

An Initial Investigation into the Baraminology of Snakes: Order – Squamata, Suborder Serpentes

Tom Hennigan*

Abstract

Evolution theory predicts that the ancestry of organisms can be traced down a hypothetical evolutionary tree and eventually back to the first living cell. Creation theory postulates that ancestry can be traced back only a limited distance to a starting organism of that type. Instead of a “tree” the creation model has a “forest” of unrelated organisms with vast genetic potential. I hypothesize that the snake taxon originated from one or more originally created “trees” or “kinds” that have diversified into the snakes of today and that snakes are unrelated to any other group. In order to test this hypothesis, the snake taxon was analyzed using a discontinuity matrix and the data suggest that snakes can be considered a group unto themselves. Subsequently, a literature search was begun in order to determine additive evidence for relatedness. Three families were identified for their interspecific and intergeneric hybridization tendencies and within each family certain genera and species were classified into subgroups of related snakes. This initial investigation indicates that many snakes have the ability to hybridize, even when they are reproductively isolated over great distances, and are capable of a large degree of variation within a “species.” As more data are gathered and quantified, I predict that evolutionary hypotheses will continue to be frustrated because of faulty metaphysical assumptions and will strongly suggest that snakes began from one or a few originally created kinds, just a few thousand years ago.

Introduction

Historically, the evolution model of common descent predicted that we should see continuity among all organisms and that species could be traced along the evolutionary tree to a single-celled ancestor. That prediction has not born itself out. The whole question of just what a “species” is has come under fire for many years. Evolutionary taxonomists maintain that the species taxon is the “currency” of biology

at the same time that they realize the term “species” has more than twenty meanings, each of which is vigorously debated among biologists (Agapow et al., 2004). Much of the difficulty arises from the presuppositions of the evolutionary worldview, which is built upon the metaphysic of materialism.

Creation theory, to the contrary, postulates a “forest” of organisms in which each “tree” began with an originally created pair designed with vast genetic potential for variation but discontinuous with (not related to) the other created “kinds.” Although there is great variation within each “tree”, there is a limit to biological change and those limits cause serious problems for an evolutionary model involving common ancestry (Lester and Bohlin, 1989). The creationist

* Tom Hennigan, 125 Hennigan Lane,
Georgetown, NY 13072, tdhennigan@citlink.net
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begins his scientific inquiry with a Biblical understanding of our world and interprets it from a theistic metaphysic.

The materialistic and the theistic worldviews present very different visions when trying to understand how life progressed on earth. Concepts of morality, God, and even biosystematics can have grossly different explanations and interpretations based on different worldviews. The materialist view postulates that snake ancestry can be traced along the evolutionary tree to the lizards. Up until recently, the prevailing belief was the marine hypothesis, which stated that snakes evolved from limbless marine lizards. Many evolutionists, however, are interpreting new data that favor snakes having descended from terrestrial lizards (Ross, 2004). There is little evidence for either the marine or terrestrial hypotheses in the fossil record however, and much snake morphology appears highly designed and unique to the snake group.

Baraminology is a creationist method of biosystematics that begins with Genesis 1:24–25 and predicts that we should see major unrelatedness, or discontinuity, among various taxa because God made them after their kinds. The purpose of baraminology is to discover the boundaries of the created kind or holobaramin. A *holobaramin* is defined as all the organisms within the group that are related with each other but not related to any other group. In other words, all members of that group began with an original created pair. Humanity is an example of a holobaramin group in that the members are related by common descent to the originally created Adam and Eve.

The *monobaramin* is a group of organisms related to one another by common descent, but not necessarily all of them (ReMine, 1993). For example, if a tree represents the human holobaramin, then one or more branches representing specific people groups (such as Caucasians and Ethiopians) would each represent a subset of all humans or a human monobaramin (Frair, 2001).

