An archaeal origin of eukaryotes supports only two primary domains of life

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Preface

The discovery of the Archaea and the proposal of the three-domains "universal" tree based on ribosomal RNA and core genes mainly involved in protein translation catalyzed new ideas for cellular evolution and eukaryotic origins. But accumulating evidence suggests that the three-domains tree may be incorrect: evolutionary trees made using better methods place eukaryotic core genes within the Archaea, supporting hypotheses in which an archaeon participated in eukaryotic origins by founding the host lineage for the mitochondrial endosymbiont. These results provide support for only two primary domains of life: Archaea and Bacteria, because eukaryotes arose through partnership between them.

Introduction

Since their discovery by Carl Woese and his co-workers in 1977, the Archaea have figured prominently in hypotheses for eukaryotic origins[1,2]. Though similar to Bacteria in terms of cell structure, molecular phylogenies for ribosomal RNA and a small core of genes, that mainly play essential roles in protein translation[3], suggested that the Archaea were more closely related to the eukaryotic nuclear lineage; that is, to the host cell that acquired the mitochondrion[4]. The idea that Archaea and eukaryotes are more closely related to each other than either is to Bacteria depends on analyses suggesting that the root of the tree should be placed on the bacterial stem, or within the Bacteria[5-12], implying that the prokaryotes - cells that lack a nucleus - are a paraphyletic group[13]. The main question now debated is whether core components of the eukaryotic nuclear lineage descend from a common ancestor shared with Archaea, as in the three-domains tree[14] (Figure 1) which is also often called the "universal tree" or "tree of life"[15-17], or from within the Archaea, as proposed by archaeal-host hypotheses for eukaryotic origins[2]. The archaeal-host scenario with the greatest phylogenetic support is the eocyte hypothesis[18], which proposes a sister group relationship between eukaryotes and the eocytes (or Crenarchaeota[14]), one of the major archaeal divisions (Figure 1). But the three-domains-eocyte debate remains controversial because different phylogenetic methods have delivered different results,

often from the same data[19]. This disagreement is due, at least in part, to the difficulties associated with resolving ancient divergences in phylogenetic trees.

Challenges of reconstructing ancient relationships

A major issue in reconstructing ancient relationships is the strength and quality of historical signal remaining after the millions of years since the divergence of Archaea and eukaryotes. The earliest fossils identified as eukaryotic appeared by about 1.8 billion years ago[20]; over this enormous span of time, the accumulation of multiple substitutions in DNA and protein sequences might have erased any signal that would allow the relationship between archaeal and eukaryotic core genes to be established[21]. However, more recent simulations and empirical studies suggest there are reasons to be cautiously optimistic that this is not the case: functional constraints vary across real DNA and protein sequences so that sites evolve at different rates[22-25]. Fast evolving sites are indeed quickly saturated but the slowest sites can still retain useful phylogenetic information, explaining why we are able to align some genes over the entire tree of life. Analyses of molecular sequences might therefore be able to distinguish between the alternative hypotheses for eukaryotic core gene origins, but the phylogenetic methods used and the types of data analyzed are likely to be of critical importance in attempts to recover any historical signal[22-26].

The problems associated with phylogenetic reconstruction come into particularly sharp focus when comparing support for the three-domains and eocyte trees. The first studies to investigate this question generally recovered the three-domains tree, in which eukaryotes emerge as the sister group to Archaea[27,28], but the parsimony and distance methods used carried unrealistic assumptions, including constancy (homogeneity) of base compositions across lineages and of evolutionary rates across sites. These assumptions are clearly violated by key phylogenetic markers such as small subunit rRNA genes, which contain a mixture of fast- and slowly-evolving sites[29] and for which GC-content varies widely among the three domains[12]. Compositional heterogeneity can cause phylogenetic error when not taken into account, because sequences of similar base or amino acid composition may group together in the tree even when they are not closely related[30-32]. Two pioneering studies used methods to mitigate possible convergence in the universal tree due to shared

compositional biases in nucleotide sequences and, interestingly, both recovered an eocyte tree[33,34].

