbi.nlm.nih.gov/nuccore/NC_004920.1 and http://www.ncbi.nlm.nih.gov/nuccore/AJ428944.1

[5] http://www.ncbi.nlm.nih.gov/nuccore/NC_010304.1 and http://www.ncbi.nlm.nih.gov/nuccore/AM904729.1
The blastn test was run on each sequence individually using default parameters.

subfamily within Dasyuridae. Apart from its color pattern, it seems to fit in the same cognitum as other dasyurids. Its karyotype (2n=14) is similar, but this same pattern is seen in other marsupial orders as well. It is distinctive from dasyurids in its serology, though to a degree more commonly found at the subfamily level. Major reasons for placing it in a separate family are distinctive dental and basicranial features (Archer and Kirsch 1977). They are considered a separate kind here because they do have some distinctive features and we have chosen to prefer splitting to lumping, especially above the family level.

There are several things worth noting here. First, Archer and Kirsch (1977) attribute much of the increase in marsupial families to the fact that the marsupial designation is now above the level of the order. This has provided more "room" and many subfamilies have been promoted to the family level. Second, they note that changes in morphology, serology, and karyology often don't keep pace with each other. So, while the banded anteater has a karyotype like dasyurids, and the serology only differed as would be expected on the subfamily level, the separate family placement was based on some unique characteristics of the molars and basicranium.

Creationists can also find it challenging to interpret differences in morphology, serology, and karyology. For example, even if we assume that each created kind originally had a uniform karyotype, there is not a uniform karyotype within all created kinds today. Animals can have similar or identical morphology, even belonging to the same species, and have different karyotypes (Lightner 2006a). Perhaps the most extreme documented example is in the South American marsh rat, *Holochilus brasiliensis*, where 26 distinct karyotypes were observed in the 42 animals tested (Nachman and Myers 1989). So clearly animals with differing karyotypes can belong to the same created kind. On the other hand, what are we to make of similar karyotypes? Within different marsupial orders are individuals with a very similar karyotype (2n=14). Many of these animals have a rodent-like morphology, making it a challenge to see clear divisions when looking at the live animal without supporting laboratory data. Might this be a hint that the level of the kind may be higher and include several orders of marsupials? At the same time, there is no biblical reason why God could not have created several marsupial kinds with essentially identical karyotypes. This highlights the need for considerable creationist research to address these types of questions.

Fig. 9. Banded anteater (*Myrmecobius fasciatus*). Martin Pot, "Numbat," https://commons.wikimedia.org/wiki/File:Numbat.jpg, CC BY-SA 3.0.

Dasyuridae (Marsupial mouse kind)

Size: *body length 12cm (4.7in); tail length ~12cm (4.7in)*

Dasyuridae is divided into two subfamilies, each of which is composed of two tribes. There are a total of 69 species placed in 20 genera within this family (Wilson and Reeder 2005). Many look similar to mice, though the quolls (*Dasyurus* species) tend to be larger with some having a body shape similar to that of the banded anteater. From an appearance standpoint, the most unique member of this family is the Tasmanian devil, *Sarcophilus harrisii*. The head and body of this creature look like that of a small bear (Nowak 2005a). It would be tempting to split the Tasmanian devil out on the basis of the cognitum, but taxonomically it fits well in the tribe Dasyurini, along with the quolls and several other genera (Wilson and Reeder 2005). For this reason, the kind is considered to be at the level of the family.

Here again there are important questions that can be raised. Taxonomists have reason to believe the Tasmanian devil is closely related to the quolls, despite

Fig. 10. Spotted quoll (*Dasyurus maculatus*). Sean McClean, "Spotted Quoll 2005," https://commons.wikimedia.org/wiki/File:SpottedQuoll_2005_SeanMcClean.jpg, CC BY-SA 3.0.

its bulkier body build. Are the unusual features of the Tasmanian devil from variation within a kind? It has been assumed so here since other members of the same tribe (Dasyurini) look similar to members of the other tribe (Phascogalini) within this family. When two taxonomic categories are bridged, all members of both categories are assumed to be in the same kind. On the other hand, what differences distinguish one created kind from another? Since Scripture never tells us specifically, we are left to conjecture in most cases.

Some progress has been made on these questions by examining variation in kinds identified by hybrid data. We know that domestic dogs vary tremendously in size, color, and muzzle shape. Wild animals vary in size and color as well. What types of cranial and dental variation are found in created kinds? Are there certain features that are distinct and tend to not change? Do some changes within created kinds result in certain members that look a bit like other kinds? Considerably more research is necessary to better answer these questions. In marsupials, the family Macropodidae has documented intergeneric hybrids. This should provide an excellent place to start assessing morphologic, serologic, and genetic variation within marsupials linked by hybrid data.