The *apobaramin* consists of a group of creatures that do not share ancestry with any other group. For example, turtles are an apobaramin because they share no common ancestor with any other group, such as birds, or snakes. But it also means that within the turtle apobaramin there may be one or more created holobaramins. The apobaramin is different than the holobaramin in that the apobaramin may be made up of creatures that were derived from one or more originally created kinds. In contrast, the holobaramin has been identified as such because all members have been traced back to one created pair. Therefore, humans are not only a holobaramin because they can be traced to the originally created Adam and Eve but also they are an apobaramin because they share no common ancestor with any other group (Frair, 2001).

The purpose of this paper is to view snake biosystematics from the creationary standpoint and to initiate an investigation of snake baraminology upon the premise that God produced life according to specific created kinds (Genesis 1:24–25). In the case of snakes, it is unclear whether all snakes came from one or a few originally created pairs. I hypothesize that snakes are discontinuous with any other group and are therefore an apobaramin. The goal is to determine if all snakes came from one or a few original created pairs by grouping related snake taxa using additive evidence and separating unrelated snake taxa using subtractive evidence in order to identify one or more snake holobaramins. Eventually I would like to develop a creationary model of snake biosystematics that would be more consistent with the taxonomic data, and that would avoid the ambiguous species concept. Hopefully, it would likewise have a more robust predictive value than the current evolutionary origins model.

Serpents in the Bible

In order to determine true discontinuity, baraminologists have an analysis called the Discontinuity Matrix (Wood and Murray, 2003). The serpentes taxon was analyzed using this matrix and the results are summarized in Table I.

The first step was to find out what the Bible says about snakes. Although the Bible does not claim discontinuity for snakes, it implies discontinuity, suggesting that snakes are unrelated to other organisms. The Hebrew transliteration for “serpent” in Genesis 3:1 is *Nachash* or *Nahash* meaning “shining whisperer”, and referring to serpent or snake (Harris et al., 1980). It is derived from the assumed Hebrew root *nhsh*. Revelation 12:9 unveils the identity of the serpent as the devil, Satan, and is not referring to a wild snake that talks. It is unclear, however, whether it was a snake whom Satan indwelt in Genesis or whether “snake” was just another name for Satan.

Nehushtan is used over 30 times in the Old Testament and is the most common word for “snake” (Harris et al., 1980). Certain snake characteristics used in conjunction with this word, include stealth (Genesis 49:17), poisonous bite (Prov. 23:32), snake “charming” (Eccl. 10:8), climbing ability on a smooth surface (Amos 5:19), “licking the dust” (Isa. 65:25), and making a hissing sound (Jer. 46:22) (Harris et al., 1980). Though once in a while there are other creatures to which this Hebrew word might refer, the above list suggests that the Bible implies snakes are a group of their own, discontinuous with other groups.

Other questions that may determine discontinuity also were asked. As a taxon, snakes have many unique characteristics that include: 120 to over 400 preloacal vertebrae,

Table I. Discontinuity Matrix for Serpentes.

Does the Bible claim discontinuity for snakes?		No
Does the Bible imply discontinuity for snakes?	Yes	
Do most of the members of the group exhibit a novel metabolic pathway not found in other groups or only in groups known to be discontinuous?	Unknown	
Is the similarity of ingroup comparisons significantly greater than ingroup vs. outgroup comparisons?	Yes	
Do most members of the group possess novel cell types or structures not possessed by other groups or only in groups known to be discontinuous?	Yes	
Do most members of the group possess novel organs or anatomical structures not possessed by other groups or only in groups known to be discontinuous?	Yes	
Is the overall morphological similarity within the group significantly greater than the similarity of the group with other groups?	Yes	
Does the group occupy an environment notably different from other organisms?		No
Are stratomorphic intermediates that would connect the group to other groups mostly absent?	Yes	
Is the lowest member of the proposed ancestral group found in a higher layer than the lowest member of the group of interest?		No

Compiled from (Wood and Murray, 2003, p.95)

a branch of the trigeminal nerve that is enclosed within the braincase, a lack of muscles in the ciliary body of the eye, the left arterial arch larger than the right, and the brain enclosed in a rigid box made of bone (Pough et al., 2004).

