

<https://creationismeweersproken.blogspot.com/2023/03/de-rode-panda-en-cserhati-17-baramin.html>

## THE RED PANDA AND CSERHATI (17): BARAMIN

Cserhati advances several proposals for 'baramin' in his CRSQ article, and provides an interesting comment about recognizability of baramin.

Proposal 1            Musteloidea als baramin (pp 78, 79), first interpretation of the WGKS data

Proposal 2            A mustelid cluster of the red panda with the Mustelidae species, an interpretation of the WGKS and cytochrome b analyses (pp 81, 82)

Proposal 3            The red panda as a separate baramin, as indicated by the mtDNA analysis (page 82)

Proposal 4            How do you recognize 'lineage' versus 'baramin'? (p.81)

### Ad Proposal 1

The Musteloidea as baramin appear in the first interpretation of the WGKS results, but this possibility is not further discussed.

### Ad Proposal 2

In the WGKS revised interpretation and the cytochrome b interpretation, the red panda and the mustelids cluster together. Cserhati considers them to belong to one baramin. So, he considers the red panda to be related to the mustelids (by definition of baramin), and not related to the raccoons and the skunks. Cserhati realizes that the red panda can be found not inside but next to the Mustelidae family in the heatmaps of these two analyses, somewhat on the outside of the group.

Cserhati proposes an explanation for the red panda being somewhat different from the mustelids, visible as a lower correlation.

*The reason for the low mean PCC (correlation) value between A. fulgens and all other mustelids might be its geographic isolation in the mountainous areas of Nepal, India, and China. This could have allowed for greater genetic change to take place.*

It remains to be seen whether the geography of the red panda is quite so isolated, in red panda terms, and whether geographic isolation would explain the difference of the red panda from the mustelids. The hog badger *Arctonyx*, from around the same area as the red panda, falls neatly within the mustelid family. The sea otter *Enhydra* can also be called geographically isolated, but also falls neatly within the mustelids. All in all, although geographic isolation may lead to a separate genetic lineage, it is not certain that this accounts for differences between mustelids and the red panda. In any case, no 'greater genetic change' – that is not documented -, only 'different genetic change'.

### Ad Proposal 3

The red panda as a separate holobaramin is a possible conclusion according to the mtDNA heatmap.

*Alternatively, A. fulgens could be the only known member of its own holobaramin ...*

The red panda subspecies are the only living representatives of the Ailuridae family according to science. This is supported by the heatmap of mtDNA in the CRSQ article.

Cserhati considers a holobaramin with only one species to be possible.

*When a taxon, as in this case, a holobaramin loses a large portion of its constituent species, during a mass extinction, such as the Genesis Flood, it loses its capability to re-diversify after the extinction.*

This statement of Cserhati leaves loose ends.

Genesis 7:14 says that of the unclean animals according to their kind (KJV) one pair, a male and a female, go into the Ark. All predators are unclean, so the family Mustelidae with 65 or so now living species and the family Ailuridae with one species would have been both present on the Ark with one pair for their baramin. In the case of the Mustelidae, this would involve a re-diversification to the most species-rich and diverse family within the order Carnivora, and in the case of the Ailuridae, the family would be stuck at one species.

Cserhati thinks it's possible that with a large loss of species in a mass extinction, the remaining species are somehow unlucky and have little genetic variation left for diversification. The question then arises whether the Ailuridae or the Mustelidae lost "a large portion of its constituent species" during a mass extinction. It should be possible to verify this using fossils of the families

Ailuridae and Mustelidae. Fossils of both families are known. Nothing in the fossil record of these families indicates a mass extinction.

