

<https://creationismeweersproken.blogspot.com/2023/01/de-rode-panda-en-cserhati-10-wasberen.html>

## THE RED PANDA AND CSERHATI (10): PROCYONIDAE WGKS?

In the introduction to his BMC Genomics article, Cserhati cites Flynn et al (2000), Yu and Zhang (2006), Sato et al (2009) and Yu et al (2011). The four articles give the raccoon families Procyonidae and mustelid families Mustelidae as sister groups of each other, together called Musteloidea *sensu stricto*. In addition, all the articles mentioned list the Musteloidea *sensu lato* as a superfamily with the four families red panda Ailuridae, skunks Mephitidae, Procyonidae and Mustelidae.

For Cserhati, too, the question should therefore have been what the mutual order of the Ailuridae, the Mephitidae and the Musteloidea *sensu stricto* is within the Musteloidea *sensu lato*.

Cserhati emphasizes the importance of Whole Genome data.

*The advantages of using a genomics-based algorithm to analyze the WGS of these organisms is that it takes all the information present in the WGS, as opposed to just a handful of genes, utilized in gene studies*

A WGKS profile for all families within the Musteloidea, the four families red panda Ailuridae, skunks Mephitidae, Procyonidae and Mustelidae, was therefore indicated in order to find the place of the red panda. The raccoons are missing from Cserhati's WGKS analysis. Why?

One answer is that no whole-genome study of the raccoon family was available. At least, no whole genome study of the raccoon family was available when Cserhati wrote his BMC Genomics article. Publishing history for the BMC Genomics article is given as: Received: 18 May 2020 Accepted: 14 March 2021.

The only paper I can find on whole genome sequencing for the raccoon family appeared when Cserhati's BMC Genomics paper was under review, online December 17, 2020:

Tsuchija et al, 2021. Whole-Genome Sequencing of Procyonids Reveals Distinct Demographic Histories in Kinkajou (*Potos flavus*) and Northern Raccoon (*Procyon lotor*) Genome Biology and Evolution 13, January 2021, evaa255, Published online: 17 December 2020

Alertness would have been required to notice this in time to add the Procyonidae WGKS to the BMC Genomics paper. However, time was quite sufficient for Procyonidae WGKS to be added to the CRSQ paper.

However, does it matter that the raccoons are missing from the WGKS analysis?

The raccoons are always the sister family of the mustelid family. The possible divisions of the superfamily Musteloidea are:

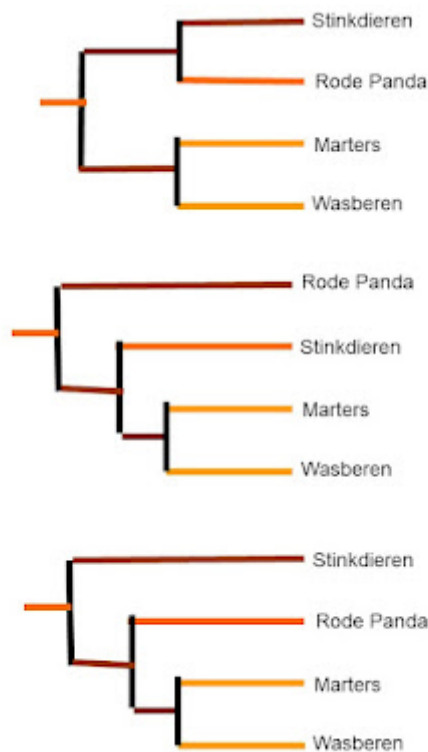


Figure 1 The three distinct configurations of the phylogenetic tree of the Musteloidea. If the Procyonidae are absent, the three configurations are still distinct. (Wasberen = Procyonids; Marters = Mustelids; Rode Panda = Red Panda; Stinkdieren = Mephitids)

In the absence of a species of the raccoon family, a sister group relationship of the red panda Ailuridae with the Mustelidae appears in the lowest diagram for the Musteloidea phylogenetic tree. This agrees with the phylogenetic tree of

Law et al (2018). This means that the raccoons are not strictly necessary to see what placement of the red panda yields the WGKS data.

However, the presence of one or more species of the raccoon family could have prevented a sister group relationship between the red panda and the mustelid family from being misinterpreted as if the red panda belonged to the mustelids.

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Cserhati, M., 2021, A tail of two pandas – whole genome k-mer signature analysis of the red panda (*Ailurus fulgens*) and the Giant panda (*Ailuropoda melanoleuca*), BMC Genomics 22: 228

M.T.N. Tsuchiya, R.B. Dikowkow, K.P Koepfli, P.B Frandsen, L.L Rockwood, J.E Maldonado, 2021. Whole-Genome Sequencing of Procyonids Reveals Distinct Demographic Histories in Kinkajou (*Potos flavus*) and Northern Raccoon (*Procyon lotor*) Genome Biology and Evolution, Volume 13, Issue 1, January 2021, evaa255; Published online: 17 December 2020