All are carnivorous. Their respiratory system consists of a stunted left lung and a longer right lung (Pough et al., 2004). Compared to other reptiles, whose livers and stomachs are S-shaped, the snake liver and stomach are fusiform. These unique snake characteristics, coupled with the Biblical data and the poor fossil record connecting snake and lizard ancestry, (Pough et al., 2004; Ross, 2004) show that six out of ten discontinuity criteria, with one unknown, can be answered in the affirmative on the Discontinuity Matrix (see Table I). This suggests that the snakes can be considered an apobaramin or a group unrelated to all other groups.

Snake Monobaramins

It has been estimated that there are about 2300 species of snakes in the world (Conant and Collins, 1998). Depending on the taxonomic source, there are about 15 families of snake species. Trying to identify snake species is in continual flux and can be controversial, as is true of most taxa. One's definition of "species" often determines the identification of same.

In baraminology, there are many characters of organisms that determine continuity or relatedness. The ability to hybridize was the main character investigated for this paper. Hybridization suggests a close biochemical relationship between two organisms and is an important additive evidence for ancestry within a "kind" in the identification of monobaramins. It is also realized, however, that just because two organisms are unable to hybridize does not mean they are unrelated. There are many environmental, behavioral, biochemical and morphological reasons why hybridization might not be possible between related organisms. For this reason, baraminologists look at the creature holistically and analyze as many characters as possible including morphology, anatomy, behavior, environmental niche, and biochemistry. A holistic view that allows the organism to be classified based on the totality of real data effectively eliminates much of the subjectivity and bias possible.

A literature search was done in order to document the ability of snakes to hybridize, both in the wild and in captivity. From this initial search, three families were identified: Boidae (Table II), Colubridae (Table III), and Viperidae (Table IV). Many snake taxa were capable of hybridization interspecifically, intraspecifically, and/or intergenerically within each family.

Snake breeders frequently cross various members of snake taxa in order to discover the variation that can be

Table II. Hybridization in *Boidae*

Hybrid Pairing	Artificial/Natural	Fertility	References
<i>Morelia spilota metcalfei</i> x <i>Morelia s. bredli</i>	Artificial	Fertile	Hoser, 2001
<i>Morelia s. metcalfei</i> x <i>Morelia s. mcdowelli</i>	Artificial	Fertile	Hoser, 1999
<i>Antaresia childreni</i> x <i>A. maculosus</i>	Artificial	Fertile	Hoser, 1993
<i>Antaresia childreni</i> x <i>A. stimsoni</i>	Artificial	Fertile	Hoser, 1993
<i>A. maculosus</i> x <i>A. child./maculosus hybrid</i>	Artificial	Fertility assumed	Hoser, 1993
<i>Morelia s. spilota</i> x <i>M. amethystina</i>	Artificial	Fertility assumed	Hoser, 1988
<i>Morelia s. spilota</i> x <i>Liasis fuscus</i>	Artificial	Fertility assumed	Hoser, 1988
<i>Morelia s. spilota</i> x <i>Liasis mackloti</i>	Artificial	Fertile	Banks and Schwaner, 1984
<i>Morelia s. spilota</i> x <i>Morelia amethystinus</i>	Artificial	Fertile	Banks and Schwaner, 1984
<i>Boa c. constrictor</i> x <i>Boa c. imperator</i>	Artificial	Fertile	Meyer-Holzapfel, 1969
<i>Python regius</i> x <i>Python breitensteini</i>	Artificial	Fertile	Chernof, 2004

produced and to sell those variants profitably. Breeder websites such as kingsnake.com have ongoing discussions of many current crosses hobbyists have accomplished. Tables II–IV contain summaries of some of the known hybrids from the professional literature though a few are from personal correspondences with herpetoculturalists and field herpetologists.

Family Boidae (Table II) consists of about 17 genera with 75 or more species (Museum of Zoology, Ann Arbor, Michigan). Members of the genus, *Morelia* (carpet pythons) in that family, readily hybridize interspecifically with each other, and intergenerically with *Liasis* (Australian and rock pythons), producing fertile hybrids.

