

In search of the created snake kinds

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Figure 1. *Agkistrodon contortrix* is a species of venomous snake endemic to eastern North America, commonly known as the copperhead. Photograph by Tom Hennigan.

ABSTRACT

Baraminology is the study of the created kinds. Initial research on the baraminology of snakes has focused on their ability to hybridise with one another, which has been considered a criterion indicating membership in the same baramin (or created kind). This research is in its infancy, but has led to the identification of some likely monobaramins (subsets of created kinds).

INTRODUCTION

For the Christian researcher who loves Jesus, enjoys the beauty of God’s creation and bases life on the foundation of God’s Word, it is an exciting time. There is a strong movement in the Christian science community toward building a scientific model of origins based on the authority of the Bible and for the glory of God.

A scientific model is a way to visualise complex natural processes in a simplified manner. Models can take the form of mathematical calculations, diagrams and computer programs. They can help scientists improve explanations for natural processes, make better scientific predictions and test ideas about complex natural systems.

For example, the better we understand the complexity of Earth’s atmosphere, the better our computer models will be. As atmospheric computer models improve, better

predictions can be made about how pollution affects Earth temperatures. However, it is important to note that interpretations of data generated by models can depend on the worldview of the researcher and we see this in all modelling, including models of biological origins.

For example, you might be familiar with the neo-Darwinian tree model for the origin of biological diversity. The base of the tree represents the assumed first cell, produced over a long period by random chemical reactions. Over time, the assumed first cell was the precursor of the life we see today, as random genetic changes in evolving organisms were either selected for survival or weeded out by natural processes.

The model is in the form of a tree to show how everything is related to everything else. Just like having the potential ability to trace your ancestry back hundreds of years, so each organism alive today can theoretically be traced to their first-cell ancestor. This concept is known as universal common ancestry by researchers who have worldviews that reject the supernatural or who feel that the Genesis account is poetry and not meant to be an historical description of the origin of biological life.

Of course, with the enormous amount of new data, Darwin’s initial tree model is being visualised as more bush than tree, but that is to be expected as

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models are continually updated with new understanding (Hennigan 2017). With the tree/bush model in mind, and the assumption that every living thing is related to every other living thing, predictions can be made, the fossil record can be described and DNA investigations can be accomplished in order to study creature relatedness and how they are connected by their ancestry.

In other words, these researchers predict universal relatedness or *continuity* between creatures and interpret data with that underlying assumption. To be sure, and maybe to the consternation of some believers in Christ, there is evidence consistent with the idea of universal common ancestry (continuity) when studying things like skeletal structure comparisons or DNA similarities.

However, it is possible to produce a different model of biological origins from a different perspective with different interpretations that are also consistent with what is observed. The purpose of this article is to highlight some initial research that offers a different model for interpreting organisms in the context of snakes.

Creation researchers who take Genesis 1 at face value and hold the Bible to be authoritative for the origin of biological life have a completely different view of the world than researchers who feel that only natural processes are involved. Creation biologists have keyed in on God's creative phrase, 'according to their kinds' (Genesis 1:24–25).

Rather than all creatures of today being related to an original cell, the Genesis account has a very different story of God creating discrete and fully-formed creatures called *kinds* (Hebrew *mîn*). Any similarities between all organisms could be interpreted as products of universal common design rather than universal common ancestry. But there also should be evidence of significant differences or gaps. Let's look at this created kind model.

THE CREATED KIND MODEL FOR THE ORIGIN OF SPECIES

If God created discrete groups of creatures, then not all creatures are universally related. If true, there should be gaps or discontinuities between created kinds. Young-age creationists, assuming that Genesis 1 is an accurate view of the origin of biological life, have proposed an orchard model rather than a tree/bush model (Wise 1990).

Hennigan (2017) uses the following imagery:

Picture an orchard where each tree represents a different biblical kind. These trees are not related to each other, but branches on individual trees represent variations within the same kind. Each kind is a masterpiece of design, containing immense genetic diversity and potential. It looks as

if God gave organisms a treasure trove of diverse and potential traits – like a Swiss Army knife – that allowed them to respond to changing needs with specialized tools.

The study of the created kinds is called baraminology, from the Hebrew *bara* (to create) and *mîn* (kind). In order to put the tree/bush and forest models in perspective, biologists must grapple with the definition of species. The whole question of just what a 'species' is has been under discussion for many years.