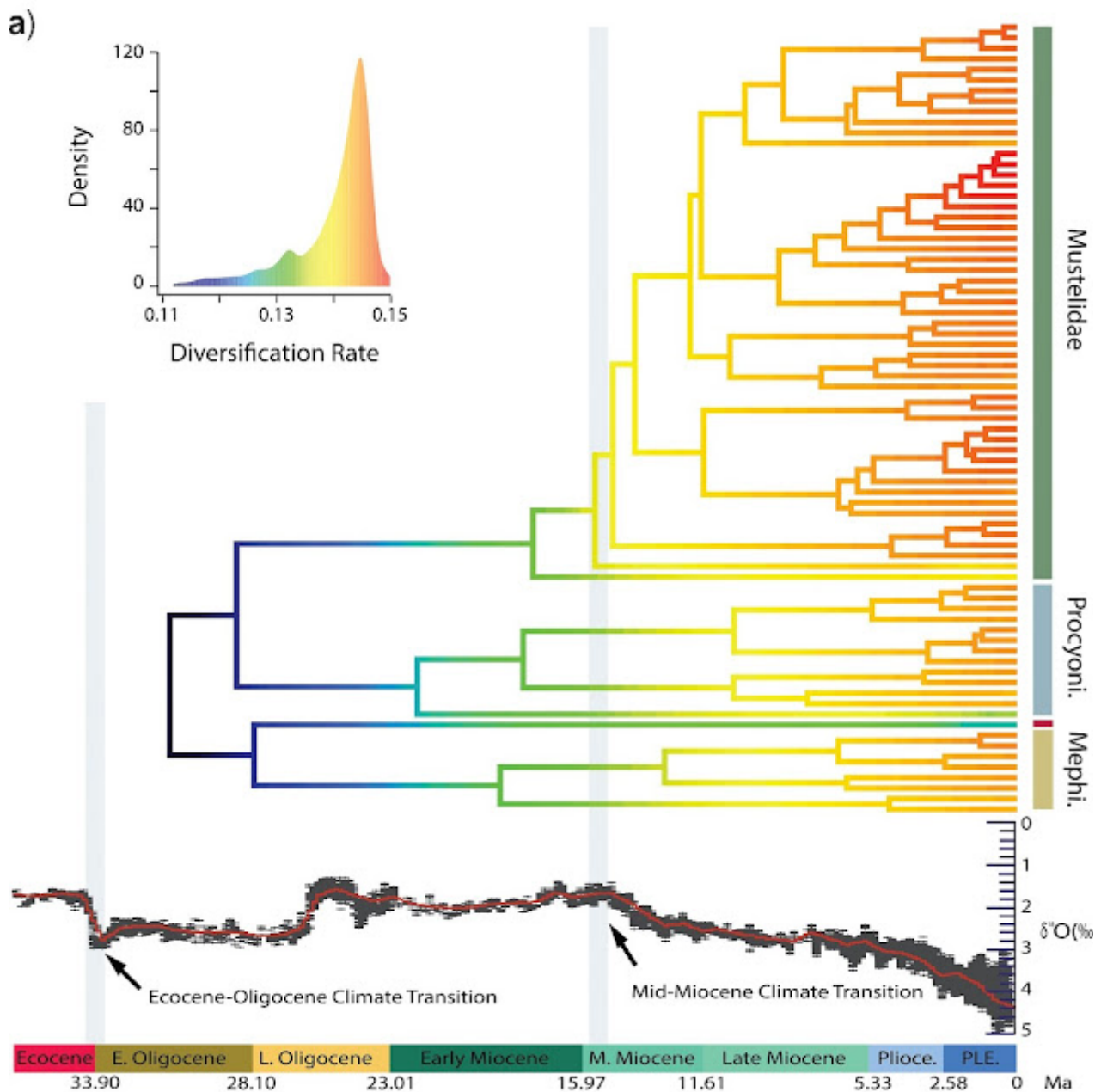


Figure 1. Diversification in fossil Musteloidea. Red, in the lay-out tussen Mephi. en Procyon., Ailuridae are indicated . Figuur 3a van Law et al (2017)

Proposed creationist End-Flood boundaries are the Pliocene-Pleistocene boundary and the Cretaceous-Paleogene boundary. At the Pliocene-Pleistocene boundary, species diversity in the Mustelidae and Ailuridae is close to current (see figure 1). At the Cretaceous-Paleogene boundary, the orders of mammals and therefore the families Ailuridae and Mustelidae did not exist.