The children's pythons (*Antaresia sp.*), also in Boidae, hybridize interspecifically producing fertile hybrids in both f_1 and f_2 generations. Crosses between various subspecies of *Boa* have produced fertile offspring in zoos. Interestingly, the Borneo python (*Python breitensteini*) and ball python (*Python regius*) have produced hybrids in captivity. This is surprising for many because these two species are reproduc-

tively isolated in the wild. The Borneo python is native to Sumatra and Malaysia, while the ball python is indigenous to Western and West Central Africa. From these data *Morelia/Liasis*, *Python*, and *Antaresia* were identified as three probable monobaramins, within the Boidae taxon.

The Colubridae family (Table III) is the largest snake taxon comprising about 1700 species which is more than 74% of all snake species. Many genera readily hybridize both naturally and in captivity. Members of the *Nerodia* complex of water snakes, for example, often intergrade in the wild. Some have even adapted to saltwater while others thrive in fresh water, demonstrating an interesting genetic variation in related species (Lawson et al., 1991). Herpetoculturalists have crossed at least 14 different species, in captivity, across the three genera *Pantherophis*, *Pituophis*, and *Lampropeltis* (Table III). They often question the taxonomic conclusions of what defines a species.

Historically the genera *Toluca* and *Conopsis*, which are Mexican endemics, have been differentiated by one single character, a groove on each posterior maxillary tooth.

Table III. Hybridization in *Colubridae*.

Hybrid Pairing	Artificial/Natural	Fertility	References
<i>Nerodia fasciata</i> x <i>N. sipedon</i>	Natural intergrades	Fertile	Lawson et al., 1991
<i>N. f. confluens</i> x <i>N. sipedon</i>	Natural intergrades	Fertile	Lawson et al., 1991
<i>N. f. pictiventris</i> x <i>N. sipedon</i>	Natural intergrades	Fertile	Lawson et al., 1991
<i>Nerodia f. confluens, fasciata, pictiventris</i> x <i>N. clarkii, taeniata, compressicauda</i>	Natural intergrades	Fertility between salt and freshwater snakes	Lawson et al., 1991
<i>Zamenis persicus</i> x <i>Z. situla</i>	Artificial	Fertile	Ryabov, 1998
<i>P. guttatus</i> x <i>P. obsoletus</i>	Artificial	Fertile	Sidelva et al., 2003
<i>Elaphe schrenckii</i> x <i>Elaphe anomala</i>	Artificial	Fertile	Sidelva et al., 2003
<i>P. climacophora</i> x <i>E. anomala</i>	Artificial	Fertile	Sidelva et al., 2003
<i>P. situla</i> x <i>Z. persicus</i>	Artificial	Fertile	Sidelva et al., 2003
<i>P. o. obsoletus</i> x <i>P. quadrivittata</i>	Natural Intergrades	Fertile	Conant, 1998
<i>Lampropeltis g. getula</i> x <i>L. g. floridana</i>	Natural Intergrades	Fertile	Conant, 1998
<i>L. t. triangulum</i> x <i>L. t. elapsoides</i>	Natural Intergrades	Fertile	Conant, 1998
<i>L. t. triangulum</i> x <i>P. g. guttatus</i>	Artificial	Fertile	Batton, 2000
<i>L. getula splendida</i> x <i>L. holbrookii</i>	Natural Intergrades	Fertile	Cole, 2004
<i>P. o. lindheimerii</i> x <i>P. bairdi</i>	Natural Intergrades	Fertile	Cole, 2004
<i>L. getula holbrookii</i> x <i>L. g. nigra</i>	Natural Intergrades	Fertile	Cole, 2004
<i>Diadophis punctatus arnyi</i> x <i>D. p. regalis</i>	Natural Intergrades	Fertile	Cole, 2004
<i>Storeria decayi subspecies</i>	Natural Intergrades	Fertile	Cook, 1993
<i>Thamnophis subspecies</i>	May integrate in NW California	Fertile	Morrison et al., 1998.
<i>Pantherophis, Pituophis, Lampropeltis</i>	Artificial breeding across genera common	Fertile	Kingsnake.com
<i>Pituophis catenifer annectens</i> x <i>P. melanoleucus</i>	Artificial	Fertile	Kennard, 1980

