



ANSWERS RESEARCH
MONOGRAPH SERIES 1
BARAMINOLOGY



EXTANT ARK KINDS

Amphibian and Reptile Kinds

VOLUME 2

Dr. Andrew A. Snelling | Editor

Extant Ark Kinds



ARMS

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EXTANT ARK KINDS AMPHIBIAN AND REPTILE KINDS

ANDREW A. SNELLING, *Editor*



Petersburg, Kentucky, USA

Answers Research Monograph Series
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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.

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FEBRUARY, 2018

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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.

The underlying Hebrew word for kind here is מִין, *mîn*. It, along with the Hebrew word for create (בָּרָא, *bārāʾ*), 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 מִין is a technical term (Turner 2009; Williams 1997). Both Williams (1997) and Turner (2009) suggest that מִין 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 (זָרַע, *zeraʾ*), 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; זָרַע, *zeraʾ*). Word-for-word translations render זָרַע 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 מִין 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

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

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 underestimating the number of kinds represented on the Ark.

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

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

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

to divide the birds up for taxonomic purposes. This seems a reasonable explanation for why the statistical tests based on that dataset divided birds that were connected by hybrid data.

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

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

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

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

Soli Deo Gloria!

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An Initial Estimate Toward Identifying and Numbering Amphibian Kinds within the Orders Caudata and Gymnophiona

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Abstract

Biosystematics is in great flux today because of the plethora of genetic research continually shedding light on organism relationships. Despite the large amount of data being published, the challenge is having enough knowledge about genetics to draw conclusions regarding the biological history of organisms and their taxonomy. Despite these uncertainties, an initial attempt to count and identify biblical kinds in amphibian orders Caudata and Gymnophiona were estimated using current information and several key assumptions and guidelines. They include focusing on monophyly based on morphological and genetic characters, maintaining taxonomic stability, relying on authors who demonstrate expertise in systematics, considering the usefulness and general acceptance of nomenclature, using hybridization data as evidence that organisms are of the same kind, and using statistical baraminology as a tool to assess significant holistic continuity and discontinuity amongst and between organisms. With the above parameters, and ever changing systematics data from extant amphibians, a cautious estimate suggests that Noah had 53 extant Caudate kinds and 1 extant Gymnophionan kind on the Ark. In no way is this the final word and much baraminological research must be done to improve the precision of these estimates.

Keywords: Ark Encounter, baraminology, biosystematics, Lissamphibian, Caudata, Gymnophiona, Caecilian

Introduction

Creation research is guided by God's Word which is foundational to the scientific models that are built. As Christian scientists, we believe God has communicated important highlights of earth history, such as the worldwide Flood described in Genesis 6–9, and which is consistent with the geological data (Snelling 2009). The Flood of Noah has many implications that must be considered when building a Creation model of biology. In light of these implications, The Ark Encounter Project has tasked creation researchers to investigate several questions, some of which include:

- What did God mean by kind when He told Noah to bring two of each and seven—sevens of clean animals on board (Turner 2009; Williams 1997)?
- How have organisms diversified from their Ark ancestors (Wood 2003)?
- How can the Ark kind be recognized from today's organisms (Brophy and Kramer 2007, 10–11; Lightner et al. 2011; Sanders and Wise 2003)?
- How many kinds were taken on board the Ark (Woodmorappe 1996)?

The purpose of this paper is to make an initial estimate of the identification and number of the kinds taken on board the Ark using all available information. Here I address extant amphibian Orders; Caudata (salamanders) and Gymnophiona (Caecilians or worm-like amphibians) and explain the rationale

for my conclusions. Future papers will address the extant Anuran kinds (frogs and toads) and the extant sauropsids that include lizards, tuataras, crocodiles, snakes, and turtles.

The State of Biosystematics and Taxonomy Today

Biosystematics is the science of discovering, classifying, and organizing biological diversity. The science of identifying taxa and naming organisms is taxonomy. There is no universally accepted procedure for organism classification (Amphibiaweb 2013). Currently, these disciplines are in great flux as researchers are putting more importance on new genetic data being accumulated for phylogeny development and much is being changed accordingly. Therefore, how organisms are named and organized today may change tomorrow. Major sources for amphibian classification include; Blackburn and Wake (2011, 38–54); Dubois (2005); Duellman (1999); Duellman and Trueb (1986); Frost (1985); Frost et al. (2006) and Pyron and Wiens (2011). Herpetologists at Amphibiaweb (2013), using these sources, have outlined the following criteria for their taxonomic recommendations:

- Of primary importance is to focus on monophyly and identify the clade consisting of species and their descendants based on morphological and genetic characters.

- Maintain stability as it pertains to the association of names and their taxa.
- Rely on authors who demonstrate expertise in systematics.
- Consider the usefulness and general acceptance of nomenclature by amphibian researchers.
- Focus on “tree” thinking rather than nested hierarchies.

Refining the Baraminological Research Approach

Since Frank L. Marsh (1899-1992) coined the term *baramin*, much has changed in creationist approaches toward the study of the created kind or baraminology. For a full discussion of the history of baraminological research, concept development, defined terms, and statistical analysis see Wood et al. (2003). For the purposes of this monograph, let us identify and define the concepts and terms that reflect a refined baramin concept (Wood et al. 2003). Key terms for this discussion include continuity and discontinuity. If God created distinct organisms that are not genetically related, then one of the tasks of creation research is to detect discontinuity, a foreign concept to naturalists because of their belief in universal common ancestry. Discontinuity is defined as significant, holistic differences between two organisms. Holistic is most important in that it is beneficial to obtain as much data about organisms, from all different perspectives (e.g., anatomical, morphological, behavioral, genetic, developmental) so that significance is better statistically quantified. At the same time, continuity between two organisms (defined as having significant holistic similarities) must also be detected. For example, the ability to hybridize between taxa suggests that creatures have holistic and significant similarity at the anatomic, genetic, and developmental levels that allow them to produce offspring. In this light, a monobaramin is a group of known organisms that share continuity with other organisms, an apobaramin is a group of known organisms surrounded by discontinuity with others, and a holobaramin is a group of known organisms that share continuity with at least one other member and bounded by discontinuity. The *baramin* is a theoretical idea that describes any organisms that have existed in earth history. Unfortunately, studies in quantifying the holobaramin are sparse, but where they have been done, they will be referenced in this paper.

Though there are taxonomic overlaps with baraminologists and naturalists at Amphibiaweb, creation biologists differ in our assumptions in that we focus on “forest” thinking (rather than tree thinking) and are interested in how creatures have diversified from the originally created baramins and more specifically, the archetypes that left the Ark.

Below is an outline of baraminological guidelines, in descending priority:

Creation biologists differ in our assumptions in that we focus on “forest” thinking and are interested in how creatures have diversified from the originally created baramins and more specifically, the archetypes that left the Ark. Though there are overlaps with the above criteria, Lightner et al. (2011) outline the following guidelines, in descending priority, from a baraminological perspective:

- Assess characters to determine significant holistic continuity and discontinuity amongst and between organisms using statistical baraminology (Wood 2006a, 2006b).
- Biblical evidence suggests that living things reproduce after their kinds and therefore the ability to hybridize in extant creatures suggests that they are the same “kind” (Genesis 1 and 7). Baraminologists consider hybridization as a special category of biological significance and recognize the limitations of hybridization assessment. For example, there are many reasons why taxa can become reproductively isolated but that doesn’t mean they were not part of a created “kind” in the past.
- Identify the cognitum because God created His image bearers with the ability to group things together through human cognitive senses (Sanders and Wise 2003).