Fig. 11. Brown antechinus (*Antechinus stuartii*). Glen Fergus, "Brown Antechinus," https://commons.wikimedia.org/wiki/File: Brown_Antechinus.jpg, CC BY-SA 2.5.

Order Peramelemorphia *(Bandicoot kind)*

Size: *head and body 20 cm (7.8 in); tail 7–10 cm (2.7–3.9 in)*

In bandicoots the second and third digits are syndactylous, bound together by skin so only the tops of the joints and nails are separate. It works somewhat like a single digit and the animals will use it for grooming. This is also a feature of Diprotodontia, and previously animals in this order were placed at a lower rank in an order beside those of Diprotodontia. However, the teeth of bandicoots are polyprotodont, having more than one pair of lower incisors, much like members of Dasyuromorphia. For this reason, these animals were placed in their own order. Bandicoots are interesting in that they form a chorioallantoic placenta in addition to the yolk sac placenta. The only other marsupials known to form this type of placenta are koalas and wombats, both from the order Diprotodontia. However, these placentas are not as well developed as in placental mammals as marsupials have a comparatively short gestation time (Nowak 2005a).

This mix of characteristics can be interpreted several ways in the creation model. It could be interpreted as indicating that the level of the kind is above the level of the order for at least some of the marsupials. Since many marsupials are rodent-like and the average student of nature probably would not be able to, by looking at pictures, place them in separate groups that match their current taxonomic position; this possibility is worthy of further investigation. It should be pointed out, however, that this would place the Tasmanian wolf in with some very rodent-like animals. In contrast, it could be taken as evidence that these animals were created separately with a mix of features so they would clearly be distinct from other groups. Since bandicoots do have some distinctive features, including a long, pointed muzzle and hind limbs longer than forelimbs, they will be considered here to be a separate kind.

Fig. 12. Southern brown bandicoot (*Isoodon obesulus*). John O' Neill, "Southern Brown Bandicoot (Isoodon obesulus) 2, Vic, jjron, 09.01.2013," https://commons.wikimedia.org/wiki/File:Southern_Brown_Bandicoot_(Isoodon_obesulus)_2,_Vic,_jjron,_09.01.2013.jpg, Public Domain.

There has been considerable disagreement over how the 18 species in this order should be grouped into families (Wilson and Reeder 2005). Aplin, Helgen, and Lunde (2010) give a relatively detailed account of this history. In 1990, based on morphologic details, it was proposed that two families are appropriate: Peroryctidae and Peramelidae. Some genetic and serologic studies that followed supported this. Later studies resulted in placing the members of Peroryctidae as a distinct subfamily within Peramelidae. Also, two genera were removed from Peramelidae to form the families Thylacomyidae (*Macrotis* spp.) and Chaeropodidae (for recently extinct *Chaeropus*). Aplin, Helgen, and Lunde (2010) point out that future studies to resolve these taxonomic issues should include, among other things, a more complete consideration of extant species. Because of the controversy over family status and the cognitum being unhelpful in dividing this order, the level of the kind was placed at the level of the order.

Order Diprotodontia

The name for this order comes from a dental characteristic of its members, namely two large lower incisors that point forward. Usually there are no other incisors or canine teeth in the lower jaw, but if they appear they are small. This leaves a gap between the incisors and cheek teeth. As mentioned previously, they are syndactylous as are members of Peramelemorphia (Nowak 2005a). It is the largest of the marsupial orders with 143 recognized species in 39 families (Wilson and Reeder 2005).

Phascolarctidae (Koala kind)

Size: *head and body 60cm (23.6in)*

The koala, *Phascolarctos cinereus*, was once placed in the family Phalangeridae with the Australian possums and cuscuses. It has since been moved into its own family and is now believed to be more closely related to wombats. Although there is only one species, it is distinctive enough to be easily recognized by most people and will be considered a created kind here.

Fig. 13. Koala (*Phascolarctos cinereus*). Arnaud Gaillard, "Koala ag1," https://commons.wikimedia.org/wiki/File:Koala-ag1.jpg, CC BY-SA 4.0.

Vombatidae (Wombat kind)

Size: *head and body 70cm (27.5in); tail 2.5cm (0.9in)*

There are three species of wombats which are placed in two genera. Like the koala, they lack the long obvious tail characteristic of most diprotodonts. They have a stocky bear-like body. Their teeth are similar to those of rodents in that they are rootless and ever growing. They also chew with rapid side-to-side movements like rodents. Since they have these unique features they are considered a separate created kind here.

Fig. 14. Common wombat (*Vombatus ursinus*). JJ Harrison (jjharrison89@facebook.com), "Vombatus Ursinus-Maria Island National Park," https://commons. wikimedia.org/wiki/File:Vombatus_ursinus_-Maria_ Island_National_Park.jpg, CC BY-SA 3.0.

