



# Reply to Ku and Sun: Ancestors of modern giant and large eukaryotic dsDNA viruses infected proto-eukaryotes

Julien Guglielmini, Anthony C. Woo, Mart Krupovic, Patrick Forterre, Morgan Gaia

## ► To cite this version:

Julien Guglielmini, Anthony C. Woo, Mart Krupovic, Patrick Forterre, Morgan Gaia. Reply to Ku and Sun: Ancestors of modern giant and large eukaryotic dsDNA viruses infected proto-eukaryotes. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117 (6), pp.2749-2750. 10.1073/pnas.1920855117 . hal-02464290

**HAL Id: hal-02464290**

**<https://hal.science/hal-02464290>**

Submitted on 9 Jun 2020

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

## **Reply to Ku and Sun: Ancestors of modern giant and large eukaryotic dsDNA viruses infected proto-eukaryotes**

Julien Guglielmini, Anthony C. Woo, Mart Krupovic, Patrick Forterre<sup>a</sup>, and Morgan Gaia<sup>a</sup>

To whom correspondence may be addressed. Email: [morgan.gaia@live.fr](mailto:morgan.gaia@live.fr) or [patrick.forterre@pasteur.fr](mailto:patrick.forterre@pasteur.fr)

### **Text**

In Guglielmini et al. (1), we analyze the evolutionary relationships between Nucleo-Cytoplasmic Large DNA Viruses (NCLDV) and the cellular domains based on the two largest universal markers, that is, the two largest RNA polymerase subunits (RNAP). We conclude that NCLDV diversified before the emergence of the last eukaryotic common ancestor (LECA). Our results now draw criticism from Ku and Sun (2).

They notably describe as a flaw the three-domain (3d) topology displayed by our RNAP trees, exposing an unjustified prejudice in favor of the two-domain (2d) topology. Indeed, the debate between the 2d and 3d scenarios is still open, as exemplified by the still unsolved phylogenomic challenges and the recent robust multigene phylogenies supporting the 3d topology (3, 4). Nonetheless, as repeated throughout our manuscript, our hypothesis can be interpreted in both scenarios, since proto-eukaryotes had to exist in both. Importantly, most deep evolution studies, including our own, combine single and multigene analyses to obtain complementary information required for a rational interpretation.

Ku and Sun (2) also list as flaws the “contradictory positions” of the Asfarviridae between figures 1 and 3 and figure 2 in our article (1) and the paraphyly of the Phycodnaviridae–Asfarviridae–Megavirales (PAM) superclade in figure 2 of our article. However, the position of Asfarviridae is exactly the same relative to the other NCLDV families, and the paraphyly of the PAM is due to the branching of eukaryotic RNAP-I and RNAP-II within it combined with a different rooting. This is explained in our original article, and notably illustrated in its SI Appendix, figure S12. Finally, although the three eukaryotic RNAP clades exhibit topological differences, they also display some congruent groupings. Particularly, the three eukaryotic RNAPs are monophyletic with high supports and represent the same diversity: Their branches correspond to LECA.

The “issues with phylogenetic inference” listed by Ku and Sun (2) are not flaws. They are already described, investigated, and explained in our article (1). The additional “weaknesses” they mention reveal a clear misunderstanding. Indeed, Ku and Sun (2) assimilate our scenario to an “NCLDV-before-eukaryotes hypothesis,” as if we suggest that NCLDV could parasitize contemporary prokaryotes. They fail to realize that LECA was not predated by a single proto-eukaryotic lineage resembling prokaryotes but was the end point of a long evolutionary period with increasingly complex intermediates (5, 6). Our data suggest that ancestors of modern NCLDV (containing at least the core genes that we analyze) have indeed coevolved with communities of such proto-eukaryotes (displayed as a single lineage in trees due to the lack of extant intermediates). Our hypothetical scenario could thus be labeled NCLDV-before-modern-eukaryotes, as has indeed been mentioned in the title of our article. The alternative hypothesis to this timeline hinted by Ku and Sun would posit that NCLDV obtained their RNAP after the eukaryotic diversification from LECA, a scenario rejected by all our analyses.

Finally, we have never claimed that eukaryotes were older than bacteria or archaea, and functional redundancy is a characteristic of eukaryotic cells with both multiple RNA and DNA polymerases. In

conclusion, while we remain open to questioning our results and interpretations, the points raised by Ku and Sun are irrelevant and unjustified.

### **Acknowledgments**

This work was supported by a European Research Council grant from the European Union's Seventh Framework Program (FP/2007-2013)/Project EVOMOBIL-ERC Grant Agreement 340440.

Footnotes

**Author contributions:** J.G., A.C.W., M.K., P.F., and M.G. wrote the paper.

The authors declare no competing interest.

### **References**

1. J. Guglielmini, A. C. Woo, M. Krupovic, P. Forterre, M. Gaia, Diversification of giant and large eukaryotic dsDNA viruses predated the origin of modern eukaryotes. *Proc. Natl. Acad. Sci. U.S.A.* 116, 19585–19592 (2019).
2. C. Ku, T.-W. Sun, Did giant and large dsDNA viruses originate before their eukaryotic hosts? *Proc. Natl. Acad. Sci. U.S.A.* 117, 2747–2748 (2020).
3. V. Da Cunha, M. Gaia, D. Gadelle, A. Nasir, P. Forterre, Lokiarchaea are close relatives of Euryarchaeota, not bridging the gap between prokaryotes and eukaryotes. *PLoS Genet.* 13, e1006810 (2017).
4. V. Da Cunha, M. Gaia, A. Nasir, P. Forterre, Asgard archaea do not close the debate about the universal tree of life topology. *PLoS Genet.* 14, e1007215 (2018).
5. P. Forterre, The common ancestor of archaea and eukarya was not an archaeon. *Archaea* 2013, 372396 (2013).
- A. M. Poole, S. Gribaldo, Eukaryotic origins: How and when was the mitochondrion acquired? *Cold Spring Harb. Perspect. Biol.* 6, a015990 (2014).