Critique of the latest evolutionary models of the beginning of life

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A number of recent evolutionary models are considered and reviewed. The models contradict each other as to the origins of Eukaryotes, Archaea, and Bacteria. Finding a root for the tree of life containing these three domains has proven to be elusive. A hallmark of these theories is that cellular complexity came about suddenly, with subsequent genome reduction in many cellular lifeforms in the three domains. Some evolutionists even deny the existence of a tree of life or that evolution progresses from simple to complex. Yet, they are at a complete loss as to how complexity arose so fast and so early. A better explanation that more harmoniously fits the data is that these cellular lifeforms were created separately from one another, and form different kinds which may vary within bounds, according to creation theory.

In figure 1, we see one of the latest trees of life.[1] The tree is split into three main domains: Bacteria, Archaea, and Eukarya. Archaea was discovered as a separate domain by Carl Woese who constructed a phylogenetic tree based on the 16S rRNA.[2] The 16S rRNA molecule was chosen because it is ubiquitous, functionally constant, refractory to horizontal gene transfer (HGT), and it mutates very slowly.[3] However, the choice of the 16S rRNA molecule was somewhat arbitrary, as other universal proteins exist which also could have been used, such as the 18S rRNA, or RNA polymerase subunits.[4] The informational and operational proteins (involved in translation, transcription, and replication, and metabolism and biosynthesis, respectively) of both Eukarya and Archaea are more similar to each other than are those of Eukarya and Bacteria. Furthermore, Eukarya and Archaea share proteins that are either absent in Bacteria or have non-homologous proteins with the same function. Eukarya are also called synkaryotes (literally meaning 'with a nucleus') according to some theories. This contrasts with the akaryotes (literally meaning 'without a nucleus'), which are understood to be the prokaryotes.[5]

There are presently a number of evolutionary theories which try to explain the origin of cell types from the three domains of life, but they all appear to be contradictory to some extent.[6,7] According to one theory, Eukarya and Archaea are two distinct lineages that arose from a single common ancestor (the three-domain hypothesis).[8] Another theory claims that the Archaea group together with Eukarya make up a single super-domain, 'Arkarya' (the two-domain hypothesis).[8] However, Eukarya is really a subgroup of Archaea, and a sister group of the TACK superphylum (Thaumarcheota, Aigarcheota, Crenarcheota, and Korarcheota), with poor tree resolution. This poor resolution indicates that the supposed evolutionary origin of these groups is not clear-cut, and that instead they could have been created separately. Moreover, Archaea is divided into two major phyla, the Crenarchaeota (including hyperthermophiles) and the Euryarchaeota (made up of different groups found in diverse environments and having various metabolic activities). These different groups of Archaea are fundamentally different in their metabolism. This alone indicates that these groups of organisms are distinct from one another without any evolutionary transitions between them.

According to yet another theory, the so-called eocyte hypothesis, Eukarya originated from an association between a crenarchaeote and a bacterium.[8]

On the tree shown in figure 1, six hypothetical organisms are featured which represent the last supposed common ancestors of these large domains or subdomains: LUCA, LBCA, LARCA, LACA, LECA, and FME (LBCA: last bacterial common ancestor; LACA: last archaeal common ancestor; LECA: last eukaryotic common ancestor; FME: first mitochondrial eukarya; LARCA: last arkarya common ancestor; LUCA: last universal common ancestor). The hypothetical existence of the FME implies a stage between itself and the LARCA, i.e. when eukaryotes had supposedly evolved but still did not have any energy-producing organelles like the mitochondrion.

