

<https://creationismeweersproken.blogspot.com/2023/04/de-rode-panda-en-cserhati-18-cserhati.html>

## THE RED PANDA AND CSERHATI (18): CSERHATI TRIES TO ANSWER

On November 5, 2022, Jan van Meerten wrote an article on his Dutch website 'Oorsprong' with the title: **Wetenschapper lost (creationistisch) biosystematisch raadsel van de rode panda (*Ailurus fulgens*) op**. This translates as: "**Scientist solves (creationist) biosystematic riddle of the red panda (*Ailurus fulgens*)**". A Dr. M. Cserhati had investigated the possible taxonomic position of the red panda, and published the results in the scientific journal BMC Genomics and in the creationist journal Creation Research Society Quarterly.



figure 1

Jan van Meerten described the outcome of the research as: "*The results of this study show that the red panda belongs to the mustelid family (Mustelidae).*" This was based on what Cserhati wrote in his BMC Genomics article: '*The main conclusion we can draw from this research is that at the whole genome level, A. fulgens belongs to the mustelid clade.*' And on what Cserhati wrote in his CRSQ article: '*Probably the red panda belongs to the holobaramin of the mustelids.*'

One doesn't need to know much about the red panda to know that "red panda a mustelid" can't be right. In 2010 I had looked at the molecular taxonomy of the red panda, and the classification of the red panda turned out to be not completely clear, but not too puzzling either. A club of four families form the superfamily Musteloidea: the martens, raccoons, skunks and the red panda (the red panda itself as a family). In 2020, all studies arrived at the combination (martens, raccoons), but then? Is it (red panda , (skunks , (martens , raccoons))), or (skunks , (red panda , (martens , raccoons)))? An amusing little problem: what exactly is the order of that quick split between skunks, red panda, and martens+raccoons? But the red panda a mustelid? Never in all of the scientific literature. There's something odd about what Cserhati is doing.

So I looked into Cserhati's writings a bit further, and wrote a 1000 word comment on the Panda's Thumb website (December 2, 2022). Cserhati joined the discussion on Panda's Thumb and wrote a 4000 word comment on Jan van Meerten's website 'Oorsprong' (December 13, 2022). Then in 2023 I wrote a long series on the scientific literature concerning the red panda and all the errors in Cserhati's two articles, on my website "creationisme weersproken blogspot" ('creationism contradicted blogspot').

Now Cserhati's piece on the website "Oorsprong" is due for comment.

## **Cserhati on 'Oorsprong' I: Until Figure 1**

Cserhati's first 141 words, that is, his title and the sentences above figure 1, contain eight erroneous statements. Statements by Cserhati are in **bold**.

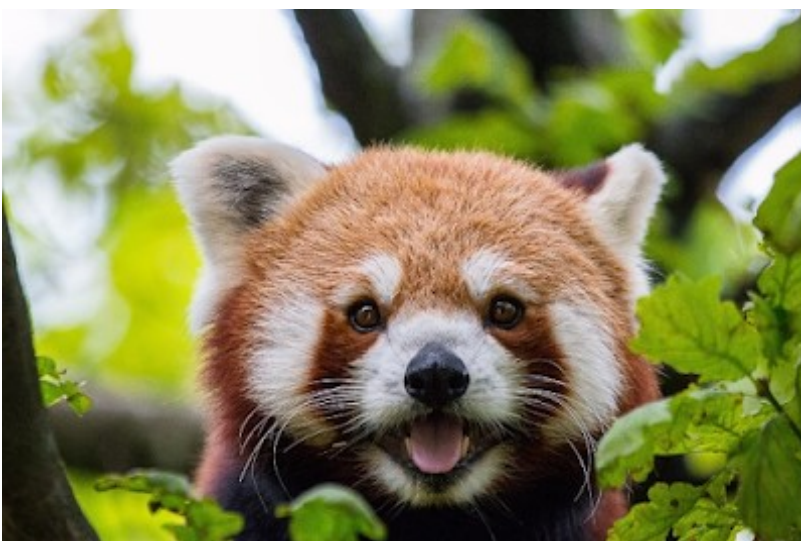


Figure 2: Figure 1 Cserhati on Oorsprong

1 The title "**Evolutionists on Panda's Thumb Attack Well-Respected Science Journal**" gives the impression that the article in Panda's Thumb is an attack on BMC Genomics. In contrast, it is critical of both of Cserhati's pieces, and that has nothing to do with the journal BMC Genomics. It has to do with the extremely poor work Cserhati has done. It is true that the question: "*One problem: how did a paper as bad as this ever get through review and published?*" appears on Panda's Thumb in the section on the BMC Genomics article, but it also applies to the CRSQ article.

2 '**Some have classified it** (the red panda) **as a cat...**' This is wrong. No one has ever classified the red panda as belonging to the cat family Felidae. It is not even claimed article by Cserhati in any of his two articles. The CRSQ article says: "*Geoffroy-Saint-Hilare and Cuvier originally classified the red panda as a member of the **raccoon** family (Procyonidae), although they ended up calling it Ailurus, because of its somewhat feline appearance*". (bold added gdj) The red panda was classified with the raccoons Procyonidae upon its first description. That was in 1825, and since then the poor red panda has been stuck with a name that means "wild cat" in ancient Greek.

3 "Some have classified it as a cat, **some as a relative of small carnivorous animals, such as minks or weasels, ...**" This is wrong. No one has ever classified the red panda with the minks and weasels or with the family that the minks and weasels belong to. Minks and weasels belong to the Mustelinae subfamily of the Mustelidae family. In the introduction to the BMC Genomics article, Cserhati gives three references for his idea that the red panda belongs to the mustelids: one misquoted - it says musteloid and Cserhati reads mustelid - , and two misinterpreted.

4 "Some have classified it as a cat, some as a relative of small carnivorous animals, such as minks or weasels, **yet others claim that it is a relative of the giant panda, Ailuropoda melanoleuca. ..**" This is wrong. Past and present are mixed up. Cserhati's source, Flynn et al (2000), makes clear that this should be 'claimed' and not 'claim'. Flynn et al (2000) write about the older literature: "*(red panda) sister taxon to the giant panda either with uncertainty about their broader relationships (Segall, 1943) or with the panda clade as sister taxon to ursids (Ginsburg, 1982 )*". References from 1943 and 1982 are a bit long ago to use the present tense in 2022.

5 " Similar to the duck-billed platypus, **biologists do not know where to put this animal, ...**". This is wrong. The red panda has been placed in the superfamily Musteloidea for at least 25 years, in a quick split between skunks, red panda, and martens+raccoons. The question was how to resolve the small

distances between the families (see blog post 2). In fact, with the article by Hassanin et al (2021), the placement of the red panda seems decided. Cserhati could have known that at the end of 2022. In 2020 or thereabouts when Cserhati wrote his articles, it was already established that the red panda belonged to the Musteloidea *sensu lato* but not to the Musteloidea *sensu stricto*. So, there were only the three possibilities that I mentioned in blog 2.

