

# Using Taxonomically Restricted Essential Genes to Determine Whether Two Organisms Can Belong to the Same Family Tree

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## Abstract

How are all life forms connected? Are they linked by one giant family tree, a web, or a forest of family trees? Here I propose to use taxonomically restricted essential genes and essential non-coding DNA elements to determine whether two organisms can be two branches of the same family tree, or can share a common ancestor that is simpler than the two organisms, based on the following reasons: 1) All essential genes and essential non-coding DNA elements of an organism are indispensable for its survival. 2) Spontaneous mutation accumulation experiments show that experimentally-identified spontaneous mutations are mostly single base substitutions, small (<13 base pairs) indels, and rearrangements of DNA segments. No novel genes have been observed to emerge. 3) Targeted mutagenesis experiments show that functional arrangements of amino acids are extremely rare; one in  $10^{77}$  for a typical protein domain with 153 amino acids. 4) Both mutation accumulation experiments and studies of symbiotic organisms show that genes that are not used tend to be degenerated or totally deleted. 5) For each constructive path to a new functional gene, there are many disruptive sidetracks. These sidetracks may prevent the cells from taking a constructive path that is of no immediate use, however beneficial it might be theoretically. In essence, the very nature of the essential genes and of the essential non-coding DNA elements of an organism, and the inability of mutation and natural selection to create novel genes, argue that two taxa, each with its own taxonomically restricted essential genes and essential non-coding DNA elements, cannot have shared and evolved from a simpler common ancestor. Analyses of the taxonomic distribution of essential genes and essential non-coding DNA elements of six bacteria and five eukaryotes show that no two of them can belong to the same family tree, which indicates that life forms on earth are best represented as a forest of family trees.

**Keywords:** common ancestor, mutations, origin of life, tree of life, lineage specific genes, orphan genes, origin of species, evolution, gene gain, gene loss

**Disclaimer:** The opinions expressed in this paper are the author's own and not necessarily those of the University of Missouri.

## Introduction

Three predominant views on the origin and relationship of organisms on earth are: 1) One family tree connects them all, 2) A forest of family trees connects them, and 3) a web connects them. The concept of a web of life, in which genes are transferred not only vertically through parents to offspring but also horizontally or laterally between different lineages, is proposed because “as the sequences from genome projects accumulate, molecular datasets become massive and messy, with the majority of gene alignments presenting odd (patchy) taxonomic distributions and conflicting evolutionary histories...the expected proportion of genes with genuinely discordant evolutionary histories has increased from limited to substantial” (Leigh et al. 2011) and “the more we learn about genomes the less tree-like we find their evolutionary history to be, both in terms of the genetic components of species and occasionally of the species themselves” (Baptiste et al. 2013). According to the web of life model, it is impossible to clearly determine, molecularly, the

phylogeny of all the organisms on earth. However, our daily experiences and experimental observations tell us that the norm of gene flow is from parents to offspring, demonstrating the reality of family trees rather than a web. Furthermore, the seemingly web-like relationship of life can be an artifact of forcing a forest of family trees into a single family tree. Therefore, determining which of the three views on the origin of life is correct can be simplified to determining whether two organisms belong to two different branches of one family tree or to two separate family trees.

With the publication of Darwin's book on the origin of species (Darwin 1859) and the works of his followers, the concept of one family tree of life has taken root in many people's hearts. Even though a group of renowned geologists, paleontologists, ecologists, geneticists, and developmental biologists concluded that what is seen in microevolution cannot be extrapolated to macroevolution (Lewin 1980), and more recently a group of distinguished evolutionists called for a paradigm shift in evolution (Baptiste et al. 2013), the concept of one family tree of life refuses

to leave the stage. Here I will use taxonomically restricted essential genes (TREGs), also called lineage-specific essential genes, and experimental observations on mutations, both spontaneous and engineered, to argue that life on earth is best described as connected by a forest of family trees.

### A. Theoretical Consideration

An essential gene is a gene in an organism that is necessary for the viability of the organism (by extension, genes responsible for its reproduction are also essential genes since a lineage terminates without reproduction). Thus, an organism dies when any one of its essential genes does not function properly and it will not exist until all its essential genes exist. A TREG is an essential gene in an organism that is unique to a specific taxon of organisms. For example, bacterial *dnaA* gene is unique to the bacterial domain; no such gene has been identified in eukaryotes (Tan and Tomkins 2015b).

A logical conclusion from the nature of essential genes is that an organism A cannot evolve into another organism B that contains organism B-specific essential genes, i.e. genes that are necessary for the survival of organism B but do not have homologs in organism A. In other words, all essential genes of an organism must have homologs in its ancestor, though these homologs may not be necessary for the survival of the ancestor.