Long branch attraction (LBA) is another pervasive artifact in molecular phylogenies, in which sequences with long branches cluster together irrespective of their evolutionary history[25,35]. LBA is especially problematic for parsimony methods, but it can also affect probabilistic methods if the model ignores among-site rate variation, or is otherwise a poor fit to the data[36]. Trees for the ribosomal RNA and protein-coding genes used to infer relationships between domains often show evidence of long branches and are therefore susceptible to LBA. Some of the early attempts to mitigate the influence of LBA in inter-domain analyses also recovered eocyte trees, although with variable support. Evolutionary parsimony, a method designed to reduce the effect of long branches on the inferred tree, recovered an eocyte topology from rRNA sequences[37], although archaeal monophyly was favoured when a related method, compositional statistics, was used to analyze RNA polymerase sequences[38]. By contrast, analyses of rRNA and RNA polymerase using models that accounted for among-site rate variation supported the eocyte hypothesis over the three-domains tree[39]. To reconcile these results, Tourasse and Gouy[39] suggested that the three-domains tree might be a phylogenetic artifact caused by LBA between the long bacterial and eukaryotic branches, forcing an artifactual clustering of the shorter archaeal branches. In other words, the eocyte tree might be intrinsically more difficult to recover using simple methods, because it requires the clustering of the short branch leading to the eocytes/Crenarchaeota with the long eukaryotic branch.

Single gene phylogenies often fail to strongly resolve the relationships between the domains[12,40], and so in order to bring more characters to bear on the problem, a number of studies have analyzed concatenations of the core set of proteins conserved on all genomes. As already described, these genes largely function in translation and gene expression, and include many of the essential RNA and protein components of the ribosome. These cellular components have been called the "genealogy-defining core"[3], the "genetic core"[41] of cells or the "functional core of genomes"[16], and their common history has been cited[3,16,41] as the strongest support for the three-domains tree. Testing the evolutionary origins of this small set of genes is

therefore critical to the three-domains-eocyte debate. Interestingly, analyses using similar sets of concatenated core genes have yielded different conclusions – for example Katoh et al.[42] obtained an eocyte tree from a set of 39 universal proteins, whereas Ciccarelli et al.[43] analyzed a similar set of proteins and obtained a three-domains tree. One reason for the conflicting results in this case may be the different methods used for making the sequence alignment: the order of alignment had previously been shown to dictate which tree (eocyte or three-domains) was recovered from elongation factor Tu sequences[44]. Ciccarreli et al.[43] aligned bacterial, archaeal and eukaryotic sequences separately before combining them into a single alignment. This step-wise procedure was criticized as potentially biasing the results towards a three-domains topology but also, when the individual alignments were combined, to have introduced alignment errors between domains[19]. Brown et al.[45] also inferred trees from a concatenation of a subset of 14 universally conserved proteins, but in this study the tree recovered depended on the phylogenetic method used; the three-domains topology was recovered using maximum parsimony, but model-based methods recovered an eocyte topology.

Over the past few years, phylogenetic models implemented in either a maximum likelihood or Bayesian framework have continued to increase in sophistication by incorporating additional features of the evolutionary process. These include relaxing the assumptions of homogeneous amino acid or base composition across sites[46] or across branches of the tree[31]. These models appear to fit molecular sequence data much better than simpler models and this may make them less susceptible to LBA and other artifacts of model mis-specification[25]. Although relatively few analyses of the core gene set have used these models so far, all of them have recovered the eocyte tree, rather than the three-domains tree[12,22,47-49].

New archaeal lineages and eukaryotic origins

In addition to improvements in phylogenetic methods, the diversity of molecular sequences from organisms related to the eocytes/Crenarchaeota has also increased dramatically, driven by the ease with which sequences from uncultured prokaryotes can now be sampled from the environment using molecular methods[50,51]. Improved sampling can have positive effects on phylogenetic reconstruction, particularly when

it helps to break up long branches[52]. Recently discovered relatives of the eocytes/Crenarchaeota include the Korarchaeota[53], the Thaumarchaeota[54] and the Aigarchaeota[55]; the "TACK" superphylum was subsequently proposed as an informal group to encompass these four taxa[47]. To date, the studies including TACK sequences have supported a version of the eocyte hypothesis extended to recognize this improved sampling, rather than the three-domains tree[47,48,56]. In this extended sense, the eocyte hypothesis implies that the closest relative of the eukaryotic nuclear lineage is one, or all, of the TACK Archaea. If this tree is correct, then an important place to look for prokaryotic homologues of eukaryotic cellular componentry should be among the TACK phyla. Consistent with this prediction, members of this group encode homologues of a number of key eukaryotic genes (Figure 2, Supplementary Table 1), including actin[57] and tubulin[58] - the essential components of the eukaryotic cytoskeleton – a ubiquitin protein modification system[55], and a number of genes involved in transcription and translation[47,59]. However, no single characterized TACK genome possesses all of these features[47,57,58], implying that gene loss and potentially HGT, have contributed to the patterns of gene sharing on contemporary archaeal and eukaryotic genomes[60,61].