For the purposes of this paper, all of the above considerations will be considered while incorporating the following precautions. Baraminologists tend to equate kinds with the family, and for many cases with good reason (Wood 2006a). However, we should carefully analyze the structures, behaviors, and physiologies of members of a putative kind and look at the genetic reasons why a certain member of a kind doesn’t have characters that the other members possess. When we better understand what mechanisms are involved in the production of the above characters, creation biologists will make more reasoned inferences about whether they were produced by post-Flood diversification through unknown genetic preprogrammed mechanisms or by direct creation. These considerations will affect the estimated number of kinds hypothesized. In the case of Caudates, there is a large variation within families and there will be an attempt to balance between lumping and splitting taxa. There will be cases where I will split because the genus seems to be the obvious cognitum and the reasons for variation are unknown. There will be other cases where I will lump and default to the Family or Order because they may be made of only one genus and/or there is hybridization, statistical baraminology and/or strong cognita that connects members.

Superclass Tetrapoda, Class Amphibia

Amphibians are non-amniotic tetrapods which are four-legged vertebrates lacking an amniotic membrane that surrounds and builds the amniotic sac of reptile, bird, and mammal embryos. Amphibians also include members with reduced and/or absent legs. The word amphibian carries the idea of having two modes of existence or “two-lives” and refers to having both a water and land stage in their life cycle. The reality is that though many do have lives divided this way; many others do not (table 1). Subclass Lissamphibia are the extant amphibians and are further subdivided into three orders; Caudata, Anura, and Gymnophiona. *Liss* refers to their smooth, scaleless skin that is crucial for respiratory gas exchange and is a derived character. Other derived characters include bicuspid teeth, unique pedicellate teeth where the crown and base are made of dentine and have an uncalcified zone at the base, poison and mucous skin glands, a single element vertebral centrum, and reduced bones at the top of the skull. All are ectothermic and because their skin easily absorbs water, they don’t need to drink. Lissamphibians are also known for having the largest range of genome size variability among terrestrial vertebrates (Litvinchuk, Borkin, and Rosenov 2004). Currently it is estimated that there are over 7000 species of Lissamphibians and at least 32% are being threatened with extinction for a host of reasons including habitat destruction (International Union for Conservation of Nature and Natural Resources 2012).

The tailed amphibians (Order: Caudata) include salamanders and newts and consists of two suborders (Salamandroidea with eight Families and

Cryptobranchoidea with two) (table 1). All together they consist of 600 species or 9% of all amphibians (Amphibiaweb 2013). Diploid chromosome numbers (2N) and many other characters may vary both between and within Families (Larson, Wake, and Devitt 2006). Salamander bodies are elongate with most having four legs and a tail, and others having reduced and/or two absent appendages. Some species are obligate water creatures from egg to adult. Others must live on land for the length of their lifetime. Still others may begin as aquatic, gilled larvae and finish their lives as terrestrial, lunged, or lungless, adults. Salamanders are being extensively studied for their ability to regenerate full limbs after they are severed and this research has important implications for human medicine (Kragl et al. 2009).

Caecilians, Latin for *caecus* meaning blind and referring to their small or non-existent eyes, are in the Order Gymnophiona. Gymnophiona, Greek for *gymnos* (naked) and *ophis* (snake) comes from a time when members were called naked snakes because they did not have outer scales. They are probably the least known amphibian order and are fossorial (adapted for terrestrial digging and burrowing) or aquatic creatures characterized by their legless, elongate bodies that resemble earthworms to some and snakes to others (Pough et al. 2004, 8). This Order currently contains ten families, 191 species, and represents 3% of all Lissamphibians. What follows is a description of each delineated salamander and caecilian kind, average total lengths, various unique characters, and the rationale behind their baraminic classification.

Table 1. A sampling of behavior and characters across families within Order Caudata.

Behavior/Characters	Suborder: Salamandroidea						Suborder: Cryptobranchoidea			
	Ambystomidae	Amphiumidae	Salamandridae	Dicamptodontidae	Plethodontidae	Proteidae	Rhyacotritonidae	Sirenidae	Hynobiidae	Cryptobranchidae
Current Number of Species	32	3	94	4	431	6	4	4	54	3
Interspecific Hybridization	yes	yes	unknown	yes	yes	unknown	unknown	unknown	unknown	yes
Fertilization	internal	internal	internal	internal	internal	internal	internal	internal	external	external
Neoteny	varies/inducible	obligate	facultative	facultative	varies/inducible	obligate	no neoteny	obligate	facultative	obligate
Parental Care of Eggs	female A. opacum	females	not reported	females	females, sometimes males	males or females	none	females	males	males
Average Total Length [TL] (cm)	14	55	15	24	10	25	6	40	13	75
Diploid Number (2n)	28	28	22 or 24	28	26 or 28	38	26	46, 52, or 64	40, 56, 60, or 62	60, 62, or 64
Respiratory Structures										
lungs	present	present	reduced	present	ABSENT	present	reduced	present	Present except Onychodactylus	present
ypsiloid	present	absent	present	present	absent	absent	present	absent	Present except Onychodactylus	present
larval gill slits	3 pairs	3 pairs	4 pairs	4 pairs	3 or 4 pairs	2 pairs	4 pairs	1 or 3 pairs	4 pairs	4 pair
adult gills	variable	1 pair gill slits	variable	variable	variable	present	none	external gills	none	absent
Skull Morphology										
lacrima bone	absent	absent	absent	present	absent	absent	present	absent	present	absent
premaxillae	separate	fused	single or separate	separate	paired or fused	separate	separate/paired	separate/paired	separate/paired	separated/paired
septomaxillae	present	absent	absent	absent	absent	absent	present	absent	absent	absent
naso-labial grooves	absent	absent	absent	absent	present	absent	absent	absent	absent	absent
operculum	present	absent	present	present	present	absent	absent	absent	absent or absent	absent
symphyseal cartilage	absent	absent	absent	absent	absent	absent	absent	absent	absent	present
pterygoid	reduced	reduced	present	present	present in larvae	present	reduced	small	absent	present
Trunk and Vertebrae										
limbs and toes	present	reduced	present	present	present	reduced	present	no hind limbs	present	present
scapula/caracoid bone of pectoral girdle	fused	reduced	fused	fused	fused	fused	fused	separate	fused	fused
ribs	bicapitate	bicapitate	bicapitate	bicapitate	bicapitate	bicapitate	bicapitate	bicapitate	unicapitate	unicapitate

Order Caudata—The Salamanders and Newts

A phenomenon common to salamanders is a process called neoteny. Neoteny (neotenic) is a word derived from the Latin referring to extended larval life, and is a process observed in many animals where adults retain juvenile characteristics. A type of neoteny found in salamanders is paedogenesis in which sexual reproduction can occur in individuals who retain a juvenile phenotype and do not fully metamorphose into terrestrial adults. These individuals are called paedomorphs. There are three types of neoteny; obligate neoteny, where all members retain their juvenile characteristics when they become adults. Obligate neotenes include all members of Amphiumidae, Sirenidae, Cryptobranchidae, and Proteidae. Inducible obligate neoteny happens when some members in Ambystomatidae and Plethodontidae can be induced to metamorphose into sexually mature terrestrial adults by manipulating the thyroid function in the laboratory or adding iodine to the environment. Facultative neoteny occurs when individuals may or may not be paedomorphic depending on environmental variables. This has been observed in Salamandridae, Dicamptodontidae, Hynobiidae, Plethodontidae, and Ambystomatidae (table 1).

Order: Caudata—Suborder Cryptobranchoidea

Cryptobranchoidea is a salamander suborder containing two Families, Cryptobranchidae and Hynobiidae. Among the major reasons they have been separated from the other eight families is because fertilization is external, like most fish, and lower jaw bones differ significantly. Consequently, they are called “primitive” salamanders.

Family Cryptobranchidae (Giant Water Salamander Kind)



Fig. 1. Giant water salamander (*Andrias japonicus*). Daiju Azuma, “*Andrias Japonicus*,” https://commons.wikimedia.org/wiki/File:Andrias_japonicus.jpg, CC BY-SA 2.5.