The dashed cross-arrow from α-proteobacteria to the FME denotes endosymbiosis of such an organism with another eukaryotic ancestor, along with the transfer of genes from it into its genome. Another dashed line points to the endosymbiosis of cyanobacteria with Plantae, the resulting organisms becoming the forerunners of chloroplasts. It is interesting to note that the PVC superphylum is a separate group within Bacteria, and it is not the ancestor of the Eukarya, despite the presence of a number of similar proteins and organelles shared between the two groups. These proteins and organelles are only analogous, being similar in

structure but not in sequence which is supposedly necessary for homology. However, this is claimed by evolutionists to be a hallmark of descent between species.[9,10] The process of thermo-reduction is believed to have occurred both in the lineage between LUCA and LCBA and the lineage between LARCA and LACA, possibly triggering reductive genome evolution.[5]

LUCA, LBCA, LARCA, and these 'common ancestors' are all hypothetical organisms, lacking descriptive binomial Latin names. They have never been directly observed or characterized, and their existence is merely speculation. Searching for them is akin to a blind man in a dark room looking for a black cat that is not there.

The problem of rooting the tree

Evolutionists must admit that finding the root for the tree of life (as depicted in figure 1) is difficult. Some advocate for a so-called 'forest of life', rather than a simple tree.[11] It has even been postulated that the three domains of life are instead monophyletic with well-resolved evolutionary relationships within each domain. However, according to trees based on the Kae1/YgjD universal protein,[12] the relationship between the three domains still remains very problematic. The relationship can been compared to that between a truck, a submarine, and an aeroplane: each one is a distinct type of vehicle suited for movement on either land, sea, or air, respectively. Just as these three types of vehicles were designed for different environments, as a result of their own special components, the three cellular domains of life are also suited to different environments. This specialization, in case of vehicle types, is the result of their own special components and, in case of the cellular domains, the result of their genetic and biochemical makeup.[13]

For example, bacteria, archaea, and eukaryotes have distinct types of ribosome (as discovered by Woese[14]) made up of different proteins, and are therefore structurally different from one another. If these three types of ribosomes are so different, why would one need to evolve into another if they already perform the same function within their respective cells?[15] Following the vehicle analogy given earlier, it would be extremely difficult to imagine how a submarine could be transformed bit by bit into an aeroplane and still remain a functioning vehicle through each intermediate step. Similarly, it is difficult to believe