Which history do universal trees represent?

In their seminal papers, Woese and Fox[1,4] recognized that the ribosomal RNA tree represented only one component, the host for the mitochondrial endosymbiont, in the composite origins of the eukaryotic cell. That composite nature has been confirmed by comparative genomics, which has demonstrated that eukaryotic genomes contain a mixture of genes with different origins[13,62-66]. Some genes are ancestrally present in all three groups or unique to eukaryotes, but many others appear to have origins through gene transfers from different bacteria, including the endosymbiotic progenitors of mitochondria and plastids, and relatively few – including the core set of conserved proteins we have been discussing – have affinities with the Archaea. From these data it is clear that no one tree is sufficient to describe the history of all of the genes on modern eukaryotic genomes[67,68]. However, even though this fact is now widely documented, the three domains tree is often still called the "tree of life" or "universal tree" in textbooks[15] and reviews[16,17].

The sequencing of genomes from across the tree of eukaryotes is beginning to provide a clearer picture of the impact on eukaryotic genomes of horizontal gene transfer (HGT) from prokaryotes[65]. These data suggest that the acquisition of bacterial genes, at least by microbial eukaryotes, has been an ongoing process that extends beyond the initial injection of genes provided by the mitochondrial and plastid endosymbionts. From the perspective of ongoing HGT, the existence of any coherent vertical signal for ancient relationships may seem surprising. However, the impact of HGT on the core genes used to reconstruct the tree of life appears rather limited. While cases of HGT have been reported[69,70], these occur mainly within rather than between domains, and at present there is little evidence that they have generally perturbed inferences of inter-domain relationships[3,12,41,69]. In addition to genuine cases of HGT, poorly-fitting phylogenetic models may also lead to disagreements between gene trees[25,26]: recent work has shown that improving the fit of phylogenetic models[48] or integrating the signal from different genes through joint inference of gene and species trees[71,72] can reduce the level of incongruence and the number of inferred HGT events.

The reasons why core genes involved in transcription, translation and related processes might be transferred (that is, fixed) less frequently than genes for metabolic pathways are currently understood in terms of their degree of functional integration into cells. Their gene products are often found in large sub-cellular complexes and therefore tend to have more interaction partners than genes for metabolic pathways; as a result, horizontal replacement of these genes is more likely to disrupt important cellular interactions and thus to be opposed by negative selection[66,73,74]. In essence, the universal core might be the largest coherent set of vertically inherited genes that can be tracked across the history of cellular life[3], and as such represents a key resource for tracing the emergence of the eukaryotic cellular lineage. Under the rooted three-domains hypothesis[14], that ancestral lineage is as old as the Archaea. By contrast, the eocyte hypothesis predicts that eukaryotes are a relatively young group because their core genes originated from within the Archaea[18].

The origin of eukaryotes in light of other data

In principle it might be possible to determine the order of events relevant to eukaryotic origins, or at least to exclude some scenarios, using the fossil and

biogeochemical record. However, this record is very incomplete and subject to deep and sometimes heated controversy. The first fossil that is indisputably eukaryotic is of a bangiophyte red alga dated to between 1.2 billion and 800 million years ago[75], but earlier microfossils with a possible eukaryotic origin are found in rocks dated to approximately 1.8 billion years ago[20]. These data are consistent with molecular dating analyses that place the last common ancestor of eukaryotes at between 1.9 and 1.7 billion years ago[76]. An earlier origin for eukaryotes had been suggested based on the presence of sterane biomarkers in 2.7 billion year-old rocks[77], but these were subsequently shown to be contaminants from younger rocks[78,79]. An early origin for Archaea has been inferred based on the presence of biological methane, today produced only by methanogenic Euryarchaeota, in rocks that are 3.5 billion years old[80]. Analyses of microfossils and stromatolites – modern versions of which harbor complex bacterial communities[81] – in 3.4 billion year old rocks suggest the presence of photosynthetic bacteria[82-84]. Thus, on the data available, Bacteria and Archaea may pre-date eukaryotes in the fossil record by almost 2 billion years.