Cryptobranchidae consists of two genera (*Andrias* and *Cryptobranchus*) and three aquatic species. They have gills as larvae and lose them through partial metamorphosis when they reach adulthood. Though they have lungs, most of their respiration occurs by oxygen diffusion through skin and are therefore

dependent on oxygen rich, turbulent streams in the wild (Jensen et al. 2008, 153). This family contains the largest salamanders in the world with an average total length of 75cm (29.5in). The hellbender (*Cryptobranchus alleganiensis*) is restricted to eastern North America and has an average total length of 50cm (19.6in) (Petranka 1998). The other two Asiatic species live in Asia. The Japanese giant salamander (*Andrias japonicus*) and the Chinese giant salamander (*A. davidianus*) can reach an average total length of 100–120cm (39–47in) and live 50 to 75 years in captivity (Larsen, Wake, and Devitt 2006). The Japanese giant salamander is revered and protected in Japan, but for many, the meat is considered a delicacy. To get around the protected status of *A. japonicus*, *A. davidianus* was introduced to Japan so that its meat could be sold at market (McNeil 2010). Consequently it is now considered an invasive species because *A. davidianus* is hybridizing with *A. japonicus* and there is mounting concern that the species “purity” of the Japanese giant salamander will be lost (McNeil 2010). From a biblical worldview, their hybridization ability connects them as the same kind.

Cryptobranchids have a unique caudate structure called a symphyseal cartilage which gives them the flexibility to suction feed with the left or right side of the mouth in their aquatic habitat (Amphibiaweb 2013). Adults are fully aquatic and reproduce by external fertilization, but they also have the ability to move across land (though rare) and gulp air. Other characters they share include; unicapitate ribs that have one head (facet) connecting to vertebrae, small lacrimal bones on the face are absent, prootic and exoccipitals skull bones are separate, fleshy skin folds are numerous, and the spiracle (external respiratory orifice in larvae) remains open in adults (Amphibiaweb 2013).

Fossils with very similar morphology as *Andrias* have been found in Cenozoic strata of the late Eocene to early Pliocene (Vasilyan, Böhme, and Winklhofer 2010) which suggests that this morphology may be a result of post-Flood diversification, if we assume the pre-Flood/post-Flood strata is denoted at the Cretaceous-Paleogene (K-Pg) boundary (Austin et al. 1994). Captive breeding and care has been done for many decades and it is possible that their archetype could have survived on the Ark. Therefore, because of their current systematics, having lungs, an ability to minimally maneuver on land, and the ability to breed in captivity, I include them on the Ark as the giant water salamander monobaramin, until further research clarifies their taxonomic relationship with other caudates.

Family Hynobiidae (Asiatic Salamander Kind)



Fig. 2. Hida salamander (*Hynobius kimurae*). Eugene van der Pijll, “Hynobius Kimurae (cropped) edit,” [https://commons.wikimedia.org/wiki/File:Hynobius_kimurae_\(cropped\)_edit.jpg](https://commons.wikimedia.org/wiki/File:Hynobius_kimurae_(cropped)_edit.jpg), CC BY-SA 2.5.

Family Hynobiidae is the other taxon of salamanders that fertilize eggs externally and current genetic data place them as a sister group of Cryptobranchidae (Amphibiaweb 2013). They are divided into two subfamilies, the Protohynobiinae (*Protohynobius*) and Hynobiinae which consists of the other nine genera. All together there are 54 species of small to medium size salamanders, endemic only to Asia, with an average total length of 12cm (4.7in). During the breeding season, males undergo a substantial increase in head width (Pough et al. 2004, 48). Larvae are aquatic, and even though facultative neoteny has been observed, most metamorphose into sexually mature terrestrial adults with eyelids, well-developed lungs (except genus *Onychodactylus* that consists of two species of lungless terrestrial salamanders) and no gill slits. Adults in genera *Batrachuperus*, *Liua*, and *Pachyhynobius* are exceptions to the terrestrial mode and are aquatic (Larson, Wake, and Devitt 2006). As a cognitum, they are easily distinguished from all other Asian salamanders which suggest that they are a kind. There are no synapomorphies for this group, but they do share the following characters: septomaxillae (bones on the front of the upper jaw), lacrimals, vomerine teeth are not parallel to marginal teeth, and ribs are unicapitate (Amphibiaweb 2013). I did not find any records of interspecific hybridization in the family, though I would expect that it occurs. More research in this area would be helpful in clarifying family relationships. I include them as the Asiatic salamander monobaramin because of several holistic similarities that may be significant. It is also possible that with further research they could be incorporated into the cryptobranchids because of sister group relationships.

Order Caudata—Suborder Salamandroidea

The remaining eight families described below belong to suborder Salamandroidea, or the “advanced” salamanders. Characters differ with Cryptobranchoidea in their jaw bone structures and reproductive behavior. Males produce spermatophores, which are little structures that house sperm, and they deposit them in their habitat. The male leads or coaxes an interested female over the deposited spermatophore. She then grasps it with the lips of her cloaca, and stores the sperm in an out-pocketing of her cloaca. As eggs pass through the cloaca they are internally fertilized. Females will deposit fertilized eggs either in water or on land, depending on the species. A few salamander species are viviparous and give birth to fully metamorphosed juveniles.

Family Ambystomatidae (Mole Salamander Kind)



Fig. 3. Spotted salamander (*Ambystoma maculatum*). Photograph courtesy of Larry Master, www.masterimages.org, “31F2001c Spotted Salamander (*Ambystoma Maculatum*),” http://www.masterimages.org/Amphibians/Spotted%20Salamander/slides/_31F2001c.jpg.

The mole salamanders contain one genus, *Ambystoma* and 32 species. They are endemic from southern Canada to Mexico and are characterized by rounded heads and broad bodies with conspicuous costal grooves, or skin folds, along their sides (Petranka 1998, 35). Statistical baraminology suggests that this family is a monobaramin and interspecific hybridization confirms this (Brophy and Kramer 2007, 10–11; Hennigan 2010; Petranka 1998, 122–129). Hybrids may be diploid, triploid, tetraploid, or pentaploid. Polyploidy in vertebrates is unique and unisexual populations consisting of females are a result and may include the following species; *A. texanum*, *A. tigrinum*, *A. laterale*, and/or *A. jeffersonianum*. Average mole salamander total length is 14cm (5.5in) and morphological characters connecting them include absent lacrimal bones, transverse oriented vomerine teeth (located on the roof of the mouth), and fused prootics, opisthotics and exoccipitals (small skull bones surrounding the inner ear) (Amphibiaweb 2013). The extinct genus

Amphitriton is known from the upper Pliocene, and fossils of the extant genus *Ambystoma* are known from the lower Oligocene, through the Pleistocene, in North America (Heying 2003).

Many mole salamanders begin as aquatic larvae which may metamorphose into sexually mature terrestrial adults with lungs like the spotted salamander (*Ambystoma maculatum*). Ambystomatid larval characteristics include, external gills, the presence of lateral line systems (sense organs used to detect underwater vibrations), and the absence of eyelids (Pough et al. 2004, 35). Some members are facultative neotenes or inducibly obligate neotenes. For example, the Axolotl (*Ambystoma mexicanum*), known for its importance in limb regeneration research (Kragl et al. 2009), is a neotene that is inducibly obligate and can metamorphose with thyroid hormones 3,5,3'-triiodothyronine (T3) and L-thyroxine (T4) in the lab (Page, Monaghan, and Walker 2009). T4 induced Axolotls will undergo metamorphic changes that include complete resorption of tail fins, gills, and dorsal ridges and will also experience reduced body mass and growth rate (Page, Monaghan, and Walker 2009). Other mole salamanders, depending on environmental variables, are facultative neotenes. I include the mole salamanders on the Ark because many have the ability to hybridize, they have a strong cognitum, and most adults are terrestrial with lungs. I identify the mole salamanders as a monobaramin because many can hybridize with one another. The data suggest, from both evolution and creation perspectives, that ambystomatid paedomorphs are recently derived from a metamorphic ancestor (Page, Monaghan, and Walker 2009; Voss and Smith 2005) and therefore ambystomatid neoteny is probably a post-Flood phenomenon.