Burramyidae (Pygmy possum kind)

At one time the members of Burramyidae were included in the family Phalangeridae (Nowak 2005a). Based on serology, Burramyidae was placed as a separate family (Kirsch 1977). In that study, the genus *Acrobates* grouped within Burramyidae, but subsequent study has placed it in a separate family, Acrobatidae (Nowak 2005a). Acrobatidae is in a separate superfamily (Petauroidea) from Burramyidae and Phalangeridae (Phalangeroidea; Wilson and Reeder 2005).

Fig. 15. Mountain pygmy possum (*Burramys parvus*). Photograph courtesy of © Dr. Linda Broome, "Mountain Pygmy-Possum Feeding," http://www.arkive.org/mountain-pygmy-possum/burramys-parvus/image-G78915.html.

Despite these shifts, the current family arrangement appears fairly well accepted. There certainly is not the degree of upheaval at the family level seen in bandicoots (order Peramelemorphia). There is, however, still considerable disagreement in how the current families are related to each other (Meredith, Westerman, and Springer 2009; Munemasa et al. 2006). One possible reason for this ambiguity is that the families are not related. However, the frequent use of possum in the common name for species in many of these families betrays the fact that there is a natural cognitum above the family level. Here the kind is tentatively placed at the family level to avoid underestimating the number of kinds on the Ark, but these issues should be looked at in more detail.

The small, mouse-like members of this family are nocturnal. Many inhabit trees, most have been observed to undergo torpor for variable lengths of time, and at least one, *Cercartetus nana*, undergoes full hibernation in the winter after storing considerable body fat, especially in the base of its tail (Nowak 2005a). It is interesting to note that studies on *Cercartetus nana*, the Eastern pygmy possum, have shown that torpor can be observed independent of season, time of day, and ambient temperature. Its body temperature drops to several degrees above ambient temperature. The duration of this period of torpor tended to increase with a drop in ambient temperature. In one experiment, a record 367-day hibernation period was recorded. The animal used 1/40th the energy normally used while awake (Harris 2008). This is not meant to imply that all marsupials slept through the entire voyage on the Ark, but some period of torpor seems reasonably likely for a number of these animals.

Fig. 16. Eastern pygmy possum (*Cercartetus nanus*). Phil Spark, "Eastern Pygmy Possum Pilliga Forest NSW," https://commons.wikimedia.org/wiki/File:Eastern_Pygmy_Possum_Pilliga_Forest_NSW.jpg, CC BY-SA 2.0.

Phalangeridae (Possum kind)

Size: *head and body 42 cm (116.5 in); tail ~38–40 cm (~14.9–15.7 in)*

At one time this family included members of what are now considered separate families. The koala (Phascolarctidae) has been moved to a different suborder (Vombatiformes) beside the wombat. As mentioned, Burramyidae is now a separate family in the same superfamily (Phalangeroidea). Members of Pseudocheiridae, Petauridae, Tarsipedidae, and Acrobatidae are in a separate superfamily (Petauroidea) in the same suborder (Phalangeriformes; Nowak 2005a; Wilson and Reeder 2005).

Currently six genera remain in Phalangeroidae. Taxonomists have recognized diagnostic features for this family, including several dental and several cranial features (Nowak 2005a). Most are not features that would be readily noticed by the average student of nature. Documented hybridization has occurred between *Trichosurus arnhemensis* and *T. vulpecula*, two of the more common species in the family (Close and Lowry 1990; Wilson and Reeder 2005). Since this is not an intergeneric hybrid, it is not listed in the hybrid tables.

Fig. 17. Common brushtail possum (*Trichosurus vulpecula*) in tree, Australia. Tom Brakefield/Stockbyte/Getty Images.

Pseudocheiridae (Ring-tailed/Greater gliding possum kind)

Size: *head and body 32 cm (12.5 in); tail ~33–36 cm (~12.9–14.1 in)*

When the members of this family were first removed from Phalangeridae, they were placed at the subfamily level in Petauridae. Based on later studies they were elevated to the family status (Nowak 2005a). There are 17 species which are placed in six genera (Wilson and Reeder 2005). All species are arboreal, and one genus contains a single species (*Petauroides volans*) which has the ability to glide. The patagium, or fold of skin used for gliding, extends from the elbow to the leg. In contrast to flying squirrels and the lesser gliding possum, the greater gliding possum glides with its elbows pointed outward and forearms pointed inward (Nowak 2005a).

Fig. 18. Lemur-like ringtail possum (*Hemibelideus lemuroides*). Wildlife Explorer, "Hemibelideus Lemuroides-Queensland 8," https://commons.wikimedia.org/wiki/File:Hemibelideus_lemuroides_-Queensland-8.jpg, CC BY-SA 3.0.