Could it be possible that organisms A and B are both derived from a simpler common ancestor, CA, that evolved through two paths, one gained A-specific essential genes and evolved into A and the other gained B-specific essential genes and evolved into B? In other words, the CA evolved into two organisms A and B, each obtaining its special essential genes that do not have homologs in CA. This, in effect, just doubles the demands, and the impossibility, than for B evolves from A. Therefore, two taxa each with its own private TREGs cannot evolve from each other or have shared and evolved from a simpler common ancestor by gene gain. That is, they do not belong to the same family tree with more primitive (or simpler) common ancestors.

Alternatively, A and B could have derived from a more complicated ancestor by gene loss. The problem with this scenario is that we then need to answer the question where the complicated ancestor came from. In other words, even proven true, it does not help to answer the question where, ultimately, various organisms with different TREGs come from.

One may argue that new genes may be generated via accumulated mutations in organism A, resulting in transitional organisms A1, A2... and, eventually, organism B. I will address this question in the sections on gene gain and gene loss.

Note that homologs are often equated to sharing a common ancestor. However, homology can be due to common design, convergent evolution, or lateral gene transfer. In this essay two genes are considered homologous as long as they share some sequence similarity, regardless of their origin. If two homologous genes are protein coding, then the protein sequence of one gene would show up as a hit with an expect (E) value of  $10^{-4}$  or smaller using the protein sequence of the other gene as a query sequence in a BLASTp (Basic Local Alignment Search Tool, protein to protein) search in the National Center for Biotechnology Information (NCBI) database (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>). E-value is a parameter that describes the number of hits one can “expect” to see by chance when searching a database of a particular size and is equal to the possibility of a hit multiplying the size of the database. The similarity between two homologs can be very limited. For example, the archaea *Haloferax volcanii* translation initiation factor aIF5A is called a homolog of eukaryotic translation initiation factor eIF5A, although only less than ten amino acids of the 124 amino acids of aIF5A (*HVO-2300*) aligned with some amino acids in eIF5A (Gabel et al. 2013; Tan and Tomkins 2015a). In a BLASTp search (performed 9/23/2015) in the NCBI non-redundant protein sequences, eIF5A did not show up as a hit as a homolog of *HVO-2300*, while in the NCBI Non-redundant UniProtKB/SwissProt sequences, eIF5A did so with E-values from  $2e-11$  to  $3e-6$  in several eukaryotes including *Caenorhabditis elegans*, *Saccharomyces cerevisiae*, and *Homo sapiens* (human). The latter search also identified elongation factor P as a hit with E-values from  $6e-5$  to 0.002 in bacteria *Campylobacter lari RM2100* ( $6e-05$ ), *Wolinella succinogenes DSM 1740* ( $7e-05$ ), *Campylobacter jejuni subsp. Jejuni* ( $3e-04$ ), and *Desulfovibrio salexigens DSM 2638* (0.002).

It is worth pointing out that taxonomically restricted non-essential genes may also be very important for the life of an organism. For example, the genes involved in human language are the very factors that made human cultures possible. However, survival and reproduction could occur without language. Thus, linguistic genes are not necessary for the survival or reproduction of humans. Similarly, other genes involved in determining our voices, fingerprints, or sound of our footsteps, length of our fingers, etc., are important for our identification, for distinguishing one person from another, or for some specific skills, but they are not required for the survival and reproduction of humans. Therefore, by focusing on TREGs, we are considering only the minimal requirement for the existence of an organism.

## B. Taxonomically Restricted Genes

Taxonomically restricted genes (TRGs) are genes that are unique to a specific taxon of organisms (Tomkins and Bergman 2013; Wilson et al. 2005, 2007). They can be at any taxonomic rank, including domain, phylum, class, order, family, genus, or species. For example, an order-specific human gene will have homologs in non-human primates but not in non-primate organisms. A species-specific human gene is one that is unique to humans. None of its homologs exist in chimpanzee or any other organisms. A few hundred of such human-specific genes have been identified and some of them are implicated in brain function and male reproduction (Demuth et al. 2006; Guerzoni and McLysaght 2011; Wu, Irwin, and Zhang 2011; Zhang and Long 2014), though the results need to be confirmed with genomic comparisons of more organisms as discussed later. Interestingly, in the search for de novo human protein-coding genes, Wu and colleagues discarded the human TRGs because no orthologous DNA sequences could be identified in chimpanzee or orangutan (Wu, Irwin, and Zhang 2011).