Cserhati gives an example of inability for extensive speciation after a mass extinction:

*When a taxon, as in this case, a holobaramin loses a large portion of its constituent species, during a mass extinction, such as the Genesis Flood, it loses its capability to re-diversify after the extinction. Such taxa include ..., and parareptiles (MacDougall, 2019).*

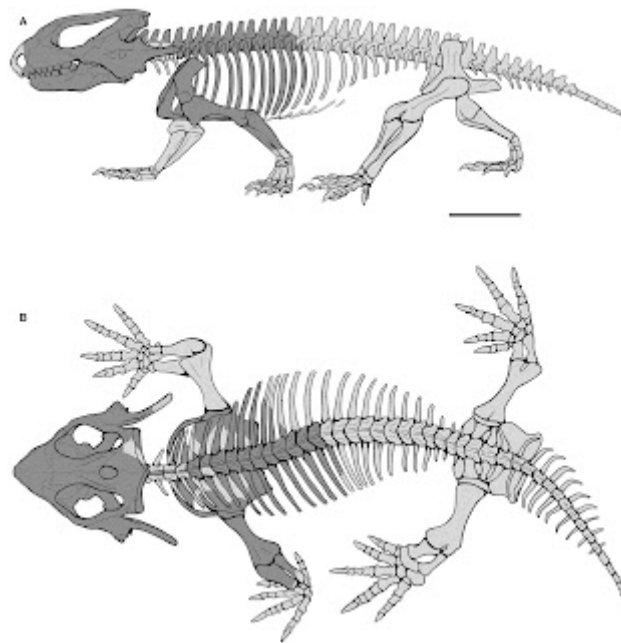


Figure 2 Fossil skeleton parareptile Kapes

The group Parareptiles differs from living reptiles and their associated fossils. The Parareptiles existed from the end of the Carboniferous 306 million years ago to the end of the Triassic period 201 million years ago. They survived the Permian-Triassic mass extinction, but with greatly reduced diversity. The phenomenon cited by Cserhati exists. But it's not such a good example for a creationist or for extinction by the Genesis Flood. The group Parareptiles originated during the Genesis Flood, and died out again during the Genesis Flood.

#### Ad Proposal 4

Cserhati gives some argument why not to stick with the mtDNA results.

*A faster mutation rate means larger differences in the mtDNA sequence in contrast with the nuclear genome. This may reveal lineages within a kind, which might appear to be separate baramins.*

Baramin or lineages within baramin surface using mtDNA. Now what are lineages, and what are baramin? The last sentence of Cserhati above is a very interesting comment (p. 81):

*lineages within a kind, which might appear to be separate baramins.*

This implies that baramin cannot be recognized. After all, it is always possible to find lineages. Hennigan (2009) lists creationist definitions to identify baramin:

*Continuity – Biologically meaningful similarity between organisms that embrace all types of biological characteristics.*

*Discontinuity – Biologically meaningful differences between organisms.*

Let us see how these ideas work out.

The red panda eats bamboo, is a vegetarian. The mustelids are carnivorous, with some degree of omnivory in some species of badgers. That is a 'biologically meaningful difference'. Then the red panda would represent a baramin whether or not the red panda clusters with the mustelids.

Is a cluster a baramin or a lineage? With clustering you can find 'lineages' and 'baramin'. Take only the family Mustelidae, and start clustering. A cluster of 'otters' appears, the subfamily Lutrinae. A baramin? Within that subfamily Lutrinae there are lineages, namely the genera. The sea otter stands alone as a species in its genus, with a different lifestyle and different teeth than all other otters. These are 'biologically meaningful differences' between the sea otter and other otters. Perhaps the genus *Enhydra* is a baramin with only one species?

In Figure 2 of the CRSQ article (Figure 3 here) we see subdivisions and subdivisions in the heat map of the WGKS correlations. The hierarchy in classification of the animal kingdom is clearly visible. The cats stand out as a dark group at the bottom left. The bears and the mustelids together color dark gray - aren't we dealing with two baramin, a cat baramin and a bear+superfamily Musteloidea baramin? Rather than with three baramin, cats, bears and Musteloidea? The bears and the mustelids both belong to the taxonomic group Arctoidea, while the cats do not. (There is no figure for the WGKS data with number of clusters on the x-axis and silhouette width on the y-axis to see what the optimal number of clusters is).