Petauridae (Gliding and striped possum kind)

***Size:** head and body 22 cm (8.6 in); tail ~25–31 cm (~9.8–12.1 in)*

Currently this family consists of 11 species placed in three genera. As with the previous family, all species are arboreal. One genus (*Petaurus*) has six species of lesser gliding possums (Nowak 2005a; Wilson and Reeder 2005). The patagium extends from the outside of the forearm to the ankle. As in the flying squirrel (*Glaucomys*), gliding is done with all limbs extended (Nowak 2005a). A hybrid has been documented between *Petaurus breviceps* and *P. norfolcensis* (Close and Lowry 1990). Since this is not an intergeneric hybrid, it is not listed in the hybrid tables.

Fig. 19. Mahogany glider (*Petaurus gracilis*). Pfinge, "Mahogany Glider," originally uploaded to French Wikipedia, https://commons.wikimedia.org/wiki/File:Mahogany_glider.jpg, CC BY-SA 2.0.

Tarsipedidae (Honey possum kind)

***Size:** head and body 7 cm (2.75 in); tail ~7.5–8.5 cm (~2.9–3.3 in)*

The honey possum, *Tarsipes rostratus*, is the only known member of this family. It is unique among the small, mouse-like Australian marsupials in its coloration and long snout. It uses its long tongue to feed on nectar and pollen from flowers. At one time it too was placed in the family Phalangeridae, but difference in morphology and serology were grounds for removing it. Other such studies identified some similarities between it and members of Acrobatidae (Nowak 2005a).

Fig. 20. Honey possum (*Tarsipes rostratus*). © 2015 Ray Wilson, www.raywilsonbirdphotography.co.uk, "Honey Possum (*Tarsipes Rostratus*)," http://www.raywilsonbirdphotography.co.uk/new_images/2015/Australia/WA/2015-09-25_O9A0911.jpg.

Acrobatidae (Feather-tailed possum kind)

***Size:** head and body 9 cm (3.5 in); tail ~10–11 cm (~3.9–4.3 in)*

This family consists of two species placed in separate genera, *Distoechurus* and *Acrobates*. At one time these species were placed in Phalangeridae, but based on serologic evidence they were removed with the family Burramyidae. Later they were considered to have affinity with Petauridae, but more recent serologic and morphologic studies suggest they have more similarity to Tarsipedidae (Nowak 2005a).

Hypsiprymnodontidae (Musky rat-kangaroo kind)

***Size:** head and body 21 cm (8.2 in); tail ~13 cm (5.1 in)*

The last three marsupial families are in the suborder Macropodiformes. The name means "big feet" which refers to the elongated hind foot. There is a strong cognitum at this level because of this trait. In addition to being evident in pictures of these animals, it is reflected in the name kangaroo which appears as rat-kangaroo for these first two families, reflecting the smaller size of their members. It would seem far more natural to place the level of the kind here, but I have resisted doing so for several

Fig. 21. Feathertail glider (*Acrobates pygmaeus*).Elias Neideck, "*Acrobates Neuneu,*" https://commons.wikimedia.org/wiki/File:Acrobates_neuneu.jpg, CC BY-SA 3.0.

reasons. First, it is at the suborder level, which is already fairly high. This first family is the most unique and also bears some resemblance to other rodent-like marsupials when noticing features such as head shape and overall body proportions. Further, these animals are less familiar to me which would increase the likelihood of me lumping them together inappropriately. For this project, we agreed to prefer splitting to lumping, especially above the family level, to avoid underestimating the Ark kinds.

The musky rat-kangaroo (*Hypsiprymnodon moschatus*), the only extant member of this family, is the smallest of the rat-kangaroos and differs from others in this suborder in that it retains the first digit of the hind foot, which is well developed, and its tail is naked and scaly. Its limbs are more equally proportioned than those of other rat-kangaroos (Nowak 2005a). It was separated taxonomically from the other rat-kangaroos, initially at the subfamily level, based on having a simple stomach and blade-like premolars (Hume 1999). The stomach has been described as more similar to that of a brushtail possum (*Trichosurus* spp; Phalangeridae) than of other rat-kangaroos (Potoroidae). The stomach does have deep grooves on either side of the esophageal opening, which seems to partially divide it. Given the foregoing discussion, it is considered a distinct kind here.

