Faculty Opinions

Origin of eukaryotes: What can be learned from the first successfully isolated Asgard archaeon

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EVALUATION OF

Landmark

Isolation of an archaeon at the prokaryote–eukaryote interface.

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The origin of cellular complexity characterizing eukaryotic cells remains a central unresolved issue in the study of diversification of cellular life on Earth. The isolation by Imachi *et al.*[1] of a member of the Asgard archaea[2] – a contemporary relative of organisms thought to have given rise to eukaryotic cells about 2 billion years ago – now promises new insight. The complete genome sequence of the isolated Lokiarchaeum strain confirms that the eukaryotic signature proteins (ESPs) previously identified in the Lokiarchaeota[3] and other Asgard archaea[2] are indeed encoded by these archaeal genomes and do not represent contamination from eukaryotes. These ESPs encode homologs of eukaryotic actins, small GTPases and the ESCRT complex proteins and are required for the functioning of complex eukaryotic cells. The new, slowly growing, anaerobic laboratory strain allows a first direct look at these organisms and provides key insights into the morphology and metabolism of an Asgard archaeal organism. The work has provided valuable information for other laboratories that aim to isolate and characterize related organisms from other environments.

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Background

The origin of the eukaryotic cell represents one of the most enigmatic events in the history of life on Earth. Models of the event propose either autogenous or symbiogenetic mechanisms for the origin of cellular complexity characterizing modern eukaryotic cells. Both are based on the assumption – now generally accepted – that mitochondria arose from a bacterium that was engulfed by the precursor of the eukaryotic lineage. In most autogenous models, however, the host evolved as an independent branch in the tree of life in parallel with Archaea and Bacteria, and already harbored cellular features characteristic of eukaryotes before the acquisition of the mitochondria. In contrast, most symbiogenetic models suggest that the host was a *bona fide* archaeon that entered a symbiotic relationship with a Bacterium, and these together gave rise to the eukaryotic cell type (see Figure 1). Direct support for either of those models has, however, been limited by sparse genomic information.

Recently, the discovery of the Lokiarchaeota by Spang *et al.*[3] and the description of other Asgard archaea[2], both based on metagenomic analysis of DNA isolated from deep sea sediments, has provided new insights bearing on this issue. Phylogenetic analyses including Lokiarchaeota and their relatives strongly support the emergence of eukaryotes from within Archaea rather than as an independent lineage in the tree of life (Figure 1). Furthermore, the genomes of Asgard archaea have been found to encode a number of so-called eukaryotic signature proteins either absent from other archaeal and bacterial genomes or more closely related to their eukaryotic counterparts than to the corresponding genes from other prokaryotes.