6 **"Similar to the duck-billed platypus,** biologists do not know where to put this animal, ....". This is wrong. The platypus is staged for no valid reason. The platypus is the only living member of the platypus family (Ornithorhynchidae) and suborder platypus (Platypoda), within the order Monotremata of mammals. Neatly classified, with a know evolutionary history. For unbiased information see wikipedia; for a biased uninformative story see the creation.com entry Cserhati alludes to

7 **"Molecular characterization of this species based on small sets of genes also did not fare any better,** and evolutionists contradicted one another again in further attempts to classify this animal." This is wrong. Flynn et al (2000) had "a total of 3450 bp ... for 17 carnivoran species" - few by current standards, but they arrived at a classification consistent with the most recent classification, that of Hassanin et al (2021) based on much more material.

8 "Molecular characterization of this species based on small sets of genes also did not fare any better, **and evolutionists contradicted one another again in further attempts to classify this animal.**" This is wrong. The red panda placement differences were never major - it's just about the red panda's place within the superfamily Musteloidea. No one makes the red panda a relative of, for example, the bear cat (*Arctictis binturong*), although the bear cat may resemble the red panda in terms of appearance, lifestyle and distribution area. The bear cat belongs to the civet family Viverridae. Cserhati tries to make a major disagreement out of a minor uncertainty.

## **Cserhati 'Oorsprong' II. Table 1**

After the eight errors above the first figure, we get:

*"To illustrate the fact that evolutionists themselves cannot make heads or furry red tails of where to place the red panda, see Table 1 below to see how various evolutionist researchers tried to classify this mysterious animal."*



Figure 3 Figure 2 Cserhati on Oorsprong

Cserhati's Table 1 does not tabulate the classifications scientists arrived at, but Cserhati's erroneous interpretation of their scientific work.

Cserhati's Table 1.

<b>Researcher(s)</b>	<b>Analysis</b>	<b>Conclusion</b>
Peng et al	13 mitochondrial genes	Either mustelid or mephitid
Fulton and Strobeck	3 nuclear and 3 mitochondrial genes	Related to <i>Mephitis mephitis</i>
Yu and Zhang	Introns 4 and 7 of nuclear FGB gene, ND2 mitochondrial gene	Sister to procyonids
Sato et al	5.5 Kbp segment containing 5 nuclear genes	Closer to mustelids or procyonids

Cserhati cites four articles and succeeds in drawing four erroneous conclusions.

Table 1 line 1

‘Either mustelid or mephitid’

The article by Peng et al (2007) deals with the placing of the giant panda in the bear family Ursidae, with a whole series of more or less related species as background, as outgroups. The Musteloidea are part of the outgroup. For the Musteloidea are represented by one species per family: the red panda for itself as family Ailuridae, the raccoon for the Procyonidae, the striped skunk for the Mephitids and the American marten for the Mustelidae. Peng provides two analyses.

This is the NJ method.

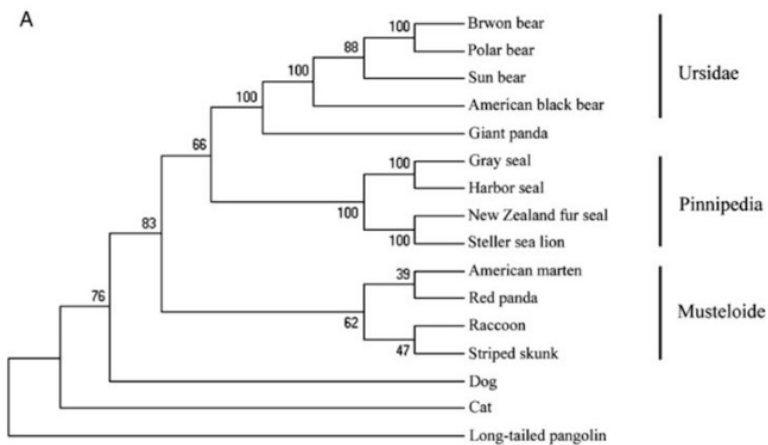


Figure 4 Figure 2A Peng et al (2007)

Here the red panda forms the sister group to the American marten, but since there is only one species of the family Mustelidae – the American marten- , it cannot be concluded that the red panda belongs to the Mustelidae: "*mustelid*" is incorrectly reasoned.

This is the ML method:

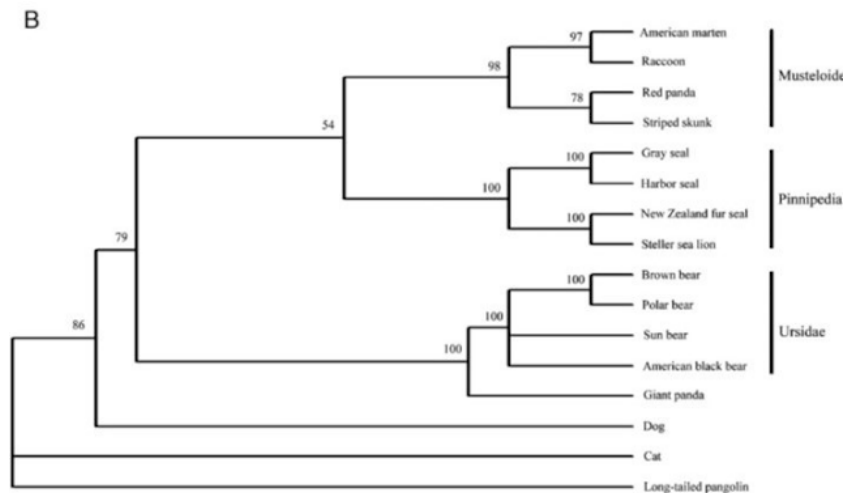


Figure 5 Figure 2B Peng et al (2007)

Here the red panda forms the sister group to the striped skunk, but since there is only one species of the family Mephitidae, it cannot be concluded that the red panda belongs to the Mephitidae: "*mephitid*" is incorrectly reasoned. It is a basal error in reasoning.

The red panda, as family Ailuridae, appears to be the sister family of the Mustelidae or the Mephitidae. No way the red panda would be part of the family Mustelidae or Mephitidae, as '*mustelid or mephitid*' suggests. Cserhati doesn't understand the sistergroup idea. Cserhati misreads the article by Peng et al (2007). Cserhati's citation of the work of Peng et al is also wrong: in the BMC Genomics article as well as the CRSQ article and on Origin, Cserhati gives the date '2017' while the article dates from 2007.

Table 1 line 2                      'Related to *Mephitis mephitis*'

Fulton & Strobeck (2007) is a study of the phylogeny within the raccoon family Procyonidae, with the red panda, two marine Carnivora (Pinnipedia) and the wolf as outgroup.