Toluca was said to have this trait while *Conopsis* did not. Otherwise, the two groups were difficult to distinguish and several taxonomists questioned whether this single trait was appropriate in the determination of its taxonomic status (Goyenechea and Flores-Villela, 2002). Consequently, a study was done, looking at a suite of characters that included snout-to-vent length, total length, number of ventral and subcaudal scales, shape of hemipenes, dorsal/ventral color patterns, and tooth grooves. In all, about 18 characters were studied in 199 members of *Conopsis* and 460 members of *Toluca* (Goyenechea and Flores-Villela, 2002). They found that all of the characters that were compared

intergenerally were variable and were found in both genera. They recommended that all ten species and subspecies be kept under one Genus called *Conopsis*.

Grismer et al. (2002) questioned the taxonomy of sand snakes (*Chilomeniscus*) after comparing four species of *Chilomeniscus* on such traits as color pattern, head scale morphology, ventral scale counts, and supra/infra labial counts. They found that these traits varied interspecifically. The authors concluded that there was no discrete difference between three of the four species of *Chilomeniscus* but maintained that *C. savagei* be separate because of its unique head scale arrangement. These four species: *C.*

Table IV. Hybridization in *Viperidae*.

Hybrid Pairing	Artificial/Natural	Fertility	References
<i>Sistrurus catenatus</i> x <i>Crotalus horridus</i>	Natural	Fertile	Klauber, 1997
<i>Crotalus adamanteus</i> x <i>Crotalus atricaudatus</i>	Natural	Fertile	Klauber, 1997
<i>Crotalus r. ruber</i> x <i>Crotalus h. helleri</i>	Artificial	Fertile	Klauber, 1997
<i>Crotalus s. scutulatus</i> x <i>Crotalus unicolor</i>	Artificial	Fertile	Klauber, 1997
<i>C. scut./unicolor</i> x <i>C. scutulatus/unicolor</i>	Artificial	Fertile	Klauber, 1997
<i>C. o. oreganus</i> x <i>C. scutulatus</i>	Artificial	Fertile	Klauber, 1997
<i>Crotalus atrox</i> x <i>Crotalus atricaudatus</i>	Artificial	Fertile	Cole, 2004
<i>Gloydus saxatilis</i> x <i>Gloydus halys</i>	Natural	Fertility Assumed. Controversial taxonomic status.	Kudryavtsev and Bozhansky, 1988
<i>Agkistrodon contortrix mokasen</i> x <i>Agkistrodon c. phaeogaster</i>	Natural	Fertile. Little molecular variation with copperhead subspecies.	LeClare, 2004
<i>Bitis gabonica</i> x <i>Bitis arietans</i> <i>Bitis gabonica</i> x <i>Bitis nasicornis</i>	Natural and Artificial	Fertile. Their ranges overlap in the wild.	Dexter, 2002

sinctus, *C. punctatissimus*, *C. stramineus*, and *C. savagei* are clearly related. To distinguish species based on a minor variation places too much emphasis on one characteristic. Likewise it draws attention to the philosophically ambiguous species concept. Based on hybridization and the great variation found in closely related snakes, I have identified the following genera as six probable monobaramins: *Nerodia*, *Pantherophis/Lampropeltis/Pituophis*, *Diadophis*, *Thamnophis*, *Toluca/Conopsis*, and *Chilomeniscus*.

Family *Viperidae* (the pit vipers) consists of about 200 species which make up about 10% of all snake species. Table IV lists four genera that hybridize with each other both in the wild and in captivity. The Massasaugas (*Sistrurus*) and the timber rattlers (*Crotalus*) have been known to produce fertile hybrids (Klauber, 1997). The copperheads (*Agkistrodon*) have little molecular variation between the subspecies which may intergrade naturally (LeClare, 2004).