Evolutionary researchers realise the term 'species' has more than twenty meanings, each of which is vigorously debated among biologists (Agapow et al. 2004). As each tree in the creation forest represents the 'kind' the branches represent how the initial kind diversified into various species, or variations, within the kind. It is a picture of limited common ancestry within a kind, but not between kinds.

THE BIBLE AND SNAKE KINDS

Though snake classification is always changing, it is estimated that there are 26 families and over 3,000 species of snakes recognised today (Uetz et al. 2018). Starting with Scripture, the Bible seems to imply that snakes are a separate (discontinuous) group and not related to anything else.

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The Hebrew word for 'serpent' in Genesis 3:1 is *nachash* or *nahash* meaning 'shining whisperer', and refers to serpent or snake (Harris et al. 1980). This Hebrew word is often used with observed snake behaviour like stealth (Genesis 49:17), venomous bite (Proverbs 23:32), snake 'charming' (Ecclesiastes 10:8), ability to climb on smooth surfaces (Amos 5:19), 'licking the dust' (Isaiah 65:25) and making a hissing sound (Jeremiah 46:22) (Harris et al. 1980; Hennigan 2005).

Field and laboratory studies suggest similar conclusions. There are serpentine traits that are not found in other animal groups and include: having 120 to over 400 vertebrae, a branch of a major facial nerve enclosed inside the braincase, transparent scales over the eyes with no eyelids, a left arterial arch larger than the right, the brain enclosed in a rigid box made of bone, a stunted or missing left lung and a worm-shaped liver (Pough et al. 2004; Hennigan 2005).

Baraminologists have proposed the idea of producing a discontinuity matrix to begin the process of looking for significant differences between snakes and other groups

Does the Bible claim snakes are a separate group from other animals?		No
Does the Bible imply snakes are a separate group from other animals?	Yes	
Do most snake members have unique body processes and functions not found in other animals?	Not known	
Is the similarity of members in the snake group significantly greater than snake vs. non-snake groups?	Yes	
Do most snakes have unique cell types or structures not found in other animal groups?	Yes	
Do most snakes have unique organs or organ structures not found in other animal groups?	Yes	
Is the overall snake shape significantly greater than the similarity of the group with other animal groups?	Yes	
Do snakes occupy an environment quite different from other organisms?		No
Are the intermediate fossils that would connect snakes to other animal groups mostly absent?	Yes	
Is the proposed ancestor of snakes found in higher rock layers than the lowest member of the snake group?		No

Table 1. A discontinuity matrix for snakes. Modified from Wood and Murray (2003) and Hennigan (2005).

of animals, beginning with what the Bible says about them (Wood and Murray 2003). Using this first method, it appears that snakes may be significantly different from other animals (Table 1). Therefore, using the forest model of snake origins, I hypothesise that snakes are a discrete group of animals created fully-formed and according to their kinds on Day Six (Genesis 1:24–25).

Just as the definition of species is currently uncertain, so too is the definition of ‘kind’ (Turner 2009). Other than discrete groups, what else is meant? The only inference we can make comes from Genesis 6–9 where males and females of each air-breathing land vertebrate ‘kind’ are to go on the Ark. The presumed reason is so they can reproduce and fill the post-Flood world.

For example, because many king snake, corn snake, and rat snake species can interbreed and produce fertile offspring, it is possible all have diversified from an

original male and female king/corn/rat snake ancestor that came off the Ark (Table 5). However, for lots of reasons, the capability of reproduction alone cannot be the only measure for determining a kind (Wood et al. 2003).

Consequently, here we will focus on just one piece of additive evidence that will allow us to explore the question of snake kinds: the ability to mate and produce fertile offspring. Hybridisation between different subspecies, species and genera suggests a close biochemical relationship between two organisms.

In baraminology, a group of known organisms that are significantly similar to one another without considering their dissimilarities with others is called a *monobaramin* (Wood et al. 2003). From the initial research on

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Species/genera that can hybridise	Hybrid fertility	Artificial/natural	Source
Bredl's python x Inland carpet python	Fertile	Artificial	Hoser (2001)
Coastal carpet python x Inland carpet python	Fertile	Artificial	Hoser (1999)
Children's python x Spotted python	Fertile	Artificial	Hoser (1993)
Children's python x Large-blotched python	Fertile	Artificial	Hoser (1993)
Diamond python x Amethystine python	Fertility assumed	Artificial	Hoser (1988)
Royal python x Borneo short-tailed python	Fertile	Artificial	Chernof (2004)
Spotted python x Children's/Spotted hybrid	Fertility assumed	Artificial	Hoser (1993)
Diamond python x Macklot's python (intergeneric)	Fertile	Artificial	Banks & Schwaner (1984)
Diamond python x Water python (intergeneric)	Fertile	Artificial	Hoser (1988)

Table 2. Hybridisation in pythons (Pythonidae family, one monobaramin). Modified from Hennigan (2005).