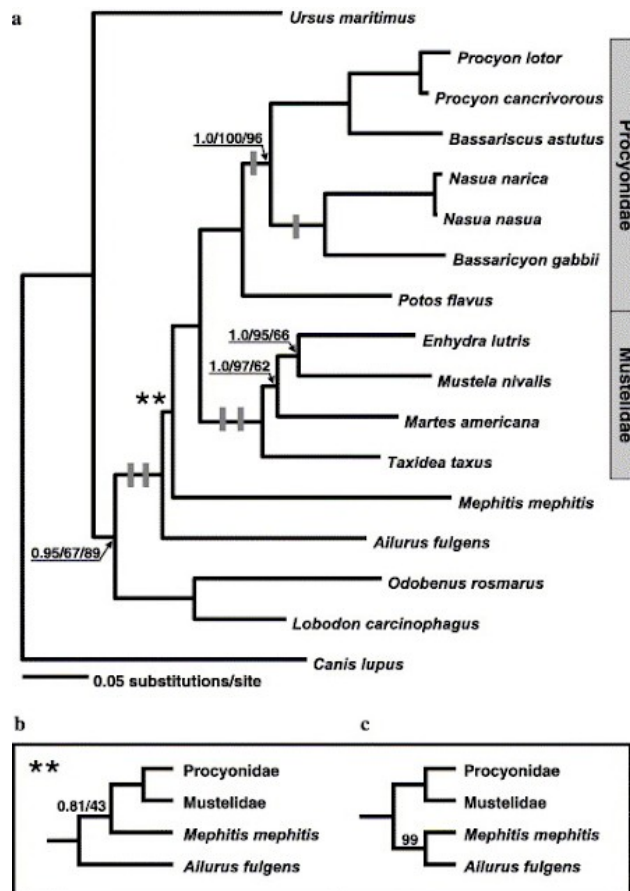


Figure 6 Figure 1 Fulton & Strobeck (2007)

Fulton & Strobeck (2007) provide several analyses. Maximum Likelihood and Bayesian give the red panda Ailuridae as a sister group of Mephitidae + Mustelidae + Procyonidae (their fig 1a,b); Maximum Parsimony lists the red panda as a sister group to the Mephitidae (their fig 1c).

"Related to *Mephitis mephitis*" - At most there is a sister-group relationship between the family Ailuridae and the family Mephitidae. The preference of Fulton & Strobeck (2007) goes to fig. 1ab, with the red panda family Ailuridae as a sister group of the three other families within the Musteloidea.

Note that in the layout of figures 1abc of Fulton & Strobeck (2007) *Ailurus fulgens* is placed next to *Mephitis mephitis*, even when the phylogenetic tree differs. Perhaps Cserhati just looked at the lay-out.

Table 1 line 3        '*Sister to procyonids*'

Yu & Zhang (2006) provide a phylogeny of the Caniformia, one of the two main groups of the order Carnivora.

In Table 1 on the website 'Oorsprong', Cserhati gives a different interpretation of the results of Yu & Zhang than in his introduction to the BMC Genomics article. Both interpretations are wrong.

In his introduction to the BMC Genomics article, Cserhati says:

*"Yu and Zhang studied introns 4 and 7 from the nuclear gene  $\beta$ -fibrinogen (FGB) as well as the mitochondrial gene NADH dehydrogenase subunit 2 (ND2) in 17 species from the order Carnivora. In their results these researchers found that A. fulgens is most closely related to procyonids based on analysis of intron 4 of the FGB gene. When the two introns were combined with analysis of the genes IRBP and TTR, A. fulgens was closest to mustelids [9]."*

In his introduction to the BMC Genomics article, Cserhati confuses three times the layout of the phylogenetic tree with the classification according to the phylogenetic tree. (See blog 5 of this series for the figures). That's quite a basic mistake.

In Table 1 on 'Oorsprong', Cserhati says: "*Introns 4 and 7 of nuclear FGB gene, ND2 mitochondrial gene - Sister to procyonids*". On 'Oorsprong', Cserhati seems to have forgotten what he said in the introduction to the BMC Genomics article, but again Cserhati confuses the layout of a phylogenetic tree with the classification according to a phylogenetic tree.

Yu & Zhang (2006) give for "*Introns 4 and 7 of nuclear FGB gene, ND2 mitochondrial gene*" the red panda as a sister group of the Musteloidea *sensu*



*stricto*: the mustelid family Mustelidae and the raccoon family Procyonidae together.

Table 1 line 4 'Closer to mustelids or procyonids'

Sato et al (2009) is the only one of the four papers listed that really deals with red panda placement. Sato et al (2009) give the following phylogenetic tree:

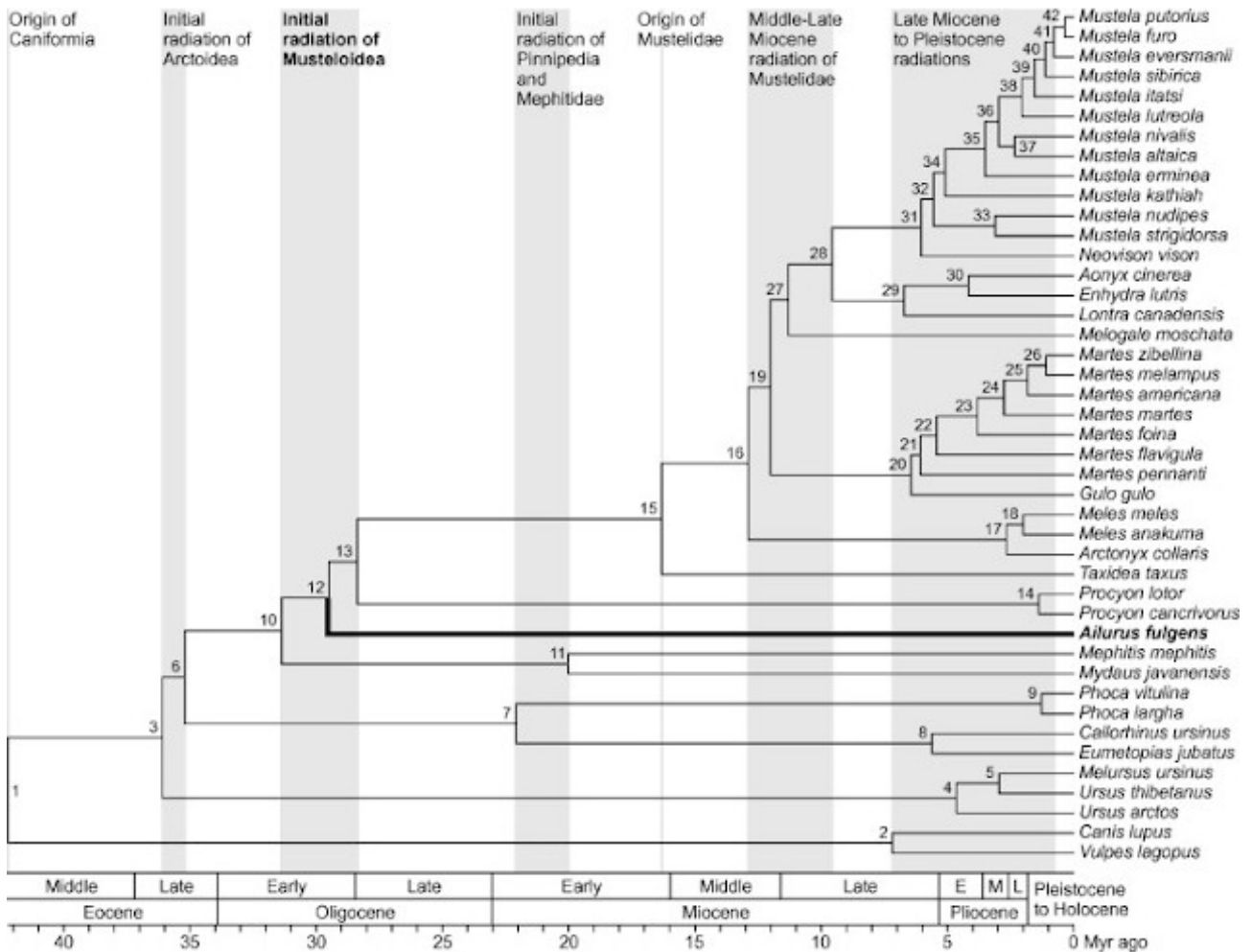


Figure 7 Figure 3 Sato et al (2009)

The conclusions by Sato et al (2009) are:

*All our phylogenetic analyses, both the probabilistic and parsimony ones, strongly supported a close relationship between the red panda and a clade containing Mustelidae and Procyonidae to the exclusion of Mephitidae (Fig. 1).*

*The close affinity of the red panda with the mustelids and procyonids to the exclusion of mephitids had been first hypothesized in our previous study (Sato et al., 2006) and a few months later was independently confirmed by Fulton and Strobeck (2006).*

Sato et al (2009) list the red panda as the sister species of Musteloidea *sensu stricto*, the families Mustelidae and Procyonidae together. To quote the conclusion of Sato et al (2009) as "Closer to mustelids or procyonids" is pure lack of understanding, not grasping sistergroups. "Closer to mustelids or procyonids" is quite wrong. What would Cserhati think Sato's "a clade containing Mustelidae and Procyonidae" means?

Yu & Zhang (2006) and Sato et al (2009) give the same phylogenetic tree, a phylogenetic tree that also occurs elsewhere in the literature; see blog 2 for that. Fulton & Strobeck (2007) give a slightly different one often found phylogeny (see again blog 2).

Table 1 was meant: *"To illustrate the fact that evolutionists themselves cannot make heads or furry red tails of where to place the red panda, see Table 1 below to see how various evolutionist researchers tried to classify this mysterious animal."*

Not so. On the contrary Table 1 is extremely useful *to illustrate the fact* that Cserhati is not able to read the scientific literature.

Note these four article are published in 2007, 2006, 2007 and 2009. Cserhati is either ignorant of more recent scientific work on the classification of the red panda, or he chooses not to cite recent papers.

### **Cserhati on 'Oorsprong' III**

Section III contains 1245 irrelevant words.



Figure 8: Figure 3 Cserhati on Oorsprong

## **Cserhati on 'Oorsprong 'IV: Cserhati's comment on post and discussion on the Panda's Thumb**

After figure 3, in section IV, Cserhati gets to the point and starts discussing blog post and the first part of the discussion that appeared on the website Panda's Thumb. Cserhati gives four propositions which he says can be found on the Panda's Thumb. Cserhati seems to disagree with those four statements. The Panda's-Thumb-statements-according-to-Cserhati are printed here in italics / bold.



Figure 9

### **IV A**

#### ***1. The red panda and the marten family (Mustelidae) are sister groups. Ailurus fulgens is not a member of Mustelidae.***

I wrote on *Panda's Thumb*: "Nowhere in his (Cserhati's) analyses does the red panda appear within the marten group. At most we see a monophyletic group of the marten and panda families." Seemingly Cserhati disagrees, as he marks this statement for comment.

Cserhati says in his BMC Genomics article:

*"The main conclusion that we can draw from this study is that on a whole genome level A. fulgens possibly belongs to the mustelid clade,"*

*"Based on this evidence, A. fulgens would belong to mustelids as a monophyletic group."*

*"In conclusion, A. fulgens possibly belongs to Mustelidae, based on the analysis of the WGKS."*

Cserhati's conclusion is pertinently wrong. Not only that, but this conclusion is based on disregarding his own results. Cserhati's own results show that the red panda forms a group of its own.

The red panda as a sister group of the Mustelidae follows directly from Cserhati's BMC Genomics figure 2 (UPGMA phylogenetic tree on WGKS, blog post 7) and figure 4 (UPGMA on mtDNA, blog post 12). The NJ and ML analyses (BMC Genomics figure 5 and figure 6) give the red panda as an independent group even with Cserhati's strange interpretation; and if the bears are taken as an outgroup – as they should have been in a correct analysis – , the red panda emerges as an independent group and sister group to the remaining three families within the Musteloidea. (See blog post 12 for further explanation). These four phylogenetic trees, Figures 2, 4, 5, 6 from the BMC Genomics article, give the actual results of Cserhati.

However, Cserhati relies entirely on the heat map of the WGKS correlations. There is no valid justifiable reason for this. First, to be valid reasoning a heat map should be suitable for classification; on the contrary, a heatmap is not suitable for classification. Second, to be valid reasoning the red panda should fall within the family Mustelidae in the heatmap; however, the red panda is not included within the mustelids in the heat map. Cserhati gives the heatmap of the WGKS correlations as his figure 1 from the BMC Genomics article and as figure 4 on Origin. This figure clearly shows that the correlations of the red panda with the species of the Mustelidae are lower than the correlations between the species of the marten family amongst each other. Cserhati agrees: "*It is true that the red panda has a mean correlation value of 0.89 with the mustelids, whereas the mean correlation among mustelids is 0.95±0.04*". The difference is significant, as I said on Panda's Thumb and when discussing the BMC Genomics results. Cserhati does not deny that. Cserhati does not understand this precludes inclusion of the red panda in the marten family Mustelidae.

Cserhati takes a completely different turn, with contorted reasoning. He refers to the difference between the black-footed cat *Felis nigripes* and the other ten species of the cat family. In his heatmap of WGKS correlations, the black-footed cat appears to differ strongly from the other cats: even significantly different.

The black-footed cat is undoubtedly a species of the cat family Felidae.

Then Cserhati reasons:

(i) apparently under WGKS a great difference between a species A and the other species of its family is possible;

(ii) then a great difference between a species B and known species of a family means that species B will belong to the same family as those other species.