Family Dicamptodontidae (Large Land Salamander Kind)



Fig. 4. Pacific giant salamander (*Dicamptodon tenebrosus*). Jeffrey Marsten, https://commons.wikimedia.org/wiki/File:Dicamptodon_tenebrosus_2.jpg, Public Domain.

Family Dicamptodontidae consists of one genus (*Dicamptodon*) and four species. Two extinct genera and the single extant genus are known from fossils in the North American Paleocene and the fossils of three extinct genera are known from the Paleocene and Miocene of Europe (Heying 2003). This Family contains the largest terrestrial salamanders with an average total length of 24cm (9.4in) (Amphibiaweb 2013; Petranka 1998, 145–156). Systematists have debated their taxonomic status for a long time (Petranka 1998, 145). Because of their strong cognita and other important characters, they used to be grouped with Ambystomatidae until recent years when they have been promoted to family status. I found one account of a breeder who has supposedly crossed *Dicamptodon tenebrosus* (Pacific Giant Salamander) with *Ambystoma tigrinum* (tiger salamander). However, because the claim is suspect, I have not found any reliable information that connects the two genera by hybridization and discount it until further evidence is gathered and verified.

Regarding interspecific hybridization within Dicamptodontidae, even though recent genetic comparisons between the Pacific giant salamander (*D. tenebrosus*) and the California giant salamander (*D. ensatus*) delineates them as separate species, they are connected by hybridization because they interbreed over a 4.7km (2.9mi) contact zone near Anchor Bay in Mendocino County, California (Amphibiaweb 2013). Gene flow is minimal and there is hybrid deficiency but the ability to interbreed suggests they are members of the same monobaramin. All four species in Dicamptodontidae are endemic to the western United States and southwestern British Columbia and live in forested habitats with fast moving, permanent streams (Amphibiaweb 2013; Petranka 1998, 145). Eggs hatch into aquatic larvae and generally metamorphose into terrestrial adults with lungs, though facultative neoteny has been documented. Adults are nocturnal, known to eat small mammals, have a “barking” noise, and shared characters that include “M” shaped vomerine teeth, lacrimal bones, and marbled dorsal patterns (Amphibiaweb 2013). It is quite possible Dicamptodontidae and Ambystomatidae are part of the same mole salamander monobaramin, especially because they share several holistic and possibly significant similarities. Now, I will denote them as the large land salamander monobaramin until further research clarifies their genetic relationships. However, keeping in mind the genetic and morphological data that distinguishes them, their current classification, and so that the number of kinds is not underestimated, I will denote them as the large land salamander kind until further research clarifies their relationship.

Family Rhyacotritonidae (Torrent Salamander Kind)



Fig. 5. Southern torrent salamander (*Rhyacotriton variegatus*). James Bettaso, U.S. Fish & Wildlife Service, https://commons.wikimedia.org/wiki/File:Rhyacotriton_variegatus.jpg, Public Domain.

The four species and one genus (*Rhyacotriton*) in Rhyacotritonidae (torrent salamanders) are small salamanders with an average total length of 6cm (2.3in). No fossils have been reported for this family and they used to be classified with Ambystomatidae and later moved to Dicamptodontidae until 1992 when it was recommended that they should be separate because of differences in biochemical and morphological characters (Good and Wake 1992). They reside in extreme western North America and adults are semi-aquatic producing fully aquatic larvae (Amphibiaweb 2013). Other shared characters include stocky build, eggs laid in cold water under rocks or in crevices, squared glands posterior to the vent, and a yellow green to bright yellow venter or belly (Amphibiaweb 2013). Their lungs are greatly reduced and they often have their vents resting in shallow water and/or always remain in saturated habitats. This is probably because *Rhyacotriton* species are probably the most desiccation intolerant salamanders known which suggests a high dependence on skin surfaces for oxygen diffusion (Amphibiaweb 2013). I was not able to locate hybrid data and much of the natural history for this family is unknown. Because of several significant similarities and the debate surrounding *Rhyacotriton*/*Ambystoma* systematics, I include them in the Ark as the torrent salamander monobaramin until future research sheds light on their taxonomy.

Family Amphiumidae (Congo Salamander Kind)

The aquatic Congo salamanders consist of one genus, *Amphiuma* with three species having an average total length of 55cm (21.6in). They are endemic to the coastal plain of the southeastern United States (Amphibiaweb 2013; Jensen et al. 2008;



Fig. 6. Two-toed amphiuma (*Amphiuma means*). Brian Gratwicke, “Amphiuma (Two-Toed),” [https://commons.wikimedia.org/wiki/File:Amphiuma_\(two-toed\).jpg](https://commons.wikimedia.org/wiki/File:Amphiuma_(two-toed).jpg), CC BY-SA 2.0.

Petranka 1998, 131). Eggs are usually laid on land under rocks or logs and near the water’s edge. Females coil around their 100 plus eggs and defend them until they hatch. Eggs are kept moist by their mother’s body and antibiotics produced by bacteria in her skin may protect them from harmful environmental fungi and bacteria (Jensen et al. 2008, 131). The length of the larval stage is variable and mostly unknown. Adults are paedomorphic and characters connecting them include laterally compressed tails, reduced pectoral and pelvic girdles, fused premaxillae (pair of small cranial bones on top of upper jaw), no eyelids, no tongue, open spiracle, lateral line systems, a single pair of gill slits, no external gills, reduced limbs, and lungs. They have variable numbers of toes per foot and this is one of the main characters that distinguish the three species. Members are the three-toed amphiuma (*Amphiuma tridactylum*), two-toed amphiuma (*A. means*), and one-toed amphiuma (*A. pholeter*) (Amphibiaweb 2013; Petranka 1998, 131). Amphiumidae contains a single extinct species in the genus *Proamphiuma* and is known from the Cretaceous (Larsen, Wake, and Devitt 2006).

Hybridization connects two of the three species (*A. pholeter* × *A. means*) in Louisiana with intermediate color patterns and toe numbers (Fontenot 2010). Some hybrid individuals had two toes on the front limbs and three on the back. These hybridization zones have highlighted the fact that amphiuman relationships are more complicated than researchers thought and much more genetic information is needed to shed light on their reproductive biology. I have included them on the Ark as the Congo salamander monobaramin because of their significant and holistic hybridization ability, in two of three species. They also have a unique ability to survive severe drought for up to three years by burrowing into the mud and secreting a mucous cocoon that encapsulates them (Amphibiaweb 2013; Jensen et al. 2008, 150).

Family Plethodontidae (The Lungless Salamanders)

Family Plethodontidae is the largest salamander group with 27 genera and 431 species having an

average total length of 10cm (3.9in). Their range extends from North, Central, and South America to Eurasia and they are subdivided into two subfamilies based on skeletal features and head muscles. Hemidactyliinae contains 20 genera and Plethodontinae has seven (Amphibiaweb 2013). Some members in Plethodontinae have aquatic larvae and other members have larvae that develop in eggs clustered under terrestrial rocks and logs. All salamanders in this family have no lungs and respiration takes place through their skin. Other shared characters include four fingers and five toes (with few exceptions), unique naso-labial grooves (grooves between each nostril and upper lip) used in chemoreception, absent pterygoids (structures on skull), absent lacrimals, and long bodies with up to 60 vertebrae (Amphibiaweb 2013). Fossils of six extinct genera are known from the North American lower Miocene to Pleistocene (Petranka 1998).

The family is quite diverse, for example, some can ballistically project their tongue to catch prey while others have web feet. Until further research sheds light on why they are so diverse, I default the kind to genus. It is probable that many will eventually be lumped into larger taxa in the future. This family may be a created kind, but until more light is shed on their taxonomy, I will break them down in the following way.

Subfamily Plethodontinae currently contains seven genera and 96 species.

A. Genus *Aneides* (6 species)

Climbing Salamander kind



Fig. 7. Climbing salamander (*Aneides lugubris*). Chris Brown, https://commons.wikimedia.org/wiki/File:Aneides_lugubris.jpg, Public Domain.