In light of the uncertainties for dating eukaryotic origins in the geological record, much attention has focused on the historical record revealed by the ultrastructure of the eukaryotic cell and in particular on the timing of the mitochondrial endosymbiosis[85]. When the three primary kingdoms and three-domains tree were originally proposed[1,14] some contemporary eukaryotes called 'archezoans'[85,86] were hypothesized to descend from eukaryotic lineages that never had mitochondria[85,86], providing modern-day evidence for the emergence of nucleated cells before the mitochondrial endosymbiosis. The 'archezoans' included the obligate intracellular parasites Microsporidia and a number of parasitic microaerophilic protists including *Entamoeba*, *Giardia* and *Trichomonas*[85,86]. However, representatives of all of these groups have now been shown to possess a mitochondrial homologue, either a hydrogenosome or mitosome, sharing common ancestry with classical mitochondria[2,87]. These results imply that the mitochondrion was acquired before the radiation of known eukaryotes; therefore, the observation that the mitochondrion descends from an endosymbiotic member of the alpha-proteobacteria[64,88] provides strong evidence that the origin of eukaryotes postdates the origin of that bacterial group[2,89]. A relatively late origin of eukaryotes compared to Bacteria is consistent with the best evidence from the geological record and with

either the three-domains or eocyte tree rooted on the bacterial stem or within the Bacteria[5-11]. Moreover, if all eukaryotes have both mitochondria and a nucleus, then we can no longer be sure which structure arose first during evolution: in other words, the host cell that acquired the mitochondrion need not have already possessed a nucleus. Indeed, there are now well-argued hypotheses suggesting that the acquisition of the mitochondrion was the key event that sparked the prokaryote to eukaryote transition[90,91]. In any case, the failure of the archezoa hypothesis removes a key obstacle to theories that propose a prokaryotic host for the mitochondrial endosymbiont, including hypotheses that are consistent with the eocyte tree[2].

The origin of eukaryotic cell membranes

The plasma membranes of Bacteria and eukaryotes predominantly contain phospholipids in which fatty acids are covalently bound to *sn*-glycerol-3-phosphate via an ester linkage. By contrast, Archaea – including the few TACK Archaea studied so far – predominantly contain phospholipids with isoprenoid chains linked to *sn*-glycerol-1-phosphate via an ether bond[92,93]. This pattern is most parsimoniously explained on the rooted three-domains tree by inferring a switch to using mainly glycerol isoprenoid ethers along the archaeal stem, with eukaryotes retaining the ancestral type. This transition may have been driven by a need to maintain membrane function at the high temperatures and acidic conditions of the habitats occupied by early Archaea[92,94]. A commonly voiced challenge to the eocyte hypothesis - and all Archaea-host models for eukaryotic origins - is how to explain the reversion of the archaeal-host membrane to a bacterial-type plasma membrane.

In fact, most of the genes needed for the synthesis of both types of lipid are common to all three groups, suggesting that neither the transition from ester to ether lipids in the common ancestor of Archaea, nor the subsequent reversion along the eukaryotic stem, would require radical genomic change[95,96]. Archaeal-type ether lipids have been detected in some Bacteria and phospholipids based upon *sn*-glycerol-1-phosphate are found in certain endomembrane components of eukaryotes, suggesting that the distinctions among contemporary membranes may not be as sharp as once thought; there is still much to be discovered about the natural diversity of lipid membranes[93,95-98]. Moreover, recent experiments have indicated that artificial

membranes containing mixtures of bacterial and archaeal lipids are stable[99], demonstrating the potential for natural mixed-membrane intermediate stages. Given these considerations, the reversion to bacterial-type membranes in eukaryotes might be explained as part of the same process whereby ancestral archaeal pathways were replaced by bacterial equivalents to yield the metabolic similarities observed between bacteria and contemporary eukaryotes[62-65,95,96,100]. This transition need not have greatly affected membrane function: in the Haloarchaea, which have obtained a large number of bacterial genes by HGT, transporters derived from Bacteria appear to function normally in the archaeal plasma membrane[101].