The Aruba Island rattler (*Crotalus unicolor*) is one of the rarest rattlesnakes in the world (Klauber, 1997). It is found off the coast of Venezuela and though geographically isolated from the Mojave rattlesnake (*Crotalus scutulatus*), the

two species, Aruba Island rattler and Mohave rattlesnake, produced a fertile hybrid in captivity.

The genus *Bitis* includes the gaboon viper (*B. gabonica*), puff adder (*B. arietans*), and rhinoceros viper (*B. nasicornis*). Their territories overlap in the wild in Africa and they are thought to intergrade. In captivity they have hybridized interspecifically (Dexter, 2002). Therefore, I suggest that the genera *Crotalus/Sistrurus*, *Agkistrodon*, and *Bitis* each be classified as a monobaramin within the pit viper taxon.

Conclusions and Further Research

A common argument leveled against creation science is that it has no predictive value. Historically, the evolution model of common descent predicted that we would see continuity among all organisms and that they could all be traced to a single-celled ancestor. Alternatively, the creation model predicts that we should see discontinuity among various taxa because God made them after their kinds. The current evidence suggests that certain organisms are discontinuous with other organisms. For example, snakes have unique

characteristics that set them apart as a taxon, making them discontinuous with other organisms and classified as an apobaramin. This initial investigation also indicates that many snakes have the ability to hybridize, even when they are geographically isolated, and are capable of a great degree of variation within a “species.” In addition to kingsnake.com there are other informal internet sources that discuss the current hybrids being produced; they can be readily located using various search engines. Hybridization and species variation show that subgroups, based on close relationships, can be identified as monobaramins within the three families researched. Within Boidae, *Morelia/Liasis*, *Python*, and *Antaresia* were identified as three separate monobaramins. *Nerodia*, *Pantherophis/Lampropeltis/Pituophis*, *Diadophis*, *Thamnophis*, *Toluca/Conopsis*, and *Chilomeniscus* were identified as six monobaramins within the colubrid taxon and in the viper family the three monobaramins were *Crotalus/Sistrurus*, *Agkistrodon*, and *Bitis*. The goal is to determine whether all snakes came from an original pair or from two or more original pairs in the quest to identify the holobaramin(s).

There is still much to be done in order to complete their baraminology. As a taxon, they must be looked at holistically and other characters must be identified. From these data baraminology techniques such as the baraminic distance method, and the Analysis of Patterns (ANOPA) will help quantify significant similarities and differences between snake taxa (Wood and Murrury, 2003). Quantitative analysis will give us a better handle on the biosystematics of serpentes, and from a Biblical perspective, I predict that a better model of snake origins will emerge. This will provide an opportunity to consider the Bible’s claims and ultimately to understand the Creator’s outline.

Glossary

Apobaramin – consists of at least one group related by common ancestry but does not share ancestry with any other member outside its own group. (Example: Snakes are hypothesized to be an apobaramin because they do not seem to share a common ancestor with any other group such as birds or fish. It is unknown, however, whether snakes are made up of one or more holobaramins because it is unclear whether they arose from one or a few originally created snake “kinds.”)

Baraminology – a creationist method of biosystematics used to identify the originally created “kinds” and incorporating discontinuity criteria and other creationist assumptions.

Discontinuity or discontinuous with – a significant difference between two groups of organisms. (Example: Turtles are distinctly different creatures than birds and therefore

turtles are discontinuous with birds.)

Holobaramin – all of the organisms in a group that are related to one another but not related to any other group. (Example: All humans are classified as a holobaramin because all are descended from the original Adam and Eve and are not related to any other organism.)

Monobaramin – a group of organisms related to one another by common descent, but do not necessarily include all of the organisms in that holobaramin. (Example: Caucasians and Amerindians would be monobaramins in the human holobaramin because they represent a subset of humans but do not represent all people in the human holobaramin.)

Morphology – the study of the form and structure of organisms.

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