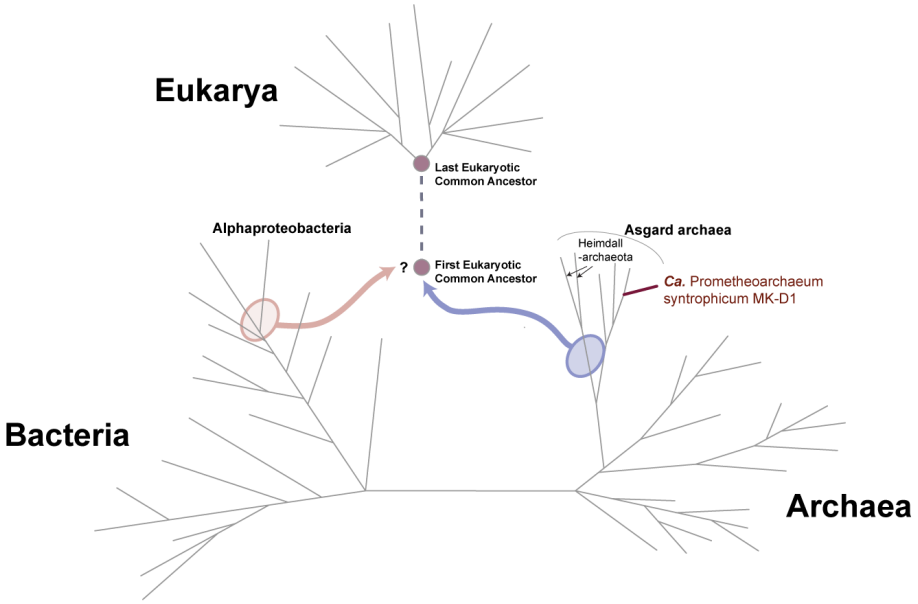

Figure 1. Tree of life

Schematic illustration of a simplified and hypothetical tree of life in which the first eukaryotic common ancestor is indicated to have emerged from a symbiosis of an Asgard archaeal host (purple arrow) and an alpha-proteobacterial symbiont (orange arrow). The last eukaryotic common ancestor stood at the root of all extant eukaryotic representatives. *Candidatus Prometheoarchaeum syntrophicum* MK-D1, which was isolated by Imachi *et al.*, is depicted in red and represents the first cultivated representative of the Asgard archaea, though on a distinct branch of the tree from that of the proposed Lokiarchaeal eukaryotic ancestor, which belongs to the Heimdallarchaeota.

However, since this analysis was solely based on inference from genomes assembled from environmental samples, many questions about the cellular features, metabolism and biology of the Asgard archaea remained unanswered.

Main contributions and importance

Through painstaking, patient trial and error over a period of 10 years, Imachi *et al*. were able to enrich for a member of Lokiarchaeota in a syntrophic culture including hydrogen-consuming *Halodesulfovibrio* (Deltaproteobacteria) and *Methanogenium* (Euryarchaeota). Through a series of transfers, the authors were able to obtain a stable co-culture consisting of the Lokiarchaeote and *Methanogenium*, which grow in syntrophy through interspecies hydrogen (or formate) transfer. The authors named this slowly growing (doubling time 1–2 weeks), anaerobic organism, which uses amino acids and peptides as growth substrates, *Candidatus Prometheoarchaeum syntrophicum* strain MK-D1 (Figure 2).

The isolation and characterization of this organism are important for several reasons:

• The genome sequence of strain MK-D1 confirms that Asgard archaea[2] comprise viable organisms whose genomes encode a diversity of eukaryotic signature proteins which are not a result of contamination from eukaryotes.

• The metabolism and syntrophic growth characteristics of strain MK-D1 verified predictions based solely on gene content analyses of the members of the Asgard archaea (e.g. 4) and support models of eukaryogenesis invoking syntrophy as a key driver for symbiotic interactions[5] that may have driven close cellular contact between Asgard archaea and the Alphaproteobacteria that are thought to have been the precursors of mitochondria.

• The methods used by Imachi *et al*. enable other laboratories to begin enriching other diverse samples for Asgard archaeal organisms.

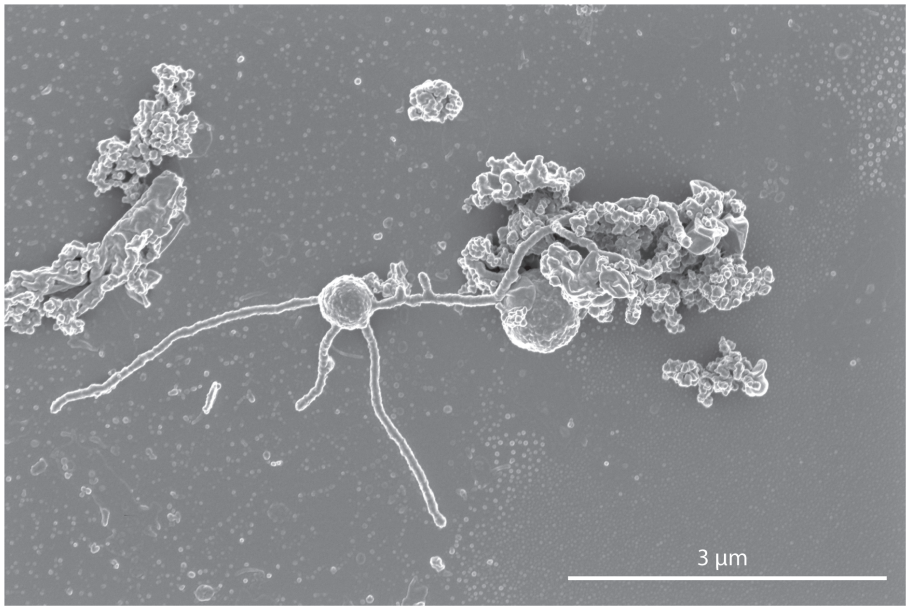

Figure 2. SEM image of strain MK-D1 of *Candidatus Prometheoarchaeum syntrophicum*

Credit: H. Imachi, M. K. Nobu, and JAMSTEC.