B. Genus *Desmognathus* (21 species)

Dusky Salamander kind

Many are linked by interspecific hybridization suggesting they are a monobaramin.

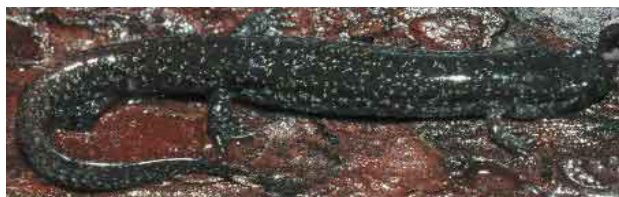


Fig. 8. Southern dusky salamander (*Desmognathus auriculatus*). USGS, https://commons.wikimedia.org/wiki/File:D_auriculatus_USGS.jpg, Public Domain.

C. Genus *Ensatina* (1 species)

Sword Salamander kind



Fig. 9. Yellow-eyed ensatina (*Ensatina eschscholtzii*). JLAuckle, “Ensatina Eschscholtzii Xanthoptica (Yellow-Eyed Ensatina) 03,” [https://commons.wikimedia.org/wiki/File:Ensatina_eschscholtzii_xanthoptica_\(Yellow-eyed_Ensatina\)_03.jpg](https://commons.wikimedia.org/wiki/File:Ensatina_eschscholtzii_xanthoptica_(Yellow-eyed_Ensatina)_03.jpg), CC BY-SA 3.0.

Ensatina eschscholtzii consists of a salamander complex made of about 7 subspecies and are found in a diversity of California habitats. They are known as a ring species because different subspecies populations can interbreed with each other when populations overlap. Where populations are furthest they generally don't interbreed, but there still may be occasional gene-flow (Alexandrino et al. 2005).

D. Genus *Karsenia* (1 species)

Korean Crevice Salamander kind



Fig. 10. Korean crevice salamander (*Karsenia koreana*). Photograph courtesy of © pintail, “Korean Crevice Salamander (*Karsenia koreana*),” <https://www.inaturalist.org/photos/111264>.

This was a surprise discovery because it is the only Asian plethodontid.

E. Genus *Hydromantes* (11 species)

Web Toed Salamander kind

Has web toes and can ballistically project tongue to capture prey.



Fig. 11. Shasta web-toed salamander (*Hydromantes shastae*). Photograph courtesy of © 2002 David Wake, “Hydromantes Shastae; Shasta Salamander,” https://calphotos.berkeley.edu/cgi/img_query?seq_num=110806&one=T.

F. Genus *Phaeognathus* (1 species)
Red Hills Salamander kind



Fig. 12. Red Hills salamander (*Phaeognathus hubrichti*). Eugene van der Pijll, https://commons.wikimedia.org/wiki/File:Phaeognathus_hubrichtii.jpg, Public Domain.

G. Genus *Plethodon* (55 species)
Woodland Salamander kind



Fig. 13. Dunn's salamander (*Plethodon dunni*). Greg Schechter, “Plethodon Dunni,” https://commons.wikimedia.org/wiki/File:Plethodon_dunni.jpg, CC BY-SA 2.0.

Subfamily Hemidactyliinae currently contains 20 genera and 335 species.

- A. Genus *Batrachoseps* (22 species)
Slender Salamander kind
- B. Genus *Bolitoglossa* (121 species)
Tropical Climbing Salamander kind
- C. Genus *Bradytriton* (1 species)
Guatemalan Salamander kind
- D. Genus *Chiropterotriton* (12 species)
Splayfoot Salamander kind



Fig. 14. Slender salamander (*Batrachoseps attenuatus*). Coveredinsevindust, “California Slender Salamander (*Batrachoseps Attenuatus*),” [https://commons.wikimedia.org/wiki/File:California_slender_salamander_\(Batrachoseps_attenuatus\).jpg](https://commons.wikimedia.org/wiki/File:California_slender_salamander_(Batrachoseps_attenuatus).jpg), CC BY-SA 3.0.



Fig. 15. Peter's climbing salamander (*Bolitoglossa adspersa*). Mauricio Rivera Correa, “Bolitoglossa Adspersa,” https://commons.wikimedia.org/wiki/File:Bolitoglossa_adspersa.jpg, CC BY-SA 2.5.

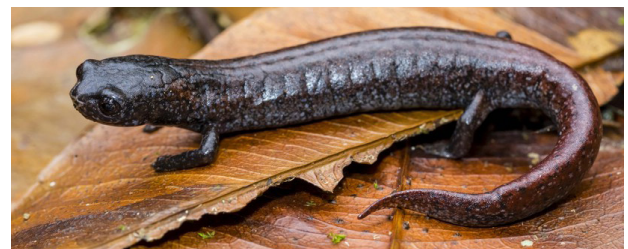


Fig. 16. Finca chiblac salamander (*Bradytriton silus*). Photograph courtesy of © 2017 Wouter Beukema, “Bradytriton Silus,” https://calphotos.berkeley.edu/cgi/img_query?seq_num=783876&one=T.



Fig. 17. Gristle-headed splayfoot salamander (*Chiropterotriton chondrostega*). Photograph courtesy of © 2014 Dr. Joachim Nerz, “Chiropterotriton Chondrostega,” https://calphotos.berkeley.edu/cgi/img_query?seq_num=615449&one=T.

E. Genus *Cryptotriton* (6 species)
Hidden Salamander kind



Fig. 18. Cortes salamander (*Cryptotriton nasali*). Photograph courtesy of © 2009 Jonathan Campbell, campbell@uta.edu, “Cryptotriton Nasalis,” https://calphotos.berkeley.edu/cgi/img_query?seq_num=297632&one=T.

F. Genus *Dendrotriton* (8 species)
Bromeliad Salamander kind



Fig. 19. Guatemalan bromeliad salamander (*Dendrotriton rabbi*). Photograph courtesy of © 2010 Carlos R. Vasquez-Almazan, “Dendrotriton Rabbi,” https://commons.wikimedia.org/wiki/File:Dendrotriton_rabbi.jpeg.

G. Genus *Eurycea* (26 species)/Genus *Haideotriton*
(1 species) Brook Salamander kind



Fig. 20. Cave salamander (*Eurycea lucifuga*). Hargle on English Wikipedia, “Eurycea Lucifuga in Natural Habitat,” https://commons.wikimedia.org/wiki/File:Eurycea_lucifuga_in_natural_habitat.jpg, CC BY-SA 3.0.

H. Genus *Gyrinophilus* (4 species)
Spring Salamander kind

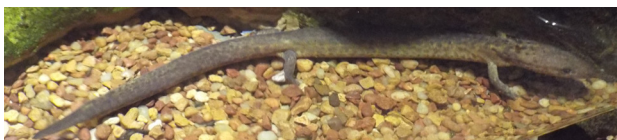


Fig. 21. Tennessee cave salamander (*Gyrinophilus palleucus*). Sesamehoneytart, “Gyrinophilus Palleucus Tennessee Cave Salamander,” https://commons.wikimedia.org/wiki/File:Gyrinophilus_palleucus_Tennessee_Cave_Salamander.jpg, CC BY-SA 3.0.



Fig. 22. Spring salamander (*Gyrinophilus porphyriticus*). John D. Wilson, [https://commons.wikimedia.org/wiki/File:Gyrinophilus_po\(1\).jpg](https://commons.wikimedia.org/wiki/File:Gyrinophilus_po(1).jpg), Public Domain.

I. Genus *Hemidactylum* (1 species)
Four-Toed Salamander kind



Fig. 23. Four-toed salamander (*Hemidactylum scutatum*). Biojoe56 at English Wikipedia, “Four-Toed Salamander Dorsal,” https://commons.wikimedia.org/wiki/File:Four-toed_salamander_dorsal.jpg, CC BY-SA 3.0.