Species that can hybridise	Hybrid fertility	Artificial/natural	Source
Red-tailed boa x Common northern boa	Fertile	Artificial	Meyer-Holzapfel (1969)
Amazon tree boa x Emerald tree boa	Unknown	Artificial	http://urbanjungles.com/bhybridtreeboasb.htm claimed, but not proven—further research necessary

Table 3. Hybridisation in boas/anacondas (Boidae family, one monobaramin). Modified from Hennigan (2005).

hybridisation, four of the 26 families were identified: the python family (Table 2); boas and anacondas from the boid family (Table 3), long-fanged snakes from the viper family (Table 4); and a few groups within the colubrid family (colubrid is Latin for ‘snake’; Table 5).

Some tables have more than one monobaramin described and in those instances, monobaramins are highlighted with a different colour. Tables 2-5 document various snake hybrids between subspecies, species and genera, which is why creation biologists place the ‘kind’ in a group more inclusive than species (e.g. genus, family or above in some organisms). Because of their ability to hybridise with one another, I propose the following.

- Python species seem to readily hybridise with one another so I suggest that the family is a monobaramin (Table 2), while red-tailed and northern boas (*Boa constrictor* subspecies) consist of another monobaramin within the Boidae family (Table 3).

- Three monobaramins are suggested in the Viperidae family (Table 4): 1) rattlesnakes in genera *Sistrurus* and *Crotalus*, 2) North American cottonmouths and copperheads in the genus *Agkistrodon* (Figure 1), 3) Asian vipers in the genus *Gloydius*, and 4) African vipers in the genus *Bitis*.

- In the colubrid groups researched (Table 5), I suggest there are six monobaramins: 1) water snake species in the genus *Nerodia*, 2) Old World rat snake species in the genus *Zamenis*, 3) New World rat snakes, king snakes and

pine snakes in the genera *Elaphe/Pantherophis* x *Lampropeltis* x *Pituophis* (Figure 2), 4) ring-necked snake subspecies, 5) brown snake subspecies, and 6) garter snake subspecies. (Note: there is still controversy surrounding the use of *Elaphe* and *Pantherophis* as genus names for the North American rat snakes, therefore I have listed both.)

CONCLUSIONS

It is an exciting time for creation research. The standard model for life’s origins has been portrayed as a tree/bush, with the belief that nature alone, selecting from genetic variations, can explain the diversity of organisms today. Assumptions in the tree/bush model include the idea that all organisms are continuous (connected) by universal common ancestry.

Though in its infancy, creation research, with the goal of building a unique creation model of origins, proposes an alternative forest model based on the authority of God’s Word and the Creator’s own testimony. An assumption in the forest model is that Genesis is an historical outline of biological life’s beginnings from the perspective of the Creator as cause and eyewitness.

Therefore, ideas within that premise include the universal common design of all organisms, deliberate design of discrete (discontinuous) kinds, and limited common ancestry within discrete kinds. Current evidence with other reptile groups suggests that certain organisms are discontinuous with others (Wood 2005).



Figure 2. (a) The Eastern rat snake (*Pantherophis (Elaphe) obsoleta*) and (b) the Eastern milk snake (*Lampropeltis triangulum*) are probably members of the same monobaramin. Photographs by Tom Hennigan.

This article outlines an initial investigation to see if the same patterns hold true for snakes.

We know that snakes have unique characteristics that set them apart from other creatures. This initial quest also indicates that many snakes have the ability to hybridise in nature and captivity. Captive hybridisation can even happen with species separated by continents in the wild. They are capable of producing a great deal of variety between species and genera.

There is much that we do not understand about how genes affect creature design, behaviour and relatedness.

A holobaramin is defined as a group with members that share significant and holistic similarity (continuity) with at least one other member and have significant holistic differences (discontinuity) with organisms outside of their group (Wood et al. 2003). The ability to identify and delineate holobaramins would greatly strengthen the forest model of biological origins.