Conclusions

Ancient phylogenies provide a fascinating window into the distant past, but are difficult to build and interpret – as evidenced by the first thirty years of debate over the tree of life in the era of molecular phylogenetics. Evolutionary biologists now have access to more data and better phylogenetic methods than ever before, although there is still much room for improvement and many uncertainties remain. These caveats apply equally to all attempts to infer ancient relationships, affecting not only the debate over whether the three-domains or eocyte tree best depicts the history of core eukaryotic genes, but also the placement of the universal root[5,9-12,21] and the relationships between major eukaryotic phyla[26,102,103]. The pioneering analyses of molecular sequence data led by Carl Woese and his co-workers culminated in the three-domains tree recognizing the Archaea, Bacteria and Eukaryota as the three primary domains of cellular life. While evidence of widespread horizontal gene transfer means that no single tree can depict the history of all genes on prokaryotic and eukaryotic genomes, the three domains tree holds a special place in biology. It appears in most textbooks and reviews, where it is often called the "universal tree" and the "tree of life". But support for the iconic three-domains tree has waned with improvements in phylogenetic methods and taxon sampling. Within the limits of methods and data, a version of the eocyte tree is now the best-supported hypothesis for the origin of the subset of genes that mainly function in translation and appear to be most resistant to horizontal gene transfer. The placement of these genes, and by extension the eukaryotic nuclear lineage, within the Archaea is consistent with only two primary lineages and with hypotheses for a symbiogenetic origin for eukaryotes

involving an archaeon and one or more bacterial partners. The eocyte tree, if correct, suggests that the TACK Archaea, currently a relatively unexplored group, might contain additional clues as to the origin of complex eukaryotic structures. It also rejects the hypothesis that eukaryotes are a primordial cellular lineage, leaving only two candidate primary domains, Archaea and Bacteria, and it identifies a key piece of the puzzle – the host lineage – in the chimeric origins of the eukaryotic cell.

Figure legends

Figure 1: Competing hypotheses for the origin of the eukaryotic host cell. (a) The rooted three-domains tree[14] depicts cellular life divided into three major monophyletic groups or domains; the Bacteria, Archaea, and the Eukaryota – the latter representing the host lineage, sometimes also called the nuclear or nucleo-cytoplasmic lineage[5], that acquired the mitochondrial endosymbiont. In this tree the Archaea and Eukaryota are most closely related to each other because they share a common ancestor that is not shared with Bacteria. (b) The rooted eocyte tree recovers the host cell lineage nested within the Archaea as a sister group to the eocytes (which Woese et al.[14] called the Crenarchaeota); this implies that, based upon the small set of core genes, there are only two primary domains of life – the Bacteria and Archaea. In its modern formulation shown here the eocyte hypothesis implies that the closest relative of the eukaryotic nuclear lineage is one, or all, of the TACK Archaea, which include newly discovered relatives of the eocytes/Crenarchaeota. Both trees have been traditionally rooted on the bacterial stem consistent with some published analyses[5-8].

Figure 2: Archaeal links in the origin of eukaryotes.

A schematic tree depicting the relationships between Archaea and the eukaryotic nuclear lineage consistent with recent analyses of core genes using new methods[47-49] and rooted using the bacteria as the outgroup[5-11]. The phylogenetic position of *Korarchaeum* was not consistently resolved in these different analyses and hence is depicted as part of a polytomy. Genome analyses have detected homologous genes in Archaea and eukaryotes that are consistent with them sharing a common ancestor to the exclusion of Bacteria. Many of these patterns of gene sharing do not distinguish