According to that sort of reasoning, an animal species B might belong to a family of plants.

Somewhere in the discussion on Panda's Thumb, Cserhati says: "*Since we know from biology that F. nigripes belongs to the cat baramin, then why can we then not infer that the red panda is a mustelid, with its smaller distance?*"

The answer is of course: "Because, if A implies B, it is not necessary that B implies A."

In the BMC Genomics artikel Cserhati remarks a propos the WGKS difference of the black footed cat and the other cats: "*Based on this (black footed cat) evidence, A. fulgens would belong to mustelids as a monophyletic group.*" It is not 'evidence' at all, far from it. Nowhere in his two articles has Cserhati any evidence that the red panda might be a mustelid, could belong to the family Mustelidae. On the contrary, the phylogenetic trees in Figures 2, 4, 5, 6 from the BMC Genomics article, phylogenetic trees that give the actual results of Cserhati, clearly contradict any such idea..

Cserhati protests on the website 'Oorsprong' and in the discussion on Panda's Thumb that I did not go into his story about the black-footed cat . I had, of course, read it, but considered this tortuous and twisted reasoning irrelevant given the clear results of the rest of the analyses.

However, the black-footed cat WGKS results lead to quite a different result. The black-footed cat raises the question of what correlations in WGKS actually refer to and how useful they are for phylogeny. Apparently under WGKS a great difference between a species A and the other species of its family is possible; this does not spell well for WGKS as a method. The UPGMA phylogenetic tree on the WGKS clearly shows that WGKS leads to classification artifacts (BMC Genomics figure 2). Cserhati should have noted that. The artefacts indicate WGKS is not valid procedure for classification.

Cserhati does not provide a data file for WGKS (Whole Genome Octamer Scores) for his 28 species with the supplementary files posted on the internet as far as I can see. That prevents anyone from gaining insight into how those octamer scores behave. It is necessary to know how the octamer scores behave in order to make heads or tails of the strange position of the black-footed cat in the WGKS analysis. In the WGKS analysis, the black-footed cat

*Felis nigripes* differs strongly from the domestic cat *Felis catus*. *Felis nigripes* is basal to all other cats in this analysis (figure 2 BMC Genomics). That is something that needs explanation, minimally some attention. Especially since Cserhati always highly praises his 'whole genome' method, without any justification that is apparent or available.

The problem with Whole Genome Octamer Scores is that it is an unvalidated method with unknown sensitivities. A neat validation study, for example a Mitochondrial DNA Octamer score, or an Octamer Score profile of a circumscribed part of the genome, is needed to see how useful octamer scores are for phylogeny. Now we have to make do with Cserhati's claim that the octamer scores are a good measure of the entire genome. Why should we take that at Cserhati's word? At a minimum, the data, the octamer scores, must be available on the internet. The question is to what extent octamer scores not so much represent the important part of the genome, but above all microsatellites, repeats and defective transposons. (Blog post 6)

Cserhati should have done a study of the influence of repeats, microsatellites, transposon numbers, on his octamer scores. Without that, the question is whether a correlation between octamer scores indicates something other than similarity or difference in number of repeats. Classifying species by number of repeats is not an obvious or immediately reliable method for phylogeny.

## **IV B**

### ***2. In the mtDNA study there is no outgroup, why was one not included?***

On Panda's Thumb I wrote the following about the mtDNA part of the BMC Genomics article.

*"The mtDNA sequences are subjected to phylogenetic analysis by UPGMA, Maximum Likelihood and Neighbour Joining. No outgroup is mentioned, and no outgroup seems to have been specified.*

*The three phylogenetic trees on mtDNA differ in the placement of the families. The mess seems the result of the lack of outgroup. When plotting an unrooted tree in a square format, the program picks the plot. The pandas do not appear within the marten family in any of the three phylogenetic trees."*

So I clearly objected to the way Cserhati uses evolutionary phylogenetic methods in the BMC Genomics article. In his answer to that obvious objection,

Cserhati only talks about baramin and baraminological methods: not a word about his phylogenetic studies in the BMC Genomics article, while the objection was undoubtedly about those.

It is unclear whether Cserhati understands why an outgroup is used. Cserhati begins with a correct description of outgroup: "*outgroup species or groups to compare the group under study to a species or group of species that are known to be unrelated to the group under study.*" Such a correct definition can be found in any textbook.

After that, however, confusion sets in: "*.. since the groups that I used (bears, cats, and martens) follow the "traditional classification" the use of an outgroup may be superfluous.*" That is total nonsense. It shows that Cserhati does not understand what an outgroup is for: to put the groups of the "traditional classification" in the correct order in a hierarchical classification.

Then something very strange happens. After giving a correct description of an outgroup Cserhati does not know how the concept is applied in any phylogenetic analysis:

*"De Jong wishes to impose her evolutionary view of classification on the species examined in this study, looking for an outlier species more basal or primitive than the species in the study".*

Three jinxes in this opinion by Cserhati. First, Cserhati changes the definition of outgroup. Second, Cserhati presents four phylogenetic trees in his BMC Genomics article, and in presenting a phylogenetic tree he is dealing with the "evolutionary view of classification" whether he recognizes it or not, and whether he wants to or not. Third, I wasn't asking for an "*outlier species more basal or primitive*" (an idiotic description for outgroup), I was asking Cserhati for a neat analysis of his own mtDNA material.

Cserhati uses Neighbor Joining and Maximum Likelihood as phylogenetic methods. "*Both trees were constructed using the MEGA-X software [29], with parameters set to default values.*" (page 9 of 12). If you run the data through a program on the default you'll get an unrooted phylogenetic tree for both NJ and ML.