Many instances of TRGs have been reported (Arendsee, Li, and Wurtele 2014; Khalturin et al. 2009; Neme and Tautz 2013; Tautz and Domazet-Lošo 2011; Toll-Riera et al. 2009; Wissler et al. 2013; Yang et al. 2013). Strikingly, opposite to earlier expectation, each newly sequenced genome adds a significant number of TRGs (Albertin et al. 2015; Arendsee, Li, and Wurtele 2014; Neme and Tautz 2013; Tautz and Domazet-Lošo 2011; Toll-Riera et al. 2009; Wissler et al. 2013).

To determine the exact number and the identity of TRGs in an organism, we need accurate sequences and careful and thorough annotations of genomes of many organisms because sequence errors or annotation errors do occur and can be very misleading (Hayashi et al. 2006). According to the Genomes Online Database, by 7/16/2015, 63851 genomes (1078 archaea, 45,076 bacteria, and 9059 eukaryotes) have been completely or partially sequenced (<https://gold.jgi-psf.org>), although most of these genomes have not been fully annotated. Improved annotation of these sequences will provide a huge amount of raw material for the identification of TRGs in many organisms.

The use of TRGs as evidence for or against two organisms belonging to the same family tree depends on the function and the origin of TRGs. If their functions are non-essential for the sustaining or propagation of their host organisms, or if, despite being functionally essential, they can be generated naturally by random mutations, then their existence cannot be used to determine whether the two organisms belong to one or two family trees. However, if they are essential and cannot be

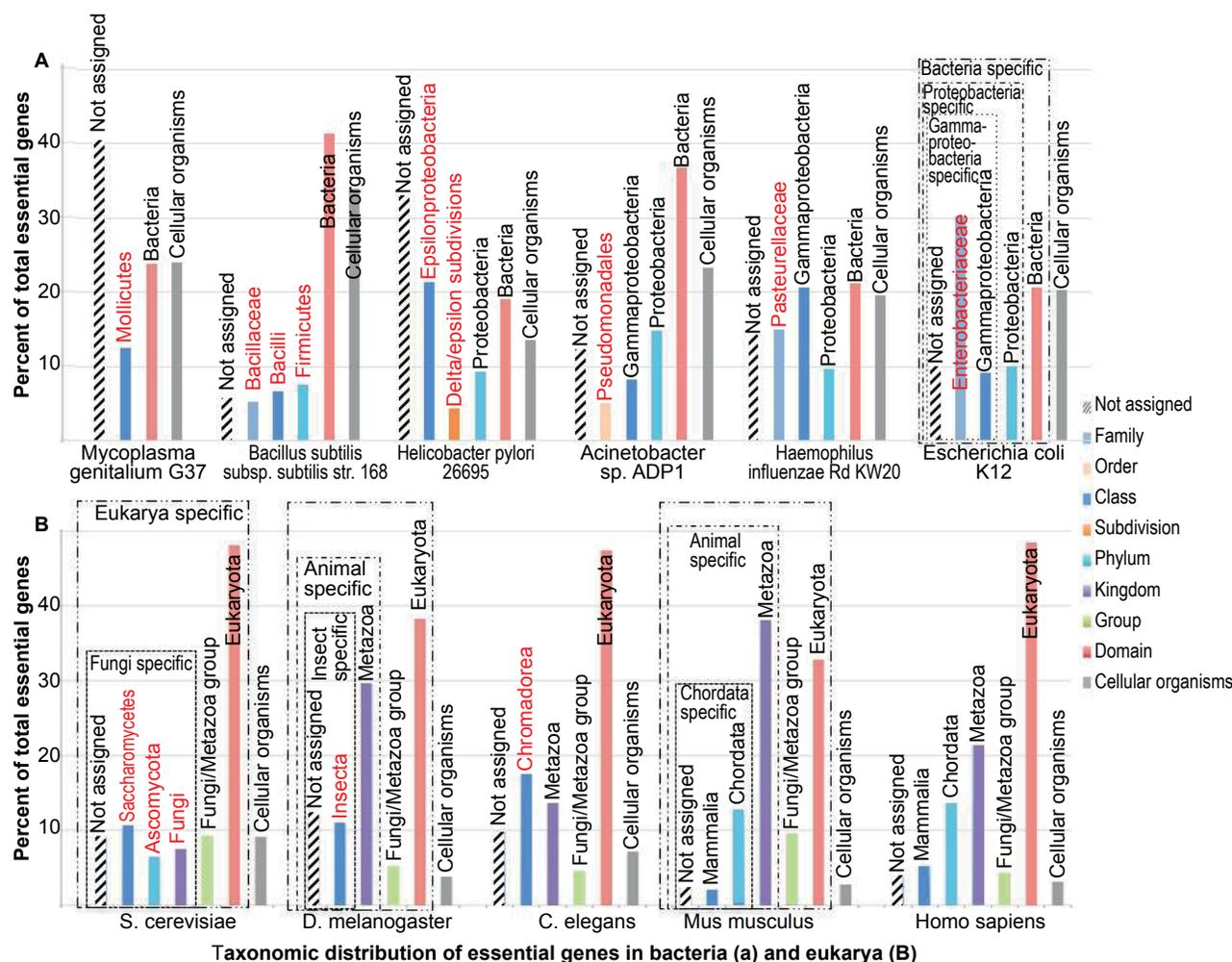
naturally generated (i.e., they are TREGs, not just TRGs), then two organisms that each contains its own distinct TREGs could not have evolved from each other or share a simpler common ancestor since each TREG creates an evolutionally unbridgeable gap between the two. In the following sections, I will first discuss the functions of TRGs in the survival of organisms (sections C and D) and then whether they can be generated via natural mutation and selection (sections E-G).

