Asgard archaea are the closest archael relatives of eukaryotes

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In their recent contribution, Da Cunha et al.¹ claim that Lokiarchaea are not the closest relatives of eukaryotes, and that phylogenetic analyses support a three-domain topology of the tree of life. We review their main arguments and show that they are untenable.

CLAIM: The first published lokiarcheal genomes⁴ are extensively contaminated.
RESPONSE: The Lokiarchaeal genome represents a composite genome of two closely related strains, as clearly mentioned in ⁴. Da Cunha et al. incorrectly interpret strain heterogeneity as sign of contamination.

CLAIM: Removing EF2 from the universal gene set breaks the Lok-Eukarya affiliation.
RESPONSE: All our analyses excluding EF2 strongly support the sister-relationship of eukaryotes and Asgard archaea, as explicitly discussed in 1, 3.

In press data from
independent group

Unpublished
novel genome data

Eukarya, Archaea, Bacteria

Three domain (3D) topology

Two primary domain (2D) topology

Bacteria Archaea Eukarya

CLAIM: The fused RNA pol A (rhoA) of Heimdallarchaeota LC3 is a contaminant from Thaumarchaeota or Batharchaeota.
RESPONSE: rhoA Heimdallarchaeota branches basal to Asgard split homologues². It thus does not represent a contaminating from other archael clades. rhoA has a complex history and underwent several split events during archael evolution.

ML phylogeny of rhoA. Rooted with bacteria (not shown). Taxa in bold face possess a fused rhoA gene. Modified from ³.

CONCLUSIONS

The results we have published in recent years are not the final word on the origin of eukaryotes. However, Da Cunha et al. use inadequate methodology, misinterpret the data, and make ad hoc decisions regarding the taxa and genes included in their analyses. Finally, they ignore the plethora of evidence and discussions presented previously², which addressed many of their points.

The publication by Da Cunha et al. provides no evidence that falsify the conclusions drawn by Spang et al. and Zarembsa-Niedzwiedzka et al.