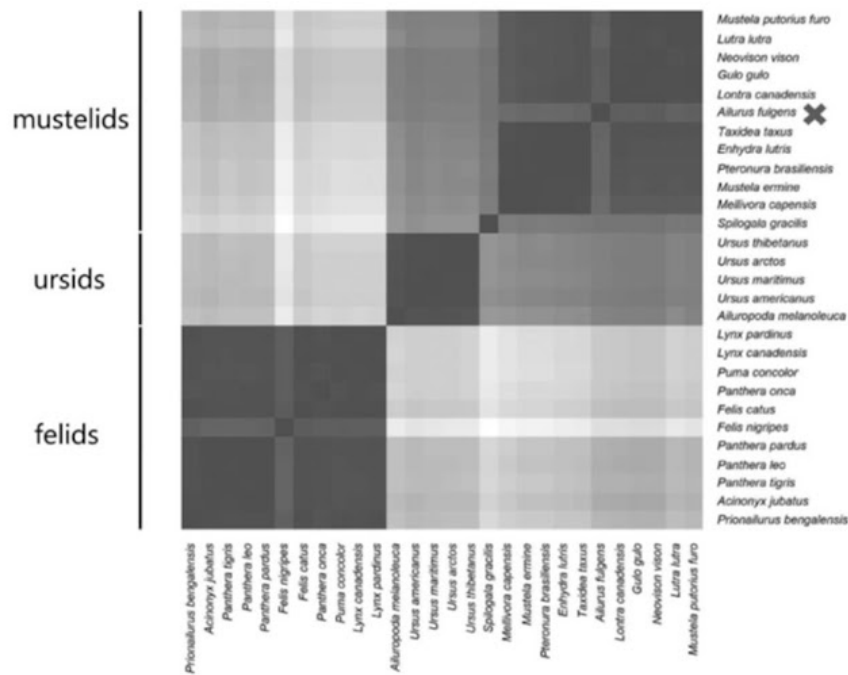


Figure 3 WGKS heatmap with hierarchical pattern

The dog family Canidae and the Arctoidea together form the group Caniformia, one of the two main groups within the order Carnivora. The other main group is the Feliformia. There are many 'biologically meaningful differences' between the main groups Feliformia and Caniformia. Are the Feliformia and the Caniformia baramin? Or the order Carnivora? Orders differ in important 'biologically meaningful differences'. Perhaps an order is a baramin?

Orders can also be clustered. Take three orders, and three species from each order. The correlations\*100 in mtDNA of the nine species are:

Red deer	100	85	86	78	79	78	72	73	73
Cow	85	100	86	79	78	78	72	73	73
Musk deer	86	86	100	78	79	78	73	74	73
Meerkat	78	79	78	100	83	84	72	73	73
Domestic cat	79	78	79	83	100	83	71	72	73
Hyena	78	78	78	84	83	100	71	72	73
Rhesus macaque	72	72	73	72	71	71	100	79	79
Human	73	73	74	73	72	72	79	100	89
Gorilla	73	73	73	73	73	73	79	89	100

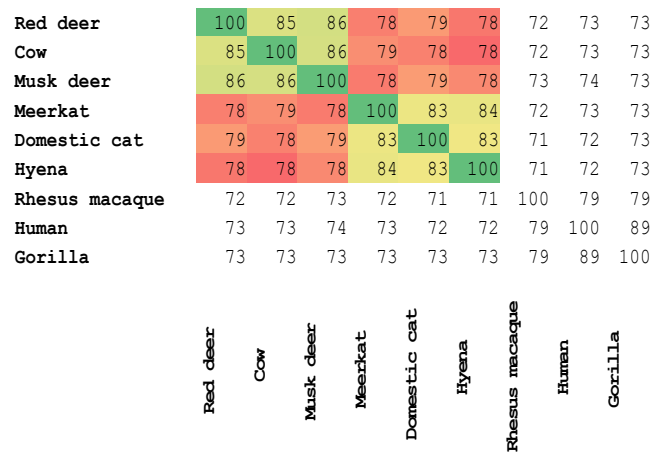


Figure 4. Nine species from three orders in three clusters; correlations \* 100 mtDNA