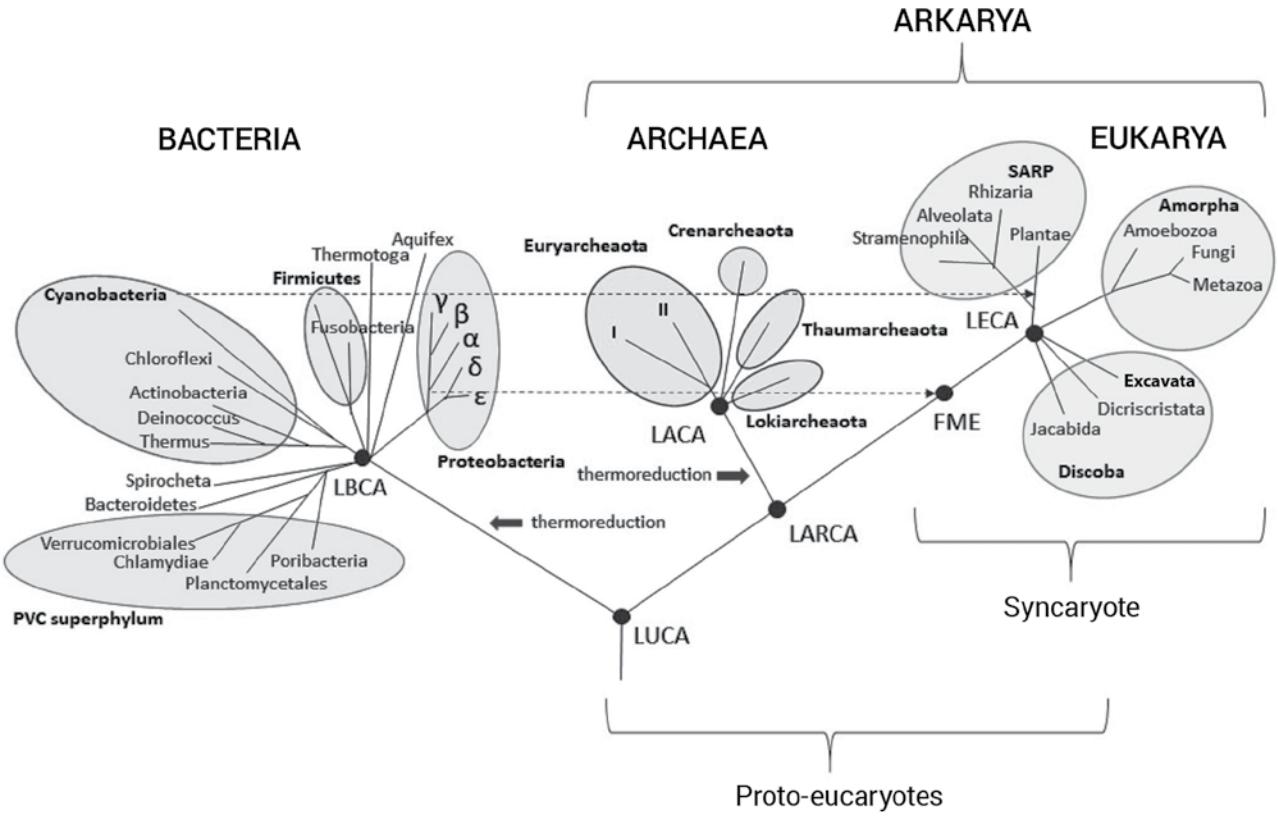

Figure 1. The latest tree of life containing the three major domains (after Forterre[1]). Bacteria are shown on the left, Archaea in the middle, and Eukarya on the right. Black dots show the last common ancestor for major taxonomical groups. Black, solid arrows show lineages where large-scale thermo-reduction happened. LBCA: last bacterial common ancestor; LACA: last archaeal common ancestor; LECA: last eukaryotic common ancestor; FME: first mitochondrial eukarya; LARCA: last arkarya common ancestor; LUCA: last universal common ancestor.

how a bacterial cell could be transformed into a eukaryotic one. The process would involve rewriting its genetic code and drastically changing its gene regulation and cellular structure, all the while keeping each intermediate step viable throughout the hypothetical process of accelerated (and unobserved, therefore unverifiable) evolution. Added to these difficulties is the fact that LUCA had some 'eukaryotic-like' features,[5] which hints at the early complexity of these hypothetical organisms, and signifies a qualitative leap from its non-eukaryotic ancestors.

It is also interesting to note that the presence or absence of certain proteins can be used as markers to distinguish between trees or sub-trees of each taxonomic group. For example, a hexameric replicative helicase, minichromosome maintenance complex, is used as a marker for the archaeal domain,[16] whereas DNA gyrase is used as a marker in the sub-phylum I of the Euryarchaeota.[17] Furthermore, and most importantly, no single protein can be used safely to reconstruct the supposed 'path of life' taken during evolution. Although the so-called 'tree of life' shows congruence in some places, it is only the case at shallower phylogenetic depths.[18] This has led some to build composite trees based on the concatenation (linking in chains) of select protein sequences. However, there is a lack of correspondence between the composite tree and the trees derived from individual proteins.[8,19] Furthermore, the more genes that are concatenated, the bigger the chance that genes involved in HGT are used.[20]

A list of such universal gene/protein families is shown in table 1 (taken from Gribaldo *et al.*[8] This list includes 35 COGS, which correspond to data sets analyzed by at least three of four groups, including Harris *et al.*,[21] Ciccarelli *et al.*,[22] Yutin *et al.*,[23] and Cox *et al.*[24], and Foster *et al.*[25] It is interesting to note that 30 of these 35 proteins are involved in translation, ribosomal structure, and biogenesis, indicating that only a small part of all the global cellular functions are represented; thus giving a biased picture of the origin of the first cell. The problem with using universal proteins is that only a small number of genes are used to construct the tree of life. Thus, the tree of life becomes what some evolutionists aptly call 'the tree of one percent'[26]—a far cry from the universal tree of life envisioned by Darwin. This is similar to issues experienced with the geological column. It is fully continuous in only 0.4% of all of the earth's surface.[27]

If evolution were true, then there should not be so many problems with generating phylogenetic trees based on protein sequences. Every single universal protein should generate exactly the same tree without exception. Yet, there are many exceptions which contradict the general rule. In summary, phylogenomics of early life does not support one common tree and, consequently, does not support one common ancestor.

