

This work by Emerling et al. attempts to unravel the genetic bases of dental regression in a group of mammals, xenarthrans, that present different degrees of reversals. The attractiveness of the system is that it exists a good characterization of the genes that are directly involved in the dental phenotype. It represents an outstanding opportunity to disentangle the genetic bases of the dental regression on xenarthrans and show the nature of the evolutionary process. I like how the introduction is written, from general aspects of regressive evolution, a description of the study system (dentition), the goodness of the selected taxonomic group, and the kind of questions that can be answered.

The taxonomic sampling is well thought out to answer the proposed questions. It includes a diverse sampling for the ingroup and also for the outgroup.

Regarding the methodology, although I understand that they accomplish the goal of getting the sequence of the genes using different approaches, adding a schematic figure showing which method was used for which species would help to understand more easily.

The dN/dS section needs to be clarified for me. How it is described does not allow the reader to create a mental image of the tree and the estimated omegas. In fact, the authors clarify not to confuse what they are describing with the free ratio model, referring to a paper that is not the best way to do it.

The result section is ok, where they described the evolutionary events related to the inactivation of genes. Figure 1 is very informative, although it is also very busy. I suggest using common names instead of scientific names. I like figure 2, which shows how the genes got inactivated in the different branches of the xenarthran tree of life. However, I am afraid that the final version will be too small to see the details easily, it is possible to show this information in two figures? I also suggest using common names.

I also like the evolutionary rationale behind reconstructing dN/dS values and when the inactivation process occurred in the xenarthran phylogeny. I recommend creating a schematic figure showing the rationale. Being more didactic will open the paper to a broader audience.

Regarding figure 3, why are the authors rooting the tree with afrotherians? Do they think the issue related to the first branching out in placental mammals is "solved"? Did they try the same analyses using Atlantogenata as a sister group of Boreoeutheria? I am also afraid that the final version will be too small to see the details, it is possible to show this information in two figures?

There is a gene called gremlin 2, for which genetic experiments have shown its role in tooth development (Brommage et al., 2014). In fact, it has been demonstrated that gremlin 2 deficient mice have upper and lower incisor teeth with a markedly reduced breadth and depth, where the upper incisors are more severely affected than the lower ones (Vogel et al., 2015). Furthermore, a study in which the evolutionary history of this gene was examined showed that gremlin2 loss coincides with a lack of upper jaw incisors in ruminants (Opazo et al. 2017). Therefore, it may be a good idea to include it in this study.

Brommage R, et al. 2014. Bone Research. PMID: 26273529.

Vogel P, et al. 2015. *Veterinary Pathology*. PMID: 24686385.

Opazo JC, et al. 2017. *PeerJ*. PMID: 28149683.