Two groups are visible in the upper heatmap: in mammalian taxonomy, those groups are the Laurasiatheria, upper left, and the Euarchontoglires, lower right. Two baramin? Those Laurasiatheria show two groups. Or should we think of three groups, from top left to bottom right, the orders ungulates Artiodactyla, predators Carnivora and apes/monkeys Primates? Three baramin? Or eight families, with eight baramin? Or nine baramin, despite the clustering?

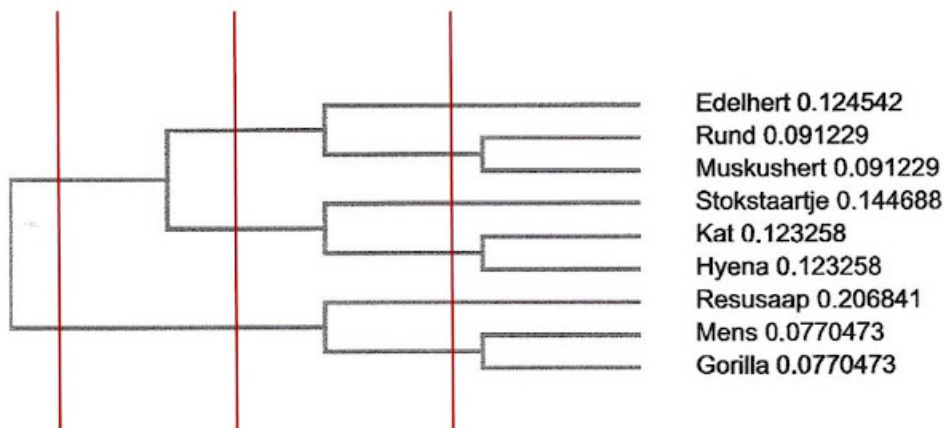


Figure 5 Hierarchical classification of the nine species. Top three species ungulates, middle three species carnivores, lower three species primates. This is a diagram, the differences between the species are in the numbers on the right, not in the line length. The red lines indicate how many groups will be found on a taxonomic level: 2,3 or 6 - compare the heatmap.

The animal kingdom is arranged hierarchically: this is how the animal kingdom is structured. Hierarchical classification is according to 'biologically meaningful similarity'. Hierarchical division allows 'biologically meaningful differences' to emerge. Clustering produces random patterns if data are hierarchical in nature - a cluster can be chosen at any level in the hierarchy (see vertical lines). Hence, clustering cannot tell what is a baramin and what is a lineage.

In fact, the hierarchical structure of life makes a fiction of the whole idea that baramin can be found by clustering.

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Cserhati, M., 2021, Classification of the Enigmatic Red Panda (*Ailurus fulgens*) Based on Molecular Baraminology-Based Analysis, Creation Research Society Quarterly 58 (2): 76-84

Hennigan, T. 2010. The case for holobaraminic status in bears (family Ursidae) and the implications within a creation model of ecology. CRSQ 46(4):271–283.

Law, C. J.; Slater, G. J. & Mehta, R. S. (2018). Lineage Diversity and Size Disparity in Musteloidea: Testing Patterns of Adaptive Radiation Using Molecular and Fossil-Based Methods. *Systematic Biology*. 67: 127–144. doi:10.1093/sysbio/syx047.

<https://en.wikipedia.org/wiki/Parareptilia>

[https://commons.wikimedia.org/wiki/File:Kapes\\_full\\_skeleton.jpg](https://commons.wikimedia.org/wiki/File:Kapes_full_skeleton.jpg)

<https://creation.com/disagreements-on-the-post-flood-boundary>