What is also striking about the tree of life is that the tempo of evolution was allegedly much faster in the eons leading up to the emergence of eukaryotes, after which it slowed down. Archaea, on the other hand, is an exception. This has been noted as follows by Patrick Forterre:

> "… whilst progressively and randomly losing some of their eukaryotic features, except for one particular lineage of Lokiarchaeota that experienced a dramatic burst of accelerated evolution and was transformed into eukaryotes."[11]

However, such mechanisms for generating accelerated bursts of evolution have not yet been identified. These explanations are akin to the theory of punctuated equilibrium at a molecular level. Intermediate stages have never been found, so the actual proof of evolution is missing.

Early complexity and genome reduction

Both Archaea and Eukarya are thought to have undergone sudden appearance of complexity, with subsequent gene loss and simplification.[28,29] For example, early-life evolutionists have proposed that the complete set of methanogenic enzymes suddenly appeared, and then were lost separately in Crenarchaeota and all non-methanogenic euryarchaeal lineages.[30] Some suggest that three main archaeal phyla (Crenarcheota, Euryarchaeota, and Nanoarcheota) should be built on comparative genomic studies. *Nanoarchaeum equitans* belongs to this latter phylum, and has a genome of a mere 490 Mb, and lacks one-third of all genes present in other archaeal genomes.[30,31] This is significant, because if this species really is related to the other two Archaeal phyla, then it must have undergone significant genome reduction.

The complex origin of eukaryotes has its own issues. As even evolutionists admit, no intermediates have been found between prokaryotes and eukaryotes, and any similarities between these two types of cells are mainly based on analogy, and not descent by homology.[10] The same appears to be the case between bacterial and archaeal cells.[32] Since no primary amitochondrial eukaryotes are known, the appearance of the first organelles poses another problem. The mechanistic difficulty of one prokaryotic cell engulfing another is formidable, making symbiotic scenarios unrealistic.[33,34]

Coupled with early cellular complexity is the widespread phenomenon of genome reduction. For example, according to evolutionary theory, mitochondria and chloroplasts have lost nearly all of their ancestral genes,[35] and hydrogenosomes and mitosomes have lost all of theirs. Bacterial genome decay is also a well-known fact, with free-living bacteria losing up to 95% of their genes during their transition to become obligate intracellular parasites.[36,37] The idea of a progressive complexity being shown by species has now been replaced by what some evolutionists call 'a drunkard's walk' model of evolution. Table 2 (after Wolf and Koonin[38]) lists several

Table 1. List of 33 clusters of orthologous groups (COGs) which have been used as universal proteins by four references (from Harris *et al.*[21], Ciccarelli *et al.*[22], Yutin *et al.*[23], Cox *et al.*[24], and Foster *et al.*[25])