J. Genus *Ixalotriton* (2 species)
Bounding Salamander kind



Fig. 24. Dwarf false brook salamander (*Ixalotriton parvus*). Photograph courtesy of ©2007 Theodore Papenfuss, “Ixalotriton Parvus,” https://calphotos.berkeley.edu/cgi/img_query?seq_num=215845&one=T, CC BY-NC 3.0.

K. Genus *Nototriton* (16 species)
Moss Salamander kind



Fig. 25. Cerro de Enmedio Moss Salamander (*Nototriton lignicola*). Josiah H. Townsend, "Nototriton Lignicola," https://commons.wikimedia.org/wiki/File:Nototriton_lignicola.jpg, CC BY-SA 2.5.

L. Genus *Nyctanolis* (1 species)
Long-Limbed Salamander kind



Fig. 26. Long-limbed salamander (*Nyctanolis pernix*). Photograph courtesy of © Renato Morales, "Nyctanolis Pernix," <https://www.flickr.com/photos/129683115@N02/31273265736/in/dateposted/>.

M. Genus *Oedipina* (36 species)
Worm Salamander kind



Fig. 27. Gamboa worm salamander (*Oedipina complex*). Photograph courtesy of © Arnaud JAMIN, "Oedipina Complex," <https://www.flickr.com/photos/necture49/5519786248/in/photolist-f5BXY9-9pLm9q/>.

N. Genus *Parvimolge* (1 species)
Tropical Dwarf Salamander kind



Fig. 28. Townsend's dwarf salamander (*Parvimolge townsendi*). Photograph courtesy of © 1969 David Wake, "Parvimolge Townsendi," https://calphotos.berkeley.edu/cgi/img_query?seq_num=26887&one=T.

O. Genus *Pseudoeurycea* (49 species)
False Brook Salamander kind



Fig. 29. Veracruz green salamander (*Pseudoeurycea lynchi*). Photograph courtesy of ©2012 Adriana Sandoval-Comte, "Pseudoeurycea Lynchi, Veracruz Green Salamander," https://calphotos.berkeley.edu/cgi/img_query?seq_num=406134&one=T.

P. Genus *Pseudotriton* (2 species)
Red-Mud Salamander kind



Fig. 30. Midland mud salamander (*Pseudotriton montanus*). Eugene van der Pijll, https://commons.wikimedia.org/wiki/File:Pseudotriton_montanus.jpg, Public Domain.

Q. Genus *Stereochilus* (1 species)
Many Lined Salamander kind



Fig. 31. Many-lined salamander (*Stereochilus marginatus*). Photograph courtesy of © 2013 Jake Scott, "Many-Lined Salamander (Stereochilus Marginatus)," <https://www.flickr.com/photos/tamers1/9889205283/in/photolist-g4SLcn-eg78zS-eg1oGv>.

R. Genus *Thorius* (24 species)
Minute Salamander kind



Fig. 32. Big-footed minute salamander (*Thorius magnipes*). Photograph courtesy of © 2014 David Wake, “*Thorius Magnipes*; Large-Footed *Thorius*,” https://calphotos.berkeley.edu/cgi/img_query?seq_num=624339&one=T.

S. Genus *Urspelerpes* (1 species)
Patch-Nosed Salamander kind



Fig. 33. Patch-nosed salamander (*Urspelerpes brucei*). Photograph courtesy of © 2014 Jake Scott, “Patch-Nosed Salamander (*Urspelerpes Brucei*),” <https://www.flickr.com/photos/tamers1/14252332618/in/album-72157644796759839/>.

**Family Salamandridae
(True Salamander and Newt Family)**

Family Salamandridae includes the newts, subfamily Pleurodelinae, the “true” salamanders, subfamily Salamandrinae, and the spectacled salamanders, subfamily Salamandrininae. The average total length of the family is 13cm (5.1in) (Amphibiaweb 2013). Their range occurs mostly in Eurasia, with some reaching northern Africa. Two genera represented in the United States and eastern Mexico are *Notophthalmus* and *Taricha* (Amphibiaweb 2013; Petranka 1998, 445). North American fossils are known from upper Oligocene, Miocene, and Pleistocene deposits and in Europe they are well represented in the Cenozoic strata (Petranka 1998, 445). Common characters shared include no nasolabial grooves, no costal grooves, two longitudinal rows of teeth extending far back into the mouth, a frontal squamosal arch on the skull,

and vertebrae that are opisthocoelous or shaped so that their anterior surface is convex and their posterior surface is concave (Amphibiaweb 2013). Some true salamanders are viviparous and include *Lyciasalamandra*, *Salamandra atra* and *S. lanzai* (Larson, Wake, and Devitt 2006). They have several specific features that distinguish them from all other salamanders and many have warty skin that produces toxins (Petranka 1998, 445). Some start as aquatic larvae, become terrestrial juveniles, and return to water as adults. During breeding they exhibit sexual dimorphism and males often perform unique courtship dances (Amphibiaweb 2013). No relevant hybridization data was found and as with Plethodontidae, because of the large variation within the family, I default the kind to genus until further research sheds light on the mechanisms for these variations.

Subfamily Salamandrininae contains 1 genus and 2 species.

A. Genus *Salamandrina* (2 species)
Spectacled Salamander kind



Fig. 34. Spectacled salamander (*Salamandrina terdigitata*). anonymous, “Brillensalamander,” <https://commons.wikimedia.org/wiki/File:Brillensalamander.jpg>, CC BY-SA 3.0.

Subfamily Salamandrinae currently contains 4 genera and 18 species.

A. Genus *Chioglossa* (1 species)
Gold-Striped Salamander kind



Fig. 35. Gold-striped salamander (*Chioglossa lusitanica*). I, Drow male, “*Chioglossa Lusitanica.005*,” https://commons.wikimedia.org/wiki/File:Chioglossa_lusitanica.005.jpg, CC BY-SA 4.0.

B. Genus *Lyciasalamandra* (10 species)
 Greco-Turkish Salamander kind



Fig. 36. Greco-Turkish salamander (*Lyciasalamandra helverseni*). Benny Trapp, “BennyTrappLyciasalamandra Helverseni,” https://commons.wikimedia.org/wiki/File:Benny_Trapp_Lyciasalamandra_helverseni.jpg, CC BY-SA 3.0.

C. Genus *Mertensiella* (1 species)
 Caucasian Salamander kind



Fig. 37. Caucasian salamander (*Mertensiella caucasica*). Photograph courtesy of © 2006 Wouter Beukema, “Mertensiella Caucasica; Caucasian Salamander,” https://calphotos.berkeley.edu/cgi/img_query?seq_num=205940&one=T.

D. Genus *Salamandra* (6 species)
 Fire Salamander kind



Fig. 38. Fire salamander (*Salamandra salamandra*). Didier Descouens, “Salamandra Salamandra MHNT 1,” https://commons.wikimedia.org/wiki/File:Salamandra_salamandra_MHNT_1.jpg, CC BY-SA 4.0.

Subfamily Pleurodelinae has 16 genera and 77 species

A. Genus *Calotriton* (2 species)
 Spanish Brook Newt kind



Fig. 39. Pyrenean brook newt (*Calotriton asper*). DAGOR53, “Tritó Pirinenc,” https://commons.wikimedia.org/wiki/File:Tritó_Pirinenc.jpg, CC BY-SA 3.0.

B. Genus *Cynops* (8 species)
 Firebelly Newt kind



Fig. 40. Chinese Fire Bellied Newt (*Cynops orientalis*). Jeff Lorch, USGS, [https://commons.wikimedia.org/wiki/File:Chinese_firebelly_newt_\(2\).jpg](https://commons.wikimedia.org/wiki/File:Chinese_firebelly_newt_(2).jpg), Public Domain.

C. Genus *Echinotriton* (2 species)
 Spiny Newt kind



Fig. 41. Anderson’s crocodile newt (*Echinotriton andersoni*). User:OpenCage, “Echinotriton Andersoni By OpenCage,” https://commons.wikimedia.org/wiki/File:Echinotriton_andersoni_by_OpenCage.jpg, CC BY-SA 2.5.