Based on overall external morphology, there is not a strong division between the musky rat-kangaroo and the rat-kangaroos of the family Potoroidae, a fact also betrayed in the common names. This highlights a need for further creation research. In addition to research delineating the variability of dental and skull characteristics within created kinds, within kind variability of the digestive tract needs to be evaluated. This issue is important in other mammalian orders too. Can a monogastric (simple stomached) creature develop a complex stomach if foregut fermentation becomes a viable adaptive strategy? If so, to what degree? Does adaptation occur in the reverse direction (complex stomach toward simple)? Within marsupials both the Potoroidae and Macropodidae are foregut fermenters with a complex stomach. What about various forms of hindgut fermentation, is there within kind variation here as well? If so, to what extent? Among marsupials hindgut fermentation is found in the wombat (Vombatidae) and arboreal folivores (tree-dwelling leaf eaters) in the families Phalangeridae, Pseudocheiridae, and Phascolarctidae (Hume 1999)

Fig. 22. Musky rat-kangaroo (*Hypsiprymnodon moschatus*). The Rambling Man, "Musky Rat-Kangaroo," https://commons.wikimedia.org/wiki/File:Musky_rat-kangaroo.jpg, CC BY-SA 3.0.

Potoroidae (Rat-kangaroo kind)

Size: *head and body 28cm (11in); tail ~25cm (~9.8in)*

This family includes 10 species placed in four genera (Wilson and Reeder 2005). Like members of Macropodidae, the tails are furred, first digit of the hind foot is absent, and they have a complex stomach. Skulls vary from short and broad to long and narrow. They are unique among the families of this suborder in that the parietal and alisphenoid bones of the skull are separated by the wide contact of the squamosal bone with the frontal bone (Nowak 2005a).

Fig. 23. Gilbert's potoroo (*Potorous gilbertii*). Mick wackers at English Wikipedia, "Gilberts Potoroo," https://commons.wikimedia.org/wiki/File:GilbertsPotoroo.jpg, CC BY-SA 3.0.

Macropodidae (Kangaroo kind)

***Size:** head and body 100cm (39.3in); tail varies, but shorter than head and body; females slightly smaller*

This family includes 65 species placed in 11 genera (Wilson and Reeder 2005). This family is also characterized by a complex stomach. Hybrid data clearly connect three genera (*Macropus*, *Thylogale*, *Wallabia*; Gray 1972; Van Gelder 1977). The genus *Setonix*, which consists of a single species, is reputed to have crossed with a species of *Macropus* at the Perth Zoo, though it has not been published and verified (Close and Lowry 1990). Hybrids within the genus *Petrogale*, which is considered closely related to *Thylogale*, are interesting because despite differing karyotypes, some hybrid females were at least partially fertile (Close and Bell 1997).

The kind is again placed at the level of the family since these species group well together. Over half the genera of this family do not currently have hybrid data recorded. Some of this may be due to the fact that they are not housed together affording them the opportunity to interbreed. On the other hand, perhaps they are unable to do so. Either way, the hybrid data that we do have provides us with valuable information. According to current baraminological understanding, this is definitive evidence they are from a common created kind. Variability among these species in morphology, serology, karyology, etc. can be examined in detail to give us a better understanding of which characteristics vary within kinds, and how they vary. With regard to morphology, Hume (1999, 352) describes variation in body size, diet, dentition, and foregut morphology between various macropods, including some identified above as having hybrid data. Further detailed investigation may prove useful in identifying the level of the kind in other marsupial orders where the family level does not match a strong cognitum.

Fig. 24. Red kangaroo (*Macropus rufus*). Rileypie, "RedRoo," https://commons.wikimedia.org/wiki/File:RedRoo.jpg, Public Domain.

EUTHERIANS

Order Afrosoricida

This order includes two families in separate suborders, the tenrecs (Tenrecidae) and the golden moles (Chrysochloridae; Wilson and Reeder 2005). At one time these small mammals were placed in the order Insectivora, alongside the families which contain true shrews, moles, and hedgehogs. Molecular evidence showed that these two families were similar to each other and more similar to animals of other African orders, including aardvarks (Tubulidentata) and elephants (Proboscidea), than to other members of Insectivora (Stanhope et al. 1998). Thus they were placed together in a separate order.

Tenrecidae (Tenrec kind)

***Size:** head and body 14cm (5.5in); tail ~10cm (~3.9in)*

The members of this family vary in body sizes and shapes and many bear a striking superficial resemblance to members of other taxa. Many are shrew-like (*Microgale* spp. and *Geogale aurita*), some are mole-like and adapted for burrowing (*Oryzorictes* spp.), and several are like hedgehogs (*Setifer setosus* and *Echinops telfairi*) except that their quills are barbed. While most species are limited to Madagascar, the otter shrews (*Potamogale velox* and *Micropotamogale* spp.) are semi-aquatic and found in other regions of Africa (Nowak 1999; Symonds 2005). Some species of tenrecs store fat in their tail and are known to undergo torpor (Marshall and Eisenberg 1996; Nowak 1999).

Although molecular evidence suggests Tenrecidae are not related to true shrews (Soricidae), moles (Talpidae), or hedgehogs (Erinaceidae), their grouping as a family seems fairly consistent. They are currently divided into three subfamilies, two of which are quite diverse morphologically. One genus, *Microgale*, displays considerable karyotypic diversity (Gilbert et al. 2007).