There is still much to be done before identifying snake holobaramins. For example, we need data that would give us a wide range of holistic characteristics that

would include comparisons in DNA, behaviour, cellular machinery, anatomy and hybridisation. From these data, baraminology techniques such as the baraminic distance method (BDC) and the Analysis of Patterns (ANOPA) will help us with a mathematical analysis of significant similarities and differences between snake groups (Wood and Murray 2003). From a biblical perspective, I predict that using the forest model of snake origins will give us a better understanding of what a kind is and how our God helped them to persist and diversify.

As we contemplate all of this, it is important for disciples of Christ to remember that scientific models are man-made and will change or be rejected as new understanding is gained. There is much that we do not understand about how genes affect creature design, behaviour and relatedness. So any conclusions must be tentative until a better understanding of genetic design is obtained.

On the other hand, the Scriptures are God-breathed and God-given, and because they are the Word of the Lord they will endure forever (2 Peter 1:23–25). As we ponder creation, God desires that his creation would

Species/genera that hybridise	Hybrid fertility	Artificial/natural	Source
Massasauga x Timber rattlesnakes (intergeneric)	Fertile	Natural	Klauber (1997)
Eastern diamondback x Timber rattlesnakes	Fertile	Natural	Klauber (1997)
Red-diamond x Southern Pacific rattlesnakes	Fertile	Artificial	Klauber (1997)
Mojave x Aruba Island rattlesnakes	Fertile	Artificial	Klauber (1997)
Mojave/Aruba hybrid x Mojave/Aruba hybrid	Fertile	Artificial	Klauber (1997)
Mojave x Pacific rattlesnakes	Fertile	Artificial	Klauber (1997)
Western diamondback x Timber rattlesnakes	Fertile	Artificial	Cole (2004)
Asian Rock mamushi x Siberian pit vipers	Fertility assumed	Natural	Kudryavtsev & Bozhansky (1988)
North American Northern x Osage copperheads	Fertile - little genetic variation	Natural	http://www.herpnet.net/lowa-Herpetology/reptiles/snakes/copperhead-agkistrodon-contortrix/
North American Cottonmouth vs. Copperhead	Fertility assumed	Natural & artificial	http://cottonmouthsnake.org/hybridization/claimed-further-research-necessary
African Puff adder x Gaboon viper	Fertile and their habitat overlaps	Natural & artificial	http://www.venomousreptiles.org/articles/93
African Gaboon x Rhinoceros vipers	Fertile and their habitat overlaps	Natural & artificial	http://www.venomousreptiles.org/articles/93

Table 4. Hybridisation in venomous vipers (Viperidae family, four monobaramins). Modified from Hennigan (2005).

Species/genera that hybridise	Hybrid fertility	Artificial/natural	Source
Banded x Common fresh and salt water - water snake species and subspecies - genus <i>Nerodia</i>	Fertile	Natural	Lawson et al. (1991)
Old World rat snake species hybridisation within genus <i>Zamenis</i>	Fertile	Artificial	Ryabov (1998) Sideleva et al. (2003)
Multiple species within New World rat snakes, king snakes and pine snakes can hybridise across the genera <i>Elaphe (Pantherophis)</i> x <i>Lampropeltis</i> x <i>Pituophis</i>	Fertile	Natural & artificial	Batten (2000) Cole (2004) Conant and Collins (1998) Kennard (1980) http://www.kingsnake.com Sideleva et al. (2003)
Ring-necked snake subspecies - within <i>Diadophis punctatus</i>	Fertile	Natural	Cole (2004)
Brown snake subspecies - <i>Storeria decayi</i>	Fertile	Natural	Cook (1993)
Garter snake subspecies - genus <i>Thamnophis</i>	Fertile	Natural	Morrison et al. (1998)

Table 5. Hybridisation in colubrids (Colubridae family, six monobaramins). Modified from Hennigan (2005).

remind us about him and redirect our thoughts and actions to worship him as Creator and Saviour (Psalm 19; Romans 1:20).

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Tom’s educational experiences in secular public schools and universities taught that the origin of life, by universal common descent and random processes, was the only way to approach the science of origins. The result of believing that perspective caused him to reject Christianity. He was soon challenged with considering the possibility of an intelligence behind the universe. This caused a worldview crisis and sparked a long journey where he tried to make sense of his university training with the truth of the Bible. His turning point came when he realised that Christianity’s basis was founded upon the historical evidence of Jesus’ resurrection. He has concluded that Jesus’s teachings give another perspective of viewing origins and are the foundation from which we can build a different origins model that gives God the glory. He resides in the mountains of north Georgia with his wife of 30 years. He has four grown children and five grandchildren.