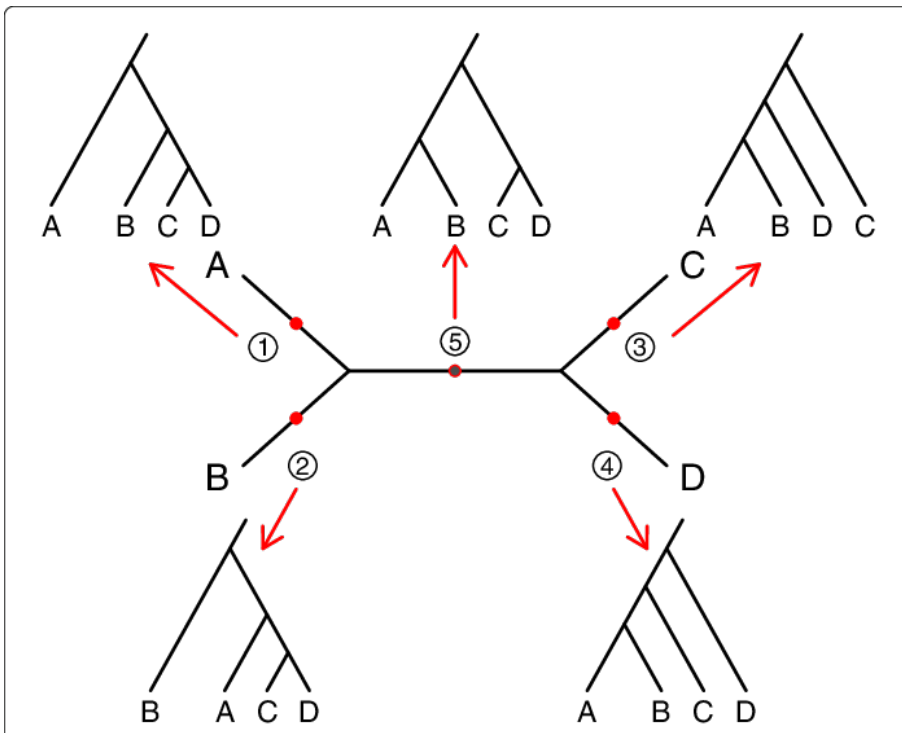


Figure 10. An unrooted tree of four Operational Taxonomic Units A B C D, and the five rooted trees associated with them. The place of the root determines the degree of relatedness.

An unrooted tree tells something but not much. With an unrooted tree mutual distances between the species are known, but not the way in which the species are related. And if you don't know how they are related, you can't classify properly.

Rooting is necessary for a good phylogenetic tree, and rooting is achieved by designating an outgroup. Here the bears are suitable as the outgroup to the superfamily Musteloidea, to find a proposal for a classification within the Musteloidea. Cserhati should have been able to tell the software to use an outgroup. Now Cserhati gets messy results, because he mistakes the efficient way the program plots an unrooted tree for the outcome of his tree. Cserhati fails to distinguish layout from result.

With the bears as an outgroup, both the NJ and ML analyzes show the red panda as a sister group to the remaining three families within the Musteloidea (See blog post 12 for further explanation).

There is a deeper problem here: a rooted phylogenetic tree provides a hierarchical classification. And no matter how you look at it, a hierarchical classification suggests evolution. That is why creationists prefer to use clustering, because clustering does not lead to a hierarchical classification.



## IV C

### ***3. The discordance between the mitochondrial DNA results and the genome shows that baraminology is useless.***

Cserhati asserts this claim can be found in my Panda's Thumb post or in the discussion that follows. I can't find where that claim is made.

Searching for 'discordance' yields only one occurrence of 'discordance' a comment:

*"The BMC Genomics paper admits that the results are tentative and that there may be differences between mtDNA and the whole genome due to nuclear-mitochondrial discordance."*

That comment is written by Cserhati. No one else says anything about nuclear-mitochondrial discordance. (By the way, it's the CRSQ paper where Cserhati talks about nuclear-mitochondrial discordance, not the BMC Genomics paper; Cserhati should have known that.)

There is no evidence of nuclear-mitochondrial discordance in Cserhati's data. First, the UPGMA on WGKS and the UPGMA on mtDNA give the same higher level classification within the Musteloidea. Thus, the direct comparison of Cserhati's 'nuclear' and his 'mitochondrial' phylogenetic tree show no discordance in red panda classification. Second, Cserhati claims that the mtDNA sequences show more differences than the nuclear genome as represented by WGKS. That is not true. Table 2 here shows the mean and minimum of the correlations between all species pairs of bears and Musteloidea in the WGKS and mtDNA analyses. WGKS and mtDNA have about the same range in correlations between species (blog post 16). This means that there is no difference between genomic divergence between species as in WGKS and mtDNA divergence between species.

TABEL 2	minimum correlation	mean correlation
WGKS	0.666	0.838
mtDNA	0.751	0.816

## IV D

### **4. Baraminology is a fictional construct, and there is nothing real behind it.**

In the discussion that followed my item on The Panda's Thumb website, a certain Henry J commented: "Well, given that "baramin" is a fictional concept, why can't they (creationists) just make up something and leave it at that." This is the only time "fictional" appears in that post on The Panda's Thumb.

So, not baraminology, but the baramin are called 'fictional'.

Baramin as creationists use that concept has little to do with Genesis 1. "Bara" ( בָּרָא ) is the verb 'to create'. Creationists have their own interpretation of the Hebrew word which is translated as 'kind', 'according to its nature' in the traditional Dutch translations. That word is mîn, and it occurs almost exclusively in this kind of context. The word is a collective, and indicates diversity:

*Thus the biblical text emphasizes the diversity of life – plants and animals – with which God filled the sky, the sea, and the dry land he had created.*

*Consistent with the basic message of Genesis 1, the emphasis rests upon God's creation of life in all its abundance and diversity. (biologos)*

The point is variety: 'as they are', 'as they live', namely herbivores, predators, frugivores, climbers and diggers. That is their 'nature'.

Baramin is a new word created by creationists to substitute a specific idea instead of the wide Biblical word 'kind'. Cserhati's interpretation of Genesis is creationist fiction: "Of course, within an individual baramin species are related to one another .... That is because Genesis 1:11, 12, 21, 24, and 25 declare that kinds form reproductive communities." Do Genesis 1:11, 12, 21, 24, and 25 really say so? Is what Cserhati says found in Scripture?

The King James Version says:

*11 And God said, Let the earth bring forth grass, the herb yielding seed, and the fruit tree yielding fruit after his kind, whose seed is in itself, upon the earth: and it was so.*

*12 And the earth brought forth grass, and herb yielding seed after his kind, and the tree yielding fruit, whose seed was in itself, after his kind: and God saw that it was good.*

*21 And God created great whales, and every living creature that moveth, which the waters brought forth abundantly, after their kind, and every winged fowl after his kind: and God saw that it was good.*

*24 And God said, Let the earth bring forth the living creature after his kind, cattle, and creeping thing, and beast of the earth after his kind: and it was so.*

*25 And God made the beast of the earth after his kind, and cattle after their kind, and every thing that creepeth upon the earth after his kind: and God saw that it was good.*

Genesis says nothing whatsoever about species within a 'kind', or that 'kinds' form closed reproductive communities. That kind of detail is non-Biblical modern creationism. It takes a high degree of imagination to get the creationist baramin out of Genesis. It is misuse of the Bible.

All in all, baramin are extra-biblical fiction.

Baraminology has two components: a statistical component, clustering, and a fictional component, the baramin, holobaramin, monobaramin, apobaramin. There exists no way whatsoever to relate a statistical cluster to Genesis. That is the fiction part. Remains the question whether statistical clustering is in any way informative or useful in scientific classification of species. Genesis is not relevant there. Creationists spend much effort on clustering, seemingly in the confused preconception that clustering will find baramin.

Cserhati doesn't like my calling baraminology a waste of effort because it does nothing but repeat evolutionary taxonomy. Cserhati denies that baraminology repeats evolutionary taxonomy. Cserhati should pay more attention.