D. Genus *Euproctus* (2 species)
Brook Newt kind



Fig. 42. Corsican brook salamander (*Euproctus montanus*). anonymous, "Korsischer Gebirgsmolch," https://commons.wikimedia.org/wiki/File:Korsischer_Gebirgsmolch.jpg, CC BY-SA 3.0.

E. Genus *Ichthyosaura* (1 species)
Alpine Newt kind



Fig. 43. Alpine newt (*Ichthyosaura alpestris*). Richard Bartz, Munich aka Makro Freak, "Alpenmolch Alpine Newt Triturus Alpestris," https://commons.wikimedia.org/wiki/File:Alpenmolch_Alpine_Newt_Triturus_alpestris.jpg, CC BY-SA 2.5.

F. Genus *Laotriton* (1 species)
Laos Newt kind



Fig. 44. Laos newt (*Laotriton laoensis*). Photograph courtesy of © 2015 Axel Hernandez, "Laotriton Laoensis," https://calphotos.berkeley.edu/cgi/img_query?seq_num=644696&one=T.

G. Genus *Lissotriton* (5 species)
Small-Bodied Newt kind



Fig. 45. Smooth newt (*Lissotriton vulgaris*). John Beniston, "Common Newt," https://commons.wikimedia.org/wiki/File:Common_Newt.jpg, CC BY-SA 3.0.

H. Genus *Neurergus* (4 species)
Spotted Newt kind



Fig. 46. Kurdistan spotted newt (*Neurergus microspilotus*). Babak Naderi, "Neurergus Microspilotus," https://commons.wikimedia.org/wiki/File:Neurergus_microspilotus.jpg, CC BY-SA 3.0.

I. Genus *Notophthalmus* (3 species)
Eastern Newt kind



Fig. 47. Eastern newt (*Notophthalmus viridescens*). Brian Gratwicke, "Redspotted Newt," https://commons.wikimedia.org/wiki/File:Redspotted_newt.jpg, CC BY-SA 2.0.

J. Genus *Ommatotriton* (2 species)
Banded Newt kind



Fig. 48. Southern banded newt (*Ommatotriton vittatus*). GoEThe, “Ommatotriton Vittatus,” https://commons.wikimedia.org/wiki/File:Ommatotriton_vittatus.jpg, CC BY-SA 3.0.

K. Genus *Pachytriton* (8 species)
Paddle-Tail Newt kind



Fig. 49. Paddle-tail newt (*Pachytriton labiatus*). KENPEI, “Pachytriton Labiatus1,” https://commons.wikimedia.org/wiki/File:Pachytriton_labiatus1.jpg, CC BY-SA 3.0.

L. Genus *Paramesotriton* (11 species)
Warty Newt kind



Fig. 50. Hong Kong newt (*Paramesotriton hongkongensis*). Drow male, “Paramesotriton Hongkongensis-Casa de las Ciencias,” https://commons.wikimedia.org/wiki/File:Paramesotriton_hongkongensis_-_Casa_de_las_Ciencias.jpg, CC BY-SA 4.0.

M. Genus *Pleurodeles* (3 species)
Ribbed Newt kind



Fig. 51. Iberian ribbed newt (*Pleurodeles waltii*). anonymous, “Pleurodeles Waltl BUD,” https://commons.wikimedia.org/wiki/File:Pleurodeles_waltl_BUD.jpg, CC BY-SA 3.0.

N. Genus *Taricha* (4 species)
Pacific Newt kind



Fig. 52. California newt (*Taricha torosa*). Connor Long, “Taricha Torosa, Napa County, CA,” https://en.wikipedia.org/wiki/File:Taricha_torosa,_Napa_County,_CA.jpg, CC BY-SA 3.0.

O. Genus *Triturus* (7 species)
Crested Newt kind



Fig. 53. Northern crested newt (*Triturus cristatus*). Rainer Theuer, <https://commons.wikimedia.org/wiki/File:Kammolchmaennchen.jpg>, Public Domain.

P. Genus *Tylototriton* (14 species)
Crocodile Newt kind



Fig. 54. Emperor newt (*Tylototriton shanjing*). Huangdaniel30, “Emperor Newt, Tylototriton Shanjing Crop,” https://commons.wikimedia.org/wiki/File:Emperor_Newt,_Tylototriton_shanjing_Crop.png, CC BY-SA 4.0.

Family Proteidae

Family Proteidae contains two genera; *Proteus* (one species) and *Necturus* (five species) with an average total length of 25cm (9.8in). Fossils have been found from the Upper Paleocene in North America and to the Middle Miocene in Europe and Kazakhstan (Larson, Wake, and Devitt 2006; Petranka 1998, 417). Proteids are paedomorphs and even though adults have lungs, they are perennibranchiate and retain filamentous gills throughout their lives (Amphibiaweb 2013). Other shared characters include; maxillae and septomaxillae absent, a reduction in the number of toes, and a diploid number of 38 (Amphibiaweb 2013). Members include the Olm or the European blind salamander (*Proteus anguinus*) which is a troglobite that may be capable of a degree of viviparity (Amphibiaweb 2013) and has a cognitum that superficially fits with certain plethodontid salamanders. The other members are waterdogs and mud puppies (*Necturus*). While it is too difficult to determine from what kind they have diversified from, their obligate aquatic morphology and paedomorphy suggest a post-Flood phenomenon and I do not include them as an Ark kind.

Family Sirenidae

The sirens are long aquatic, eel-like salamanders with an average total length of 40cm (15.7in) with small forelimbs, absent hind limbs, and no pelvic girdle (Amphibiaweb 2013). The family consists of two genera (*Pseudobranchius/Siren*) and four species that are found in the eastern United States and northeastern Mexico (Petranka 1998, 479). Fossil sirenids are known from the middle Eocene (Wyoming), middle Miocene (Nebraska and Texas), and the lower Miocene and Pleistocene (Florida) while *Pseudobranchius* fossils are known from Florida Pliocene and Pleistocene strata (Petranka 1998, 479). They are obligate neotenes, and like Proteidae, are perennibranchiate. Characters shared include no premaxillary or maxillary teeth. As with Proteidae, their obligate aquatic morphology and neoteny suggest that they are products of post-Flood diversification and therefore I don't include them as an Ark kind.

Order Gymnophiona (The Caecilian Kind)

Probably the least familiar order of burrowing or aquatic Lissamphibians, Gymnophiona (clade Apoda), currently consists of 10 Families and 191 species with an average total length of 35cm (13.7in) (Amphibiaweb 2013; Kamei et al. 2012; Pough et al. 2004, 61). Many live in moist soil and because of this fossorial existence, it is very difficult to study their life history. Common characters include long annulated (ringed) bodies, reduced or absent tails, absent limbs and girdles, reduced eyes covered by

skin or bone, reduced or absent left lungs, well ossified skulls, and scales (unique to Lissamphibians) located in the dermis below the annular grooves and next to the poison glands (Pough et al. 2004, 57–60). Their annulated body is characteristic caecilian morphology and each annulus is associated with a rib (Pough et al. 2004, 58). They also have a unique structure called a tentacle that is located between the eyes and nostrils in a little chamber that opens at the skull surface. It is a chemosensory organ that is positioned differently depending on the species and is helpful for species identification (Pough et al. 2004, 58).

They also have a unique dual jaw adductor mechanism not found in other tetrapods. This mechanism consists of two muscles; the mandibular adductors (found on ancestral tetrapods) and interhyoideus muscles (unique to caecilians) that are working together (Pough et al. 2004, 58).