Based on available photos and descriptions, no clearly discernable cognita below the family level were identified that were consistent with current taxonomic placement. For example, the otter shrews (Potamogalinae) have similarities with the web-footed tenrec (Oryzorictinae) in body proportions and habitat. Further, members of the genus *Microgale* (Oryzorictinae) are very similar in appearance to *Tenrec ecaudatus* (Tenrecinae) except that the latter species lacks a tail (Nowak 1999). This enigmatic group has posed some serious challenges for taxonomists, and it highlights important questions that creationists will need to address as well.

If these creatures are indeed a distinct kind, why do they have so many similarities to other kinds? Did one kind undergo post-Flood diversification so they now resemble one or more other kinds of animals? Which morphological features are most important in inferring created kind status? Which features tend to vary within a created kind? Further, it could also be asked if the molecular data is really as informative as it is assumed to be. Are the molecular differences that resulted in removal of Tenrecidae from Insectivora really indicative that they are from a separate kind? To answer this latter question we need more information on molecular variability within created kinds.

Wood (2008a) analyzed a dataset compiled to evaluate Tenrecidae phylogeny. It included cranial, dental, and postcranial characters from all ten extant tenrecid genera and 25 outgroup taxa. The tenrecids formed a group united by significant, positive baraminic distance correlation (BDC). Some tenrecids were positively correlated with some outgroup taxa. Another group united by significant, positive BDC included such diverse taxa as marsupials and carnivores. Interestingly, the baraminic distance between two marsupial genera *Macropus* (kangaroos and wallabies) and *Didelphis* (opposums) was greater (0.333) than the distance between *Didelphis* and the African palm civet *Nandinia*, a carnivore (0.222). Given that all three genera are likely unrelated, this is not necessarily a surprise for a creationist. However, because of the odd patterns in the results, Wood conservatively suggested that the tenrecids may be a monobaramin, but cautioned that such a conclusion might be dubious.

Recently a paper was published examining placentation in one member of each of the subfamilies of Tenrecidae as well as members of other taxa that had once been part of Insectivora (Carter and Enders 2010). Though it would be advantageous to have information on more members of this family, it does highlight the fact that this is another important anatomical area that needs evaluation. How much variation can there be in placentation within a created kind? Are there aspects of placentation that may be helpful in distinguishing between created kinds?

Fig. 25. Tenrec (*Tenrecidae*). Stephencdickson, "A Tenrec In A Defensive Mode, Horniman Museum, London," https://commons.wikimedia.org/wiki/File:A_tenrec_in_defensive_mode,_Horniman_Museum,_London.jpg, CC BY-SA 4.0

Chrysochloridae (Golden mole kind)

Size: *head and body 15cm (5.9in); no visible tail*

Golden moles are much less variable phenotypically than members of Tenrecidae, but they still raise similar questions given their resemblance to other mammalian taxa. Like Tenrecidae, they have a cloaca, which is relatively rare for eutherians. They superficially resemble moles (Talpidae), but lack a tail and have tough skin with thick fur that appears to have a metallic luster, from which the family name is derived. They appear to have several unique features for a mammal: three, rather than two, long bones in the forearm and a hyoid-dentary jaw articulation (Nowak 1999; Symonds 2005). Karyotypic diversity appears to be relatively low (Gilbert et al. 2006). Their resemblance to the marsupial mole has already been discussed.

Fig. 26. Golden mole (*Chrysochloris*). Killer18, "Taupe Doree," https://commons.wikimedia.org/wiki/File:Taupe_doree.jpg, CC BY-SA 3.0.

Order Macroscelidea

Macroscelididae (Elephant shrew kind)

Size: *head and body 20 cm (7.8 in); tail ~18 cm (7 in)*

Elephant shrews were also at one time in the order Insectivora, but were removed after more detailed study. These small mouse- to rat-sized creatures have a long flexible proboscis from which they derive their common names. The hind legs are longer that the forelegs, allowing them to hop when moving rapidly (Nowak 1999). There is a strong cognitum at the family level.

One species in this family, the golden-rumped elephant shrew (*Rhynchocyon chrysopygus*), has some relatively unique features that bring up some important issues. The largest of the elephant shrews, its back is rounded (convex) with the rump higher than the shoulders. This gives it an overall body form that has been compared to a miniature duiker or dik-dik, ruminants in the same family as cattle (Bovidae). Further, unlike most elephant shrews, *Rhynchocyon* have upper incisors that are rudimentary or absent. Ruminants, which include Bovidae and several other families, are characterized by the absence of upper incisors. Finally, *Rhynchocyon chrysopygus* has been described as having very ungulate-like anti-predatory behavior (Rathbun 1979).