between the rooted three domains or eocyte trees, as they are expected to occur under both hypotheses. Recently published analyses of the genomes of TACK Archaea, however, have increased the number of homologues shared with eukaryotes and some of these are relevant to ideas about eukaryotic origins and the evolution of their unique features. These include putative orthologues of actin[57] and tubulin[58], which in eukaryotes form the core of the cytoskeleton, as well as components of a ubiquitin protein modification system in *Caldiarchaeum subterraneum*[55]. Distant homologues of some of these genes have also been detected in Euryarchaeota[104,105], but they cluster outside the eukaryote/TACK clade in phylogenetic trees[57,58,106]. We have followed existing usage[58] in distinguishing between the FtsZ-like tubulin family members found in some Archaea and the eukaryote-like tubulin homologue found in *Nitrosoarchaeum*. Several eukaryotic genes involved in transcription and translation have prokaryotic homologues or conserved sequence features that have been found so far only among the TACK Archaea. These include four ribosomal proteins[47], the RNA polymerase subunit RpoG[59], the elongation factor Elf1[107], and a short amino acid insertion[108] in the broadly-conserved elongation factor 1-alpha that has only been found in TACK Archaea and eukaryotes as indicated by the vertical bar. Accession numbers and additional details are provided in Supplementary Tables 1 and 2.

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Supplementary Table 1: Gene presence and absence data presented in Figure 2 of the main text.

When considering patterns of gene sharing between eukaryotes and the Archaea, at least three classes of genes are evident. The first comprises cases in which orthologues of the eukaryotic gene are conserved across the Archaea, and sometimes also in Bacteria; these include among their number the core gene set used in analyses upon which the tree in Figure 2 is based. The second class includes eukaryotic genes such as actin[1], tubulin[2] and proteins of the ubiquitin modification system[3]. These genes may form large gene families, for example the tubulin/FtsZ gene family, and may have detectable dispersed paralogues among prokaryotes generally, but for which putative orthologues[2] to eukaryotic versions have so far been detected only among the TACK Archaea. The third class includes genes that have so far been found only in eukaryotes and the TACK Archaea; these include several genes involved in transcription and translation, as detailed below.

Gene	**Representative archaeal species**	**NCBI Accession (GI)**	**Reference**	**Basis for orthology inference**
Actin (Crenactin)	*Thermofilum pendens*	119719444	[1]	Tree
Tubulin (artubulin)	*Nitrosoarchaeum limnia*	494643832	[2]	Tree
Ubiquitin system (Ub, E1, E2, RING-finger containing Ub ligase)	*Caldiarchaeum subterraneum*	343485671, 343485673, 343485672, 343485674	[3]	Sequence similarity, operon structure
Elongation factor Elf1	*Sulfolobus solfataricus*	13813400	[4,5]	Not detected outside group
RNA polymerase RpoG/Rpb8	*Thermofilum pendens*	119719267	[6]	Not detected outside group
Ribosomal protein S25e	*Thermofilum pendens*	119719924	[4]	Not detected outside group
Ribosomal protein S30e	*Thermofilum pendens*	119719279	[4]	Not detected outside group
Ribosomal protein L13e	*Thermofilum pendens*	119719644	[4]	Not detected outside group
Ribosomal protein L38e	*Aeropyrum pernix*	499163706	[4]	Not detected

				outside group

Supplementary Table 2: An amino acid insertion in the elongation factor 1-alpha genes of eukaryotes and certain Archaea. An insertion[7] is present in the Thaumarchaeota, Aigarchaeota and Crenarchaeota highlighted in Figure 2; this insertion is apparently missing from *Korarchaeum cryptophilum*. The coordinates provided refer to the portion of the insertion that is readily alignable among the compared sequences.

Species	**Elongation factor 1-alpha accession**	**Amino acid coordinates**
Caldiarchaeum subterraneum	315425766	120-127
Cenarchaeum symbiosum	118575602	125-132
Nitrosopumilus maritimus	161528542	121-128
Nitrosoarchaeum limnia	494643908	121-129
Thermofilum pendens	119719557	121-128
Pyrobaculum aerophilum	18313751	131-138
Caldivirga maquilingensis	159042306	130-137
Sulfolobus solfataricus	15897164	120-127
Ignicoccus hospitalis	156937938	122-129
Staphylothermus marinus	126465710	121-128
Hyperthermus butylicus	124028427	121-128
Aeropyrum pernix	14601666	120-127