(i) In the article '*A survey of Cenozoic mammal baramins*' (Thompson & Wood 2018, cited by Cserhati), Thompson & Wood give the following result: "*Based on the successful analyses, we identified 59 putative holobaramins, 49 of which corresponded to families, seven to subfamilies (or portions of families), two to superfamilies (or multiple families), and one (Sirenia) to an infraorder (Table 3)*". Traditional evolutionary taxonomic groups are declared baramin.

- (ii) Lightner et al (2012) give the families of the mammals according to the modern molecular evolutionary classification as baramin.
- (iii) McLain et al (2018) arrive at the known dinosaur groups as baramin in feathered dinosaurs, after many unnecessary detours with repeated clustering.
- (iv) Cserhati & Carter (2020) give in their Table 1 what they call a known 'true cluster' in addition to their own clusters based on mtDNA and WGKS. That 'true cluster' is the family according to the classic, well-known, evolutionary, classification.

The animal kingdom is classified hierarchically, because the animal kingdom is structured hierarchically. The hierarchical structure of life makes a fiction of the whole idea that baramin could be found by clustering. Cserhati knows that: see the article by creationists Cserhati & Carter (2020), entitled '**Hierarchical clustering complicates baraminological analysis**'. Cserhati & Carter(2020) do not provide a solution to their problem. On the contrary. Eight significant quotes from Cserhati & Carter (2020):

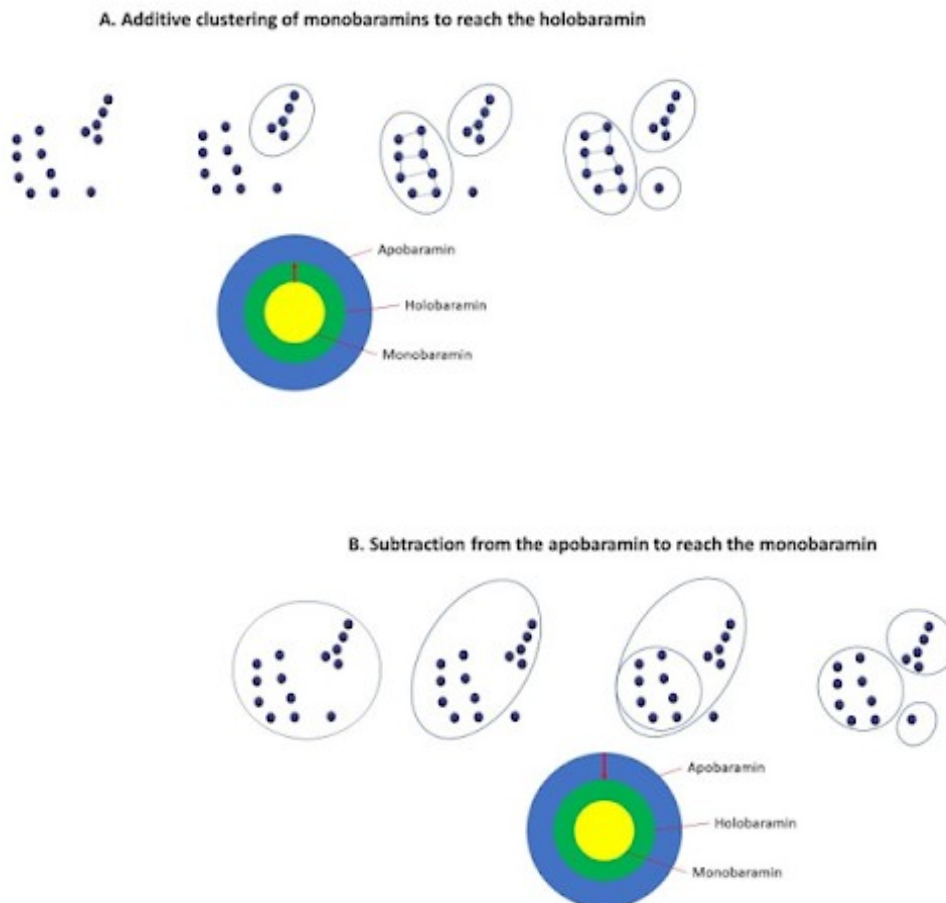
- (i) *One major issue is the hierarchical structure of species relationships. (pg 64)*
- (ii) *Yet the greatest problem facing baraminology might well be the hierarchical structure of life (pg 66)*
- (iii) *This simply means that cladistics can assemble any group of organisms into a hierarchy, regardless of whether they are truly related or not. And baraminology could be considered as just a mathematical expression of cladistics (pg 66)*
- (iv) *Baraminology was designed to elucidate the real patterns, but it had no way of making absolute judgments about the boundaries between kinds (pg 66)*
- (v) *Hierarchical clustering problems also present themselves when selecting species for baraminology studies. Species must be chosen at the right taxonomic level. If species are chosen too broadly, different clustering algorithms could put different species together which don't belong to the same baramin. Conversely, if species are chosen from one single baramin, the algorithms will still find clusters (pg 67)*
- (vi) *Thus, the promise of baraminology has not yet manifested itself. We do not yet have a way to make statistical determinations of group membership. (pg 67)*

(vii) *This study highlights one of the main problems of baraminology: the subjective classification of species into baramins (pg 71)*

(viii) *The fact that life follows a hierarchical pattern makes it hard to delimit the created kinds (pg 71)*

In those clear words, Cserhati & Carter (2020) conclude: **baraminology doesn't work**. There is no method to recognize baramin. Although Cserhati & Carter (2020) know that baraminology does not work, they stick to baramin. The conclusion that they are chasing a chimera turns out to be impossible for them. Baramin as fiction is Verboten.

In his 'Oorsprong' article, Cserhati claims that a baramin can be found by starting from two directions: start with a large group of beasts and divide them into clusters, or start with single species and make larger clusters. I have reproduced Cserhati's figure and his caption here.



**Figure 6.** The process of successive approximation. A. Starting from a larger group of species (the apobaramin) we drill down to find the holobaramin. B. Starting from individual monobaramins, we use clustering to approximate the holobaramin. When both processes meet we have the holobaramin.

Species are not dots in a plane, and this recipe, first from bottom to top and then from top to bottom until the two directions meet, does not work – precisely because the animal kingdom is hierarchically structured.

As a guide I take how Cserhati & Carter (2020) indicate how baramin should behave: “Species within the same kind should show continuity with one another on a morphological and a molecular level. They should also show discontinuity with all other species outside their kind.” This is consistent with Hennigan (2010) and seems standard creationism to me.

I’ll walk along the hierarchical structure of the animal kingdom, first from top to bottom, and then from bottom to top. I’ll use the placental mammals as example. The hierarchical classification of the mammals is shown in Figure 7.