There are numerous other anatomic details that clearly distinguish elephant shrews from ruminants, but the superficial similarities of some members of these two groups hint that creationists will have to deal with the pesky problem of convergence. In other words, creatures descended from completely different created kinds appear to have developed similarities as they have adapted to fill the earth. This is likely to make discerning created kinds more of a challenge, and may have contributed to some of the taxonomic challenges that have been described so far.

Fig. 27. Black and rufous elephant shrew (*Rhynchocyon petersi*). Joey Makalintal from Pennsylvania, USA, "Rhynchocyon Petersi from Side," https://commons.wikimedia.org/wiki/File:Rhynchocyon_petersi_from_side.jpg, CC BY-SA 2.0.

Order Tubulidentata

Orycteropodidae (Aardvark kind)

Size: *head and body 130 cm (51.1 in); tail ~60 cm (23.6 in)*

There is only one extant species of this order, *Orycteropus afer*. The name aardvark means "earth pig" in Afrikaans. This is an apt description for this medium-sized mammal has a stocky body with a short neck and arched back. It is a powerful digger and lives in burrows. It has a long snout, large ears, and a long muscular tail (Nowak 1999; Shoshani, Goldman, and Thewissen 1988).

This order and the previous two orders (Afrosoricida and Macroscelidea) are now placed in the supraorder Afrotheria along with the following two orders (Hyracoidea and Proboscidea) and sea cows (Sirenia; Wilson and Reeder 2005). The molecular similarities observed in these animals are intriguing given that all but the aquatic sea cows are found primarily in Africa. There is the possibility that some convergent evolution has taken place as these creatures have adapted to living in a similar region of the world. More information on within kind variability on a molecular level is needed to explore this possibility.

Fig. 28. Aardvark (*Orycteropus afer*). Leptictidium, "Porc Formiguer," https://commons.wikimedia.org/wiki/File:Porc_formiguer.jpg, CC BY 2.5, cropped from original image by MontageMan, "Porcs Formiguers (Orycteropus Afer)," CC BY-SA 2.5.

Order Hyracoidea

Procaviidae (Hyrax kind)

Size: *head and body 45 cm (17.7 in); tail ~20 cm (7.87 in)*

Extant species are similar in size and external appearance to rodents and lagomorphs, though some extinct forms were much larger. The soles of the feet have unique naked pads with a central portion that retracts to form a suction cup. This region is kept moist by glandular secretions and allows for excellent traction. The three extant genera form a strong cognitum. While currently evolutionists believe these creatures are most closely related to elephants and sea cows, some have argued that they are closer to odd-toed ungulates (Perissodactyla) based on morphology and fossil evidence (Nowak 1999). Given the morphologic discontinuity between these creatures and their proposed evolutionary relatives, the level of the kind seems to naturally fall here.

Extinct members of this order show more variability and a second family is recognized (McKenna and Bell 1997; Nowak 1999). These latter factors should be considered in future research on this group.

Fig. 29. Yellow-spotted hyrax (*Heterohyrax brucei*). D. Gordon E. Robertson, "Yellow-Spotted Rock Hyrax," https://commons.wikimedia.org/wiki/File:Yellow-spotted_Rock_Hyrax.jpg, CC BY-SA 3.0.

Order Proboscidea

Elephantidae (Elephant kind)

Three extant species in two genera are recognized (Wilson and Reeder 2005). Both Asian and African elephants have five toes on each foot, but they vary in the number of digits that have hooves (nails). Both generally have five on the front feet, but Asiatic elephants vary from four to five on the hind feet. African elephants have only three nails on the hind feet (Nowak 1999).

Elephants have some unusual features compared to other large domestic animals. They have a lower normal body temperature (35.9°C; Benedict and Lee 1936) and the testes remain in the abdomen of the males. The females have a pair of mammary glands just behind the front legs (Nowak 1999), rather than near the rear legs.

There is hybrid data connecting the African elephant genus with the Asian elephant. Creationists have recognized the extinct mammoths and mastodons as members of this kind as well (Oard 2004; Sarfati 2000).

Order Cingulata

Dasypodidae (Armadillo kind)

Armadillos are unique mammals with skin that is modified to contain a double-layered covering of horn and bone over the more exposed areas of the animal, serving like armor (Nowak 1999). Wilson and Reeder (2005) recognize 21 extant species in nine genera. They had been placed in two subfamilies with one containing only the genus *Chlamyphorus*, and the remaining genera in the other. More recently

Fig. 30. Asian elephant (*Elephas maximus*). The elephant kind includes African and Asian elephants. Yathin S Krishnappa, "Elephas Maximus (Bandipur)," https://commons.wikimedia.org/wiki/File:Elephas_maximus_(Bandipur).jpg, CC BY-SA3.0.

it was divided into three subfamilies, with the genus *Dasypus* in one, and several genera in each of the other two.