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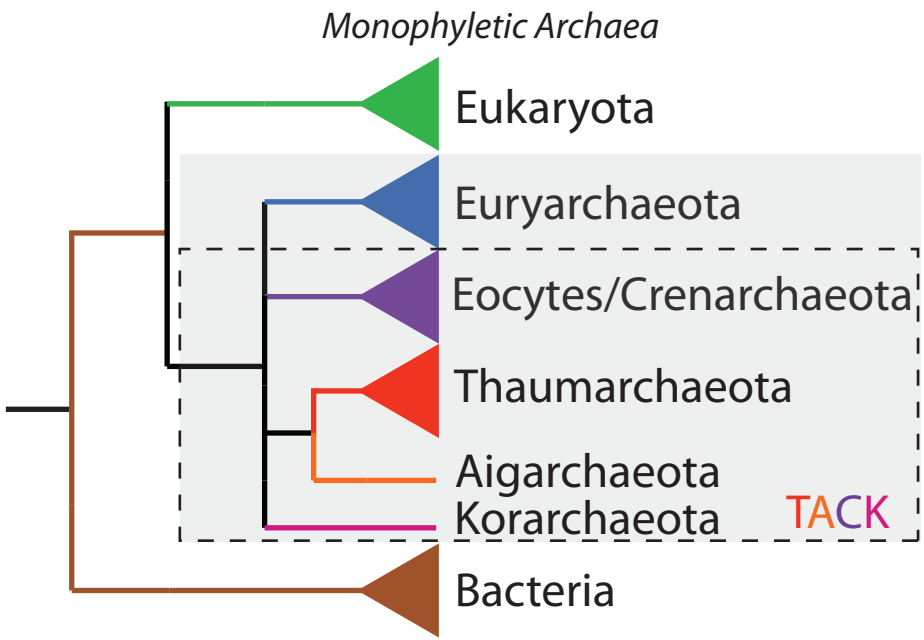
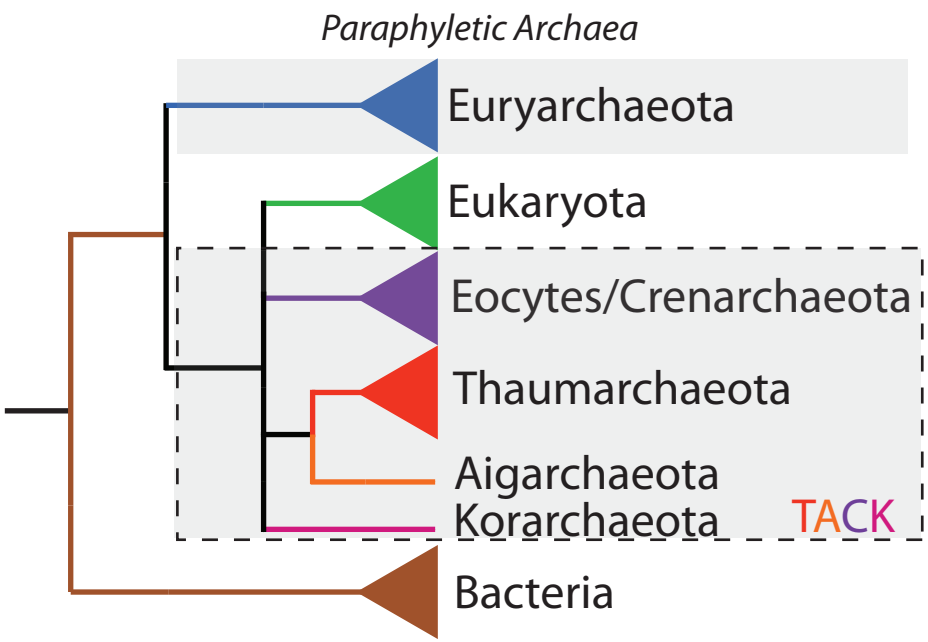
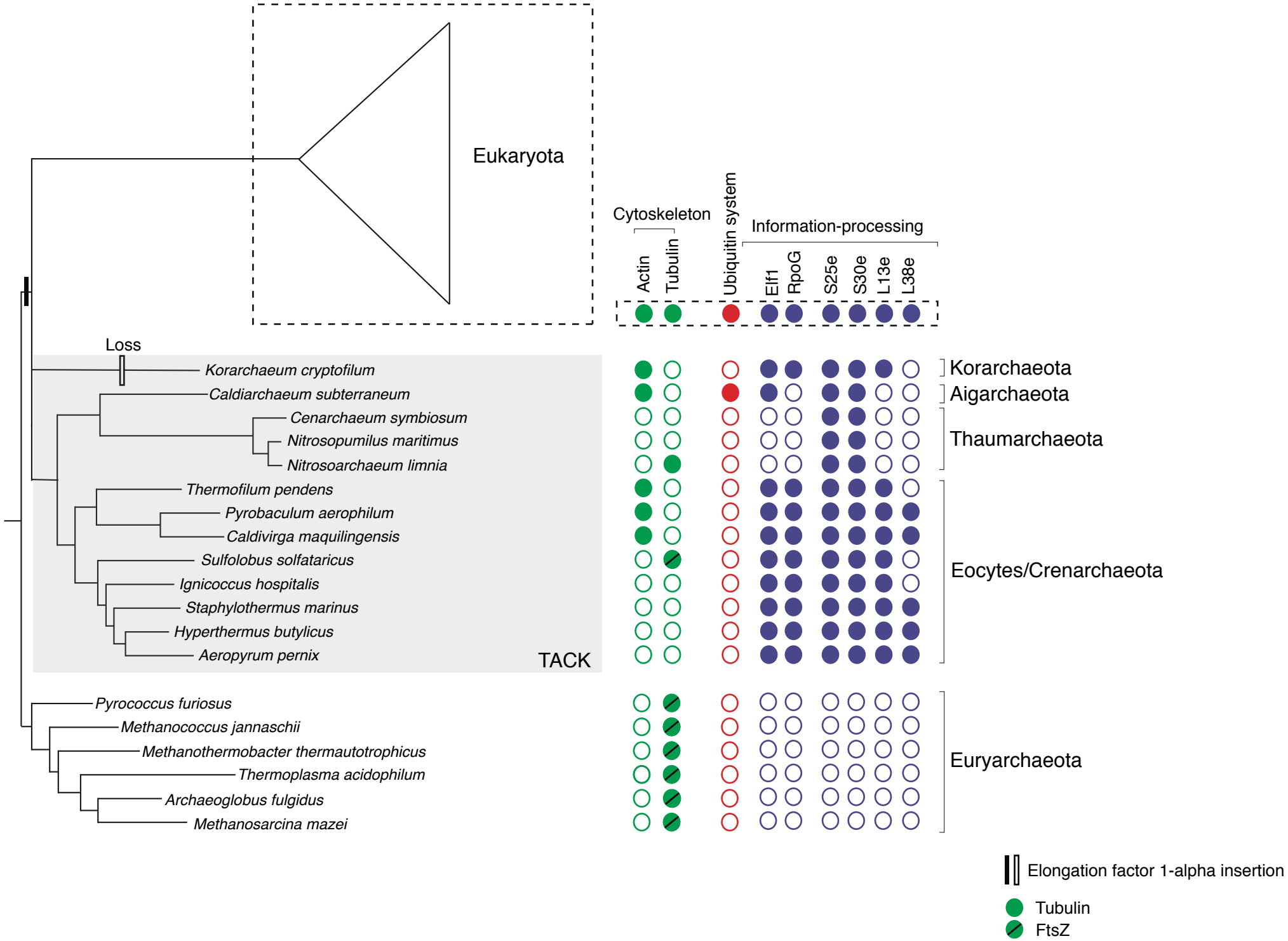


(a) Three domains hypothesis



(b) Eocyte hypothesis


Eukaryota
Cytoskeleton
Actin
Tubulin
Ubiquitin system
Information-processing
Elf1
RpoG
S25e
S30e
L13e
L38e
Loss
Korarchaeum cryptofilum
Caldiarchaeum subterraneum
Cenarchaeum symbiosum
Nitrosopumilus maritimus
Nitrosoarchaeum limnia
Thermofilum pendens
Pyrobaculum aerophilum
Caldivirga maquilingensis
Sulfolobus solfataricus
Ignicoccus hospitalis
Staphylothermus marinus
Hyperthermus butylicus
Aeropyrum pernix
TACK
Pyrococcus furiosus
Methanococcus jannaschii
Methanothermobacter thermautotrophicus
Thermoplasma acidophilum
Archaeoglobus fulgidus
Methanosarcina mazei
Korarchaeota
Aigarchaeota
Thaumarchaeota
Eocytes/Crenarchaeota
Euryarchaeota
Elongation factor 1-alpha insertion
Tubulin
FtsZ