They internally fertilize and males have a copulatory organ called a phallosome that can transfer sperm to a female. About 70% of the females are oviparous and eggs are laid in terrestrial or aquatic sites (Pough et al. 2004, 58). If eggs are laid on land, most are laid in strings and the female protects them. About 30% of the caecilians are viviparous and egg yolk volumes are much reduced compared to oviparous eggs because nutrients are supplied by the mothers from special cells in her oviduct (Pough et al. 2004, 58). Larvae have lungs, gill slits, lateral line systems, and caudal fins until they metamorphose to adulthood. Like salamanders, metamorphosis is gradual and lungs may remain (with some lungless exceptions), the tentacle develops, caudal fins and lateral lines disappear, and gill slits close (Pough et al. 2004, 60).

Fossil caecilians are known from the early Jurassic of Arizona, lower cretaceous of Morocco, late Cretaceous of Bolivia and Sudan, and from the Paleocene to the Pleistocene in Brazil and Bolivia (Pough et al. 2004, 60). The best preserved fossils, like *Eocaecilia micropodia*, come from the Jurassic and share many derived characters with extant caecilians. They differ in that *E. micropodia* have well-developed limbs and girdles, though they are reduced (Pough et al. 2004, 58, 60). A brief description of each family follows. (See also table 2).

Family Caeciliidae

Caeciliidae consists of two genera and 42 species whose range is South and Central America and average total length is unknown. However, there are very large specimens between 60–100cm (23.6–39.3in) (Amphibiaweb 2013). Shared characters include imperforate stapes (ear bones), inner mandibular teeth and eyes surrounded or covered by the maxillopalatine (upper jaw bone) regions of the skull (Amphibiaweb 2013).

Table 2. A sampling of Caecilian family traits and behavior.

All share the following traits: blunt, bullet shaped heads, cylindrical bodies, annulated rings (each associated with one vertebra), no external ear openings, reduced or absent tails, well ossified skulls, absent limbs and girdles, reduced eyes, reduced or absent left lungs, unique tentacles, unique dual jaw adductor mechanism, male copulatory organ (phallosome), internal fertilization (AmphibiaWeb 2012; Pough et al. 2003; Tree of Life n.d.; Vitt and Caldwell 2009).

	New Family									
Description	Caeciliidae	Chikilidae	Dermophiidae	Herpelidae	Ichthyophiidae	Indotyphliidae	Rhinatrematidae	Scolecophoridae	Siphonopidae	Typhlonectidae
Number of genera	42	1	4	2	3	7	2	2	7	5
Number of species	2	1	14	9	52	21	11	6	22	13
Average Total Length (cm)	unknown	unknown	50	33	32	22	25	36	contains smallest: 11	contain largest: avg. 45
stapes (ear bones)	imperforate	unknown	present	perforate	present	imperforate	present	none	imperforate	present
embryo development	ovi or viviparous	oviparous	ovi or viviparous	oviparous	oviparous	ovi or viviparous	oviparous	ovi or viviparous	oviparous	viviparous
annuli	primary/ some secondary	primary	secondary	primary/some secondary	secondary/ tertiary	primary	secondary/ tertiary	primary	primary/some secondary	primary
dual jaw adductor mechanism	2 muscle bundles	2 muscle bundles	2 muscle bundles	2 muscle bundles	2 muscle bundles	2 muscle bundles	*1 muscle bundle*	2 muscle bundles	2 muscle bundles	2 muscle bundles
dermal scales	present	present	present	present	present	absent	numerous	absent	none	none
aquatic or semi-aquatic	no	no	no	no	no	no	no	no	no	YES
intrauterine feeding by fetus	no	unknown	no	no	no	depends on species	no	depends on species	no	YES
juveniles shed gills early	no	no	no	no	no	no	no	no	no	YES

Family Chikilidae

This newly described family has only one genus and one species and little is known about them. They are very similar to other caecilians and have been found in India (Amphibiaweb 2013; Kamei et al. 2012).

Family Dermophiidae

Consisting of four genera and 14 species, they have an average total length of 50cm (19.6in). Dermophiids have secondary annuli (subdivisions of primary annuli) and are found in Africa, Central America, and South America (Amphibiaweb 2013).

Family Herpelidae

Herpelidae contains two genera and nine species and shared characters include perforate stapes, multiple small antotic foramina (skull openings), and both prefrontals and septomaxillae are separate. They are found in Africa and have an average total length of 33cm (12.9in).

Family Ichthyophiidae

Ichthyophiidae contains three genera and 52 species with an average total length of 32cm (12.5in). They have true tails, a counter sunk lower jaw, and an advanced dual jaw closing mechanism. Their range occurs in south and southeast Asia (Amphibiaweb 2013).

Family Indotyphliidae

This family has seven genera and 21 species with an average total length of 22cm (8.6in). Characters shared include; imperfect stapes, inner mandibular teeth, bicuspid teeth, an eye located at the border of the squamosal (a skull bone) and maxillopallatines, and lacks scales and secondary annuli (Amphibiaweb 2013). Some are viviparous and others are oviparous and they are found in Africa, India, and the Seychelles.

Family Rhinatrematidae

The two genera and 11 species in Rhinatrematidae are all oviparous and are found in northern South America through Brazil, Columbia, Ecuador, Peru, Surinam, Guyana, French Guiana, and Venezuela (Amphibiaweb 2013). The average total length is 25cm (8.9in) and they share the following characters; true short tails with post-cloacal vertebrae, mouth is terminal rather than countersunk, tentacular opening is adjacent to the eye rather than anterior as found in other caecilians, and primary annuli are subdivided into secondary and tertiary annuli (Amphibiaweb 2013). As was described above, all caecilians have a unique dual jaw adducting mechanism. The difference with Rhinatrematidae is that they have one bundle of muscles where all the other caecilian families (clades) have two bundles (Amphibiaweb 2013).

Family Scolecophoridae

Consisting of two genera and six species, they have an average total length of 36cm (14.1 in) and are native to western and eastern equatorial Africa (Amphibiaweb 2013). Shared characters include; countersunk lower jaws, tentacular openings far anterior on the snout, orbits are absent, eyes connected at the base of the tentacle and protrude when tentacle protrudes, lack stapes, annular grooves lack dermal scales, secondary and tertiary annuli are absent, and females have more vertebrae than males (Amphibiaweb 2013).

Family Siphonopidae

With seven genera and 22 species, Siphonopidae live in South America and are oviparous, have imperforate stapes, and lack inner mandibular teeth (Amphibiaweb 2013).

Family Typhlonectidae

Family Typhlonectidae have an average total length of 45cm (17.7in) and currently contains five

genera and 13 species. This group is aquatic or semi-aquatic and viviparous. Juveniles shed gills at an early stage, all make burrows at the water level or underwater, fetuses feed intrauterinely (extraordinary among Lissamphibians), possess tracheal lungs, have narial plugs, and lack annular scales and secondary annuli (Amphibiaweb 2013). One member of this family is known from only two specimens and is the largest lungless tetrapod (*Atretochoana eiselti*) known measuring 72.5cm (28.5in) (Amphibiaweb 2013). They are found in northern South America and some consider them nested within Caeciliidae (Amphibiaweb 2013).

No hybridization data were found, but character data suggests that taxon Gymnophiona demonstrates holistic and significant differences with other taxa and are an apobaramin. Through successive approximation, it is possible that future statistical tests may divide the group into smaller subsets of monobaramins and/or holobaramins that could suggest more than one Gymnophionan kind.

Summary and Conclusions

After looking at the most current Lissamphibian systematics and recognizing that this data is in constant flux, I have made an initial estimate as to the number and identification of kinds from Orders Caudata and Gymnophiona that may have been represented on the Ark. Of the 10 extant Caudate families, with the exception of Proteidae and Sirenidae because of probable post-Flood phenomena of their perennibranchiate morphology and obligate neoteny, the data suggest Noah had 53 Caudate kinds and 1 extant Gymnophionan kind represented on the Ark.

These conclusions are tentative. It is my contention that with a proper biblical worldview, it is probable that future baraminological research will bring us a better understanding of what the data mean and how to interpret them in the light of biosystematics and taxonomy. No matter what the numbers turn out to be, there is no question that the Creator's wisdom and desire for creatures to persist reflects his marvelous diversity, loving provision, and promised salvation.

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