Name	Description	Function	No. of studies
COG0048	Ribosomal protein S12	Translation, ribosomal structure and biogenesis	4
COG0049	Ribosomal protein S7	Translation, ribosomal structure and biogenesis	4
COG0080	Ribosomal protein L11	Translation, ribosomal structure and biogenesis	4
COG0081	Ribosomal protein L1	Translation, ribosomal structure and biogenesis	4
COG0087	Ribosomal protein L3	Translation, ribosomal structure and biogenesis	4
COG0091	Ribosomal protein L22	Translation, ribosomal structure and biogenesis	4
COG0093	Ribosomal protein L14	Translation, ribosomal structure and biogenesis	4
COG0094	Ribosomal protein L5	Translation, ribosomal structure and biogenesis	4
COG0098	Ribosomal protein L5	Translation, ribosomal structure and biogenesis	4
COG0099	Ribosomal protein S13	Translation, ribosomal structure and biogenesis	4
COG0100	Ribosomal protein S11	Translation, ribosomal structure and biogenesis	4
CGO0102	Ribosomal protein L13	Translation, ribosomal structure and biogenesis	4
COG0103	Ribosomal protein S9	Translation, ribosomal structure and biogenesis	4
COG0186	Ribosomal protein S17	Translation, ribosomal structure and biogenesis	4
COG0197	Ribosomal protein L16/L10AE	Translation, ribosomal structure and biogenesis	4
COG0201	Preprotein translocase subunit SecY	Intracellular trafficking, secretion, and vesicular transport	4
COG0256	Ribosomal protein L18	Translation, ribosomal structure and biogenesis	4
COG0016	Phenylalanyl-tRNA synthetase alpha subunit	Translation, ribosomal structure and biogenesis	3
COG0024	Methionine aminopeptidase	Translation, ribosomal structure and biogenesis	3
COG0085	DNA-directed RNA polymerase, beta subunit/ 140 kD subunit	Transcription	3
COG0086	DNA-directed RNA polymerase, beta' subunit/ 160 kD subunit	Transcription	3
COG0088	Ribosomal protein L4	Translation, ribosomal structure and biogenesis	3
COG0090	Ribosomal protein L2	Translation, ribosomal structure and biogenesis	3
COG0092	Ribosomal protein S3	Translation, ribosomal structure and biogenesis	3
COG0096	Ribosomal protein S8	Translation, ribosomal structure and biogenesis	3
COG0097	Ribosomal protein L6P/L9E	Translation, ribosomal structure and biogenesis	3
COG0184	Ribosomal protein S15P/S13E	Translation, ribosomal structure and biogenesis	3
COG0480	Translation elongation factor EF-G, a GTPase	Translation, ribosomal structure and biogenesis	3
COG0522	Ribosomal protein S4 or related protein	Translation, ribosomal structure and biogenesis	3
COG0532	Translation initiation factor IF-2, a GTPase	Translation, ribosomal structure and biogenesis	3
COG0533	tRNA A37 threonylcarbamoyltransferase TsaD	Translation, ribosomal structure and biogenesis	3
COG0541	Signal recognition particle GTPase	Intracellular trafficking, secretion, and vesicular transport	3
COG0552	Signal recognition particle GTPase	Intracellular trafficking, secretion, and vesicular transport	3

taxonomical groups as well as a characterization of their ancestor together with the kind of genome reduction that they allegedly experienced.

Genome reduction is so pervasive that Wolf and Koonin[38] posited the so-called biphasic model of genome evolution. This consists of two main phases, the first one being "genomic complexification at faster than exponential rate that is associated with stages of major innovation". The first phase is followed by a second phase of "genome simplification associated with the gradual loss of genetic material".[38] (An example is the appearance of introns which are considered to be more ancestral and supposedly underwent 'streamlining' that resulted in their current form.[29]) However, nothing much is said regarding the cause and the mechanism of rapid genomic complexification of the first phase. Evolutionists are forced to speculate and invoke a first phase in order to escape the clear implication of the special creation of such cellular complexity early on.

According to other theories, 2,500 genes existed in the genome of ancestral archaea, which is *even larger* than the genomes of most extant archaea![39] Csürös and Miklós[28] also estimate, based on known gene families in 28 archaeal genomes, that early archaeal genomes were as complex as typical modern ones, and that the genome of LACA had approximately slightly more than 2,000 gene families. This means that the genomes of archaea either remained at the same level of complexity, or underwent genome reduction. This is just the opposite of the increasing complexity that evolution posits.