• This cultivated system provides a basis for an analysis at much greater depth of the physiological and cell biological features of a representative of the Lokiarchaeota. In particular, cultivation allows further examination of hypotheses about how membrane fusion and formation events may have taken place. Notably, for example, strain MK-D1 appears to be able to form long tentacular protrusions (see Figure 2) that have led to renewed interest in a proposal by Baum and Baum in 2014[6] on the mechanism by which the ancestral archaeon acquired the bacterial precursor of mitochondria (see 7 – but see Open questions below).

In summary, Imachi *et al*. have enabled new lines of research into a fascinating group of contemporary organisms that are important for our understanding of the origins of eukaryotic cells.

Open questions

The work of Imachi *et al*. is a major contribution with longstanding impact. However, it has several limitations that leave open questions for future research.

First, the syntrophic MK-D1 strain grows very slowly, which severely limits the experiments that can be set up on this system. Hopefully, ongoing efforts will enable the isolation of other strains of Asgard archaea that grow faster and are better suited for experimental analyses and manipulation in the laboratory.

Second, the Lokiarchaeota (to which the MK-D1 strain belongs) do not represent the closest sister lineage to the eukaryotes, which instead have been suggested to share a more recent common ancestor with the Heimdallarchaeota and relatives[2,8,9]. It's also important to realise that the eukaryotic cell is thought to have originated more than 2 billion years ago, i.e. MK-D1 has diverged and evolved for an extremely long evolutionary time span since then. In turn, its phenotype may differ considerably from the one that characterised the archaeal ancestor of eukaryotes.

Likewise, it remains speculative whether the cellular protrusions of MK-D1 may bear on the mechanism of symbiont engulfment (see 6 and 7), given that the molecular machinery underlying these structures remain to be determined. Furthermore, it is unknown whether these cellular features are shared across all Asgard archaea.

We note that a variety of approaches besides cultivation can help to illuminate the biology of members of the Asgard archaea. For example, recombinant proteins of contemporary Asgard archaea or ancestrally reconstructed proteins can be expressed and purified to obtain insights into their structures and functions.

Conclusion

Imachi *et al*. have cultivated the first contemporary representative of the Asgard phylum of archaea, which includes the host organism giving rise to eukaryotes. The complete genome of this organism confirms earlier findings derived solely from metagenomic analyses of the Asgard archaea, and the obtained enrichment cultures provide a basis for investigation at greater depth of the biology of an evolutionarily pivotal group of organisms.

References

1. Landmark

Imachi H, Nobu MK, Nakahara N, *et al*. 2020. **Isolation of an archaeon at the prokaryote-eukaryote interface.** *Nature* **577**:519–525.
doi: 10.1038/s41586-019-1916-6

2. Recommended

Zaremba-Niedzwiedzka K, Caceres EF, Saw JH, *et al*. 2017. **Asgard archaea illuminate the origin of eukaryotic cellular complexity.** *Nature* **541**:353–358.
doi: 10.1038/nature21031

3. Recommended

Spang A, Saw JH, Jørgensen SL, *et al*. 2015. **Complex archaea that bridge the gap between prokaryotes and eukaryotes.** *Nature* **521**:173–179.
doi: 10.1038/nature14447

4. Recommended

Spang A, Stairs C, Dombrowski N, *et al*. 2019. **Proposal of the reverse flow model for the origin of the eukaryotic cell based on comparative analyses of Asgard archaeal metabolism.** *Nat Microbiol* **4**:1138–1148.
doi: 10.1038/s41564-019-0406-9

5. Recommended

López-García P, Moreira D. 2020. **The Syntrophy hypothesis for the origin of eukaryotes revisited.** *Nat Microbiol* **5**:655–667.
doi: 10.1038/s41564-020-0710-4

6. Recommended

Baum DA, Baum B. 2014. **An inside-out origin for the eukaryotic cell.** *BMC Biol* **12**:76.
doi: 10.1186/s12915-014-0076-2

7. Dance A. 2021. **The mysterious microbes that gave rise to complex life.** *Nature* **593**:328–330.
doi: 10.1038/d41586-021-01316-0

8. Williams TA, Cox CJ, Foster PG, *et al*. 2020. **Phylogenomics provides robust support for a two-domains tree of life.** *Nat Ecol Evol* **4**:138–147.
doi: 10.1038/s41559-019-1040-x

9. Liu Y, Makarova KS, Huang WC, *et al*. 2021. **Expanded diversity of Asgard archaea and their relationships with eukaryotes.** *Nature* **593**:553–557.
doi: 10.1038/s41586-021-03494-3