Wood (2008a) analyzed a dataset containing craniodental characters from various members of this order with two members of the order Pilosa as an outgroup. Most of the species were from extant or extinct genera within one of the three subfamilies, namely Euphractinae (McKenna and Bell 1997). There was significant, positive BDC and high bootstrapping values within Euphractinae. One species of a second subfamily, *Dasypus* of Dasypodinae, showed significant positive BDC with this group, though the bootstrap values were lower. A second member of Dasypodinae, *Stegotherium*, showed negative BDC with most of the group (all except *Dasypus*). The one species from the third subfamily, *Priodontes* of Tolypeutinae, didn't show significant positive or negative BDC with other taxa.

Unsurprisingly, the outgroup taxa from the order Pilosa showed significant negative BDC with most of the other taxa. What is surprising is that one fossil taxa that is normally placed in a separate superfamily within Cingulata (McKenna and Bell 1997), *Vassallia*, had significant positive BDC with most of the Euphractinae, and significant negative BDC with the outgroup. This is a bit unexpected given that it appears closer to members of Euphractinae than some of the other taxa which are classified in the same family as Euphractinae! For a more detailed evaluation of this dataset, the reader is referred to Wood (2008a).

From a cognitum perspective, the genus *Chlamyphorus* appears most unique. It is rather unsurprising that at one time it was placed in its own subfamily. However, this is not where it is generally placed today and the statistical baraminology analysis shows it fits well in its current placement in Euphractinae. Thus it seems the kind naturally falls at the family level, with some suggestion that extinct taxa from other families in this order may be included as well.

There is some rather interesting variation among extant members of Cingulata. The snout varies considerably in length and though most species have 7–9 teeth in each half jaw, the giant armadillo *Priodontes* may have more than 40. The forefeet have three, four, or five digits with powerful claws that make armadillos excellent diggers. The hind feet consistently have five digits with claws (Nowak 1999). The nine-banded armadillo, *Dasypus novemcinctus*, is described as having a simplex uterus like humans and primates (McBee and Baker 1982). The six-banded armadillo, *Euphractus sexcinctus*, is said to have a bicornate uterus (Redford and Wetzel 1985), the type found in cattle.

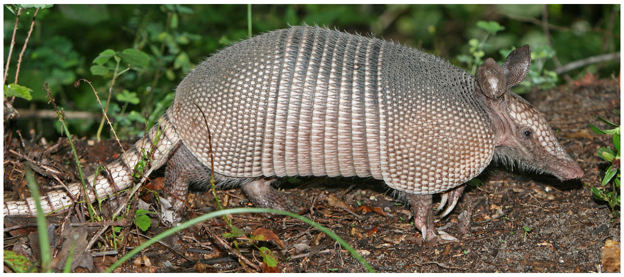

Fig. 31. Nine-banded armadillo (*Dasypus novemcinctus*). http://www.birdphotos.com, "Nine-Banded Armadillo," https://commons.wikimedia.org/wiki/File:Nine-banded_Armadillo.jpg, CC BY-SA 3.0.

Order Pilosa

This order and the previous one (Cingulata) belong to the superorder Xenarthra. Previously, Xenarthra was considered an order and sloths, anteaters, and armadillos were placed in three separate superfamilies. Xenarthra are distinguished from all other mammals by their xenarthrous vertebrae which have secondary articulations between them in the lumbar region. The ischium (bone of the pelvis) also articulates with the sacrum. All living members are found in the Americas and lack incisors and canines (Nowak 1999).

Xenarthra are also united in having long, sharp, strong claws on their digits. The females have a common urinary and genital duct. The males retain the testes in the abdomen between the bladder and the rectum. These shared features are not exclusive to this group.

Despite their distinctive morphology, studies place the anteaters and sloths closer to each other than to the armadillo (Nowak 1999). Thus they are now placed together in the order Pilosa (Wilson and Reeder 2005).

Suborder Folivora (Sloth kind)

Sloths are very distinctive creatures. There are two extant genera, both of which are arboreal (Nowak 1999; Wilson and Reeder 2005). They move very slowly and spend most of their lives hanging upside down from a tree limb. The digits are syndactylus, being bound together by skin. There are three long, sharp claws that extend from each hindfoot. Depending on the genus, there are two (*Choloepus*) or three (*Bradypus*) claws on the forefeet. The forelimbs are longer than the hindlimbs, a trait more pronounced in *Bradypus* (Nowak 1999).

The hair on sloths is directed dorsally, which helps direct water off their body as they hang inverted on a tree limb (Nowak 1999). Depending on the genus, the hairs have deep longitudinal grooves (*Choloepus*) or irregular transverse cracks (*Bradypus*) that allow for the invasion of various microorganisms and small invertebrates. Most notable is green algae, which give the animal a greenish coloration that serves as