Baraminology studies on Archaea

Despite a 'deluge of genomic data', no resolution has yet been reached concerning the problem of the origin of different basic cell types.[8] Many contradicting theories still exist as to how Bacteria, Archaea and Eukarya arose. The various genes studied also give contradictory tree topographies. Moreover, the last common ancestors of these cell types have never been identified or characterized. Thus,

Table 2. The extent and end result of genome reduction in a number of different taxonomic groups (after table 1 of Wolf and Koonin[38], with further references for each group in that paper)

Taxa	Depth of evolutionary reconstruction	Subject of evolutionary reconstruction	Outcome
Mitochondria	Proto-mitochondrial (alpha-proteobacterial) endosymbiosis, presumably, last common ancestor of eukaryotes	Genes	Deep reduction, to the point of genome elimination in anaerobic protists containing hydrogenosomes or mitosomes.
Lactobacillales	Last common ancestor of bacilli	Gene families	Complex ancestor; dominance of the reduction mode in all lineages
Anoxybacillus flavithermus	Last common ancestor of Firmicutes	Gene families	Ancestral complexification, then reduction
Rickettsia	Last common ancestor ("mother") of rickettsia	Genes	Complex ancestor, dominance of the reduction mode in all lineages
Cyanobacteria including chloroplasts	Last common ancestor of cyanobacteria	Genes	Complex ancestor, complexification in some lineages, reduction in other lineages, ultimate reduction in chloroplasts
Archaea	Last archaeal common ancestor	Gene families	Moderately complex ancestor, ancestral complexification in some lineages, more recent dominance of genome reduction in all lineages
Eukaryotes	Last eukaryotic common ancestor	Protein domain families	Complex ancestor, reduction of the domain repertoire in most lineages, expansion only in multicellular organisms
Eukaryotes	Last common ancestor of eukaryotes	Introns	Complex early ancestors, mostly reductive evolution, complexification in some, primarily multicellular lineages
Microsporidia	Last common ancestor of microsporidia	Genes	Complex ancestor, deep reduction

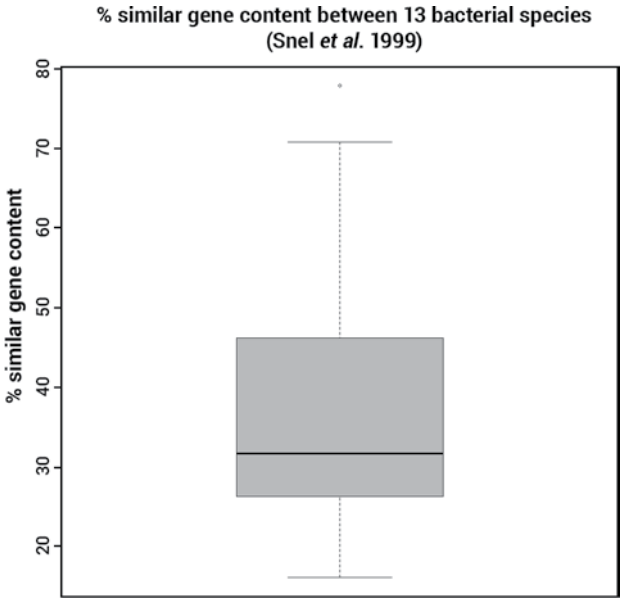

Figure 2. Boxplot of gene content similarity between 13 bacterial species from Snel *et al.*[41] All species pairs had a mean gene content similarity of 36.7%. The outlier shown at the very top represents the gene content similarity between *Escherichia coli* and *Haemophilus influenzae*, which ran at 77.8%.

the idea of the special creation of different cell types presents itself as a viable scientific alternative.