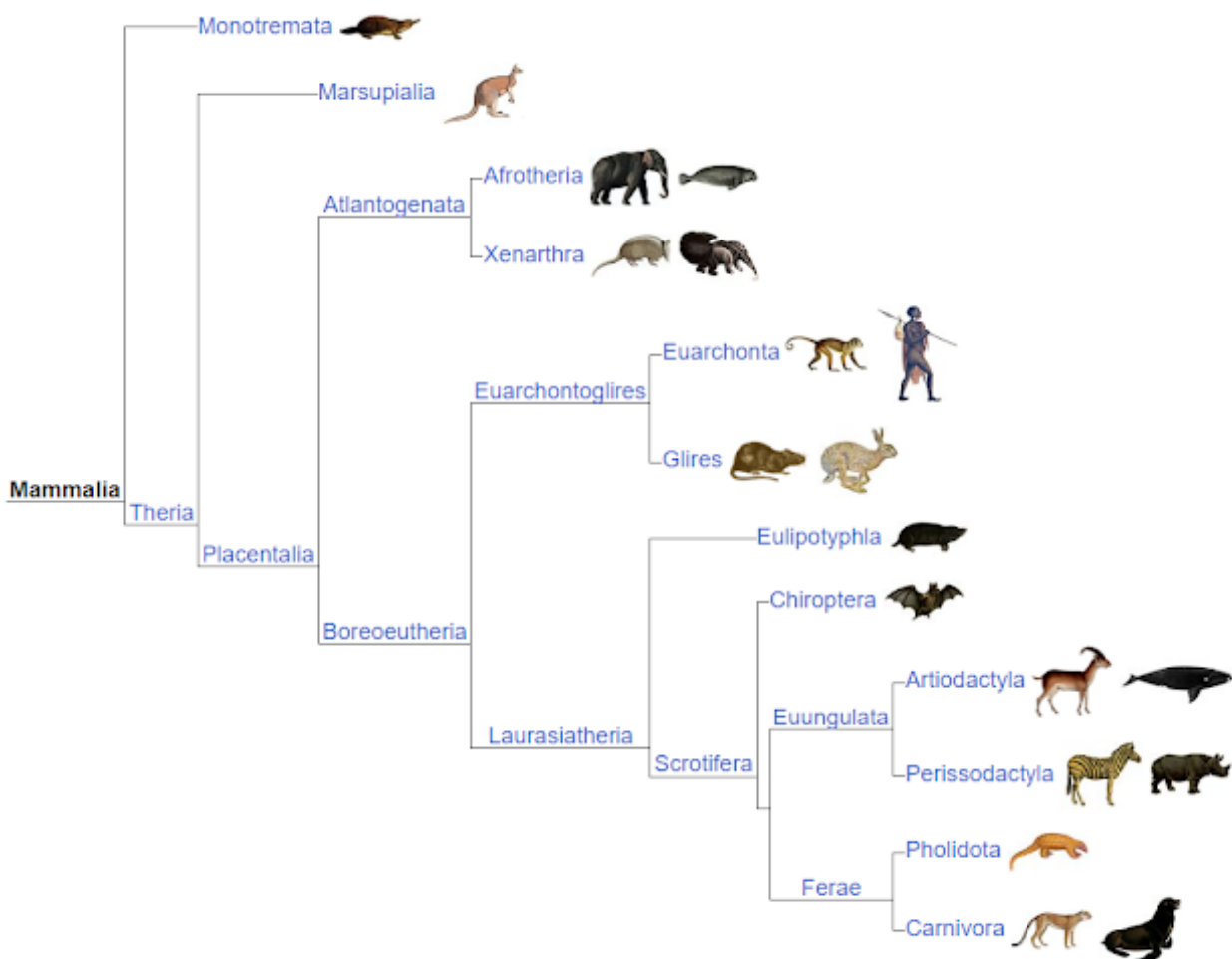


Figure 11. The hierarchical classification of the mammals. After Lv et al (2021), figure from [en.wikipedia.org/mammal](https://en.wikipedia.org/mammal)

The Theria are a group with internal continuity. Theria species have hair, differentiated dentition (incisors, canine, premolars, molars), have three ossicles in the middle ear, one bone in the lower jaw, and a relatively large brain. In addition, the Theria are molecularly genetically continuous relative to non-Theria.

In most characters the placental mammals are continuous with the marsupials and among themselves – hair, milk, etc, see under Theria. The placental mammals all have a placenta in reproduction, and are discontinuous in this characteristic with the marsupials. The placental mammals form a continuous group molecularly genetically to the marsupials, which form a different group molecularly genetically.

The placental mammals can be divided into two major groups, group Atlantogeneta and group Boreoeutheria, on molecular genetic grounds. They are continuous as placental mammal and Theria, and discontinuous on molecular grounds.

And so forth and so on. At least 15 steps down to the sea otter, in genus *Enhydra* of the subfamily Lutrinae, always with continuity at the level you look at and discontinuity below that level.

The other way, bottom to top, is also possible. Starting with the sea otter, merge the otters into the subfamily Lutrinae - a continuous group; merge the Lutrinae with the subfamily Mustelinae – together a continuous group; merge Lutrinae + Mustelinae with subfamily Guloninae – together a continuous group; add the whole of these three subfamilies together, in three steps, with three more subfamilies, and there appears the family Mustelidae – a continuous group. Climb the stairs according to the layout, and at every level of the stairs and above you have continuity. At each level in a hierarchical format, there is a continuous group.

In a hierarchical format, it is possible to move from top to bottom and bottom to top without ever getting stuck halfway: there is no privileged level. Never a privileged level appears where top-to-bottom and bottom-to-top join together: one can always go up and down in a hierarchical classification, based on the existing hierarchical structure in the animal kingdom.

That is why the idea baramin is fiction.



## **V Assessment**

The problem with Cserhati's two papers on the red panda is that it is such bad work. That is more important for the BMC Genomics article than for the CRSQ article: BMC Genomics is a scientific journal.

Cserhati neglects his own results: according to his own results the red panda forms an independent group of its own.

Cserhati prefers and adheres to his WGKS method without any justification: the UPGMA phylogenetic tree on the WGKS results clearly shows that WGKS is not a suitable method for classifying species – it gives artifacts – , but Cserhati does not even look at this UPGMA placement of the red panda.

Cserhati ignores his own statistical results: his silhouette plots indicate different numbers of clusters than he wishes to report.

Cserhati bases his main conclusion on WGKS clustering: but the silhouette plot indicates a Musteloidea cluster, not a Mustelidae+Ailuridae cluster.

Cserhati confuses the square layout of his unrooted phylogenetic NJ and ML trees with the phylogenetic trees itself.

Cserhati makes egregious errors in reading the literature; see his introduction to the BMC Genomics article and his Table 1 in the 'Oorsprong' article.

Cserhati does not cite recent scientific literature on the classification of the red panda.

How did papers as bad as these ever get through review and published?



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