Baraminology studies have been performed that identified eight putative archaeal baramins representing 168 species, based on common genes that are involved in basic metabolic processes.[40] Other approaches have been carried out to identify phylogenetic relationships between species based on the presence/absence of particular genes. These studies included only a small number of species (11 or 13) (as opposed to the baraminology study based on 168 species), and demonstrated high, statistically significant, similarity among species within a baramin in contrast to species between different baramins.[40–42]

Snel *et al.*[41] studied 13 bacterial species and found that common genes between all species pairs was spread out, with an average gene content similarity of 36.7% and a median similarity of 31.7% (figure 2). This trend implies that all these species likely belong to different baramins. In contrast, in figures 3a and 3b, we can see a swarm plot of the gene content similarity values in the baraminology study between eight archaeal baramins. They clearly show a smaller set of high values at the top for species pairs within a baramin, as opposed to the great majority of similarity values between species from different baramins at the bottom. Figure 3b does not show this tendency since the species do not clearly fall within a single holobaramin.

Conclusion

All things considered, evolutionary hypotheses of the origins of life are complicated and contradictory. Lifeforms clearly separate well into three major, disjunct domains. Early complexity and genomic reduction are widespread, which contradicts evolution. The simplest and most straightforward explanation of the data is that these lifeforms came into existence independently from each other, namely that they were created in distinct 'kinds'.

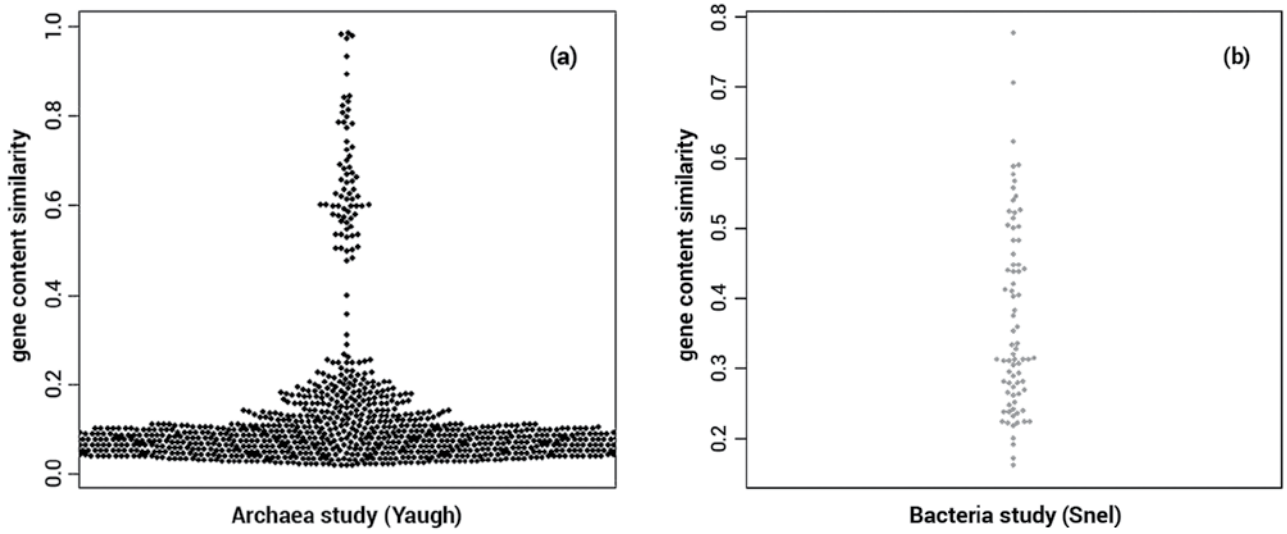

Figure 3a and **3b.** Bee swarm plots of gene content similarity values from the studies of Yaugh[41] and Snel ***et al.***[41]. In Yaugh's study (**a**) it is observed that a smaller number of higher gene content similarity values exist among species coming from the same holobaramin, with many more smaller gene content similarity values at the bottom between species from different holobaramins. In Snel *et al.*'s study (**b**), no such tendency is observed on account of the smaller number of species involved as well as the species not coming from the same holobaramin.

Materials and methods

Figure 1 was made in PowerPoint and inspired by the work of Forterre[1]. Figures 1, 2, 3a, and 3b were made in R version 3.4.3. using the boxplot and beeswarm commands.

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