## C. Taxonomically Restricted Essential Genes

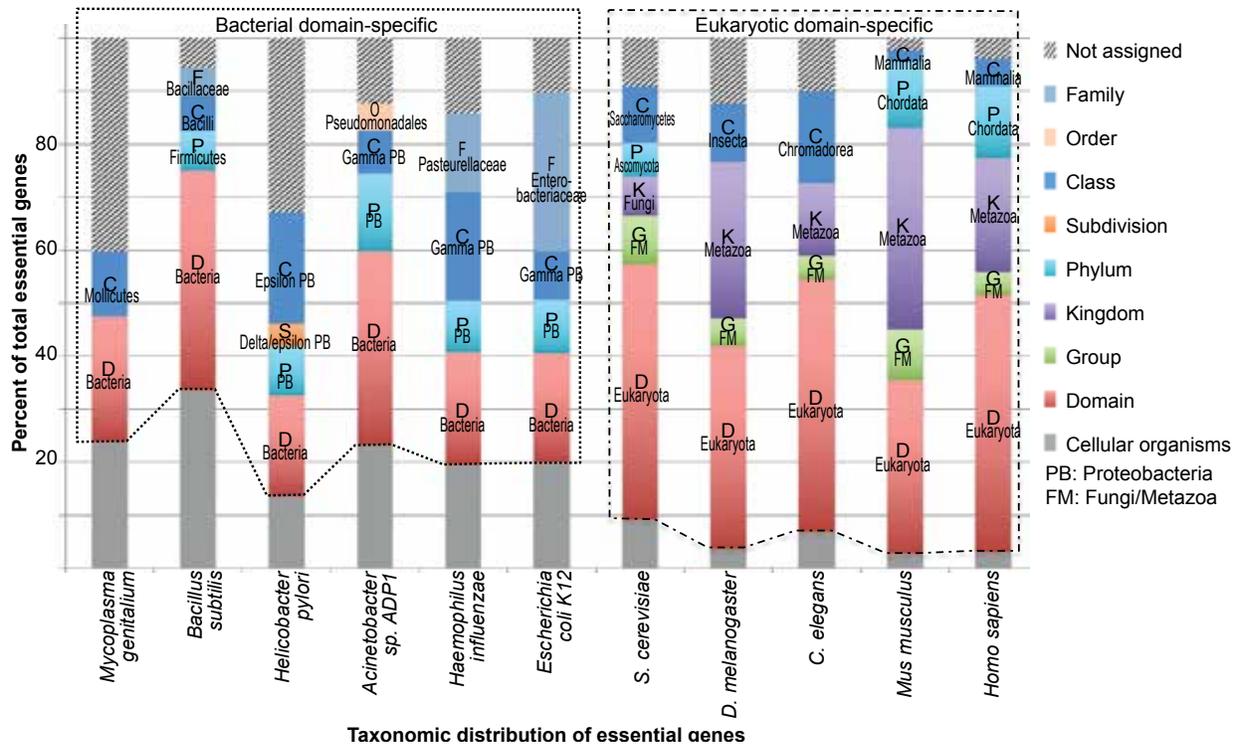
Three things should be kept in mind when considering essential genes. First, even the simplest prokaryotic cells require hundreds of essential genes. For example, the organism with the smallest known genome that can constitute a cell, the parasitic bacterium *Mycoplasma genitalium*, contains 381 essential genes, 79% of its annotated 482 protein-coding genes (Glass et al. 2006). Note that to die is not the most interesting phenotype; rather, it is an extreme phenotype. Thus, to survive is only the minimum. Second, there are many genes that are not essential on their own but are essential when deleted along with another nonessential gene. This well-known genetic phenomenon is called synthetic lethality (Tucker and Fields 2003). Therefore, we do not know how many additional genes in the *M. genitalium* genome are required for its survival, once synthetic lethality is considered. Studies in yeast show that synthetic lethal is a common phenomenon (Baryshnikova et al. 2013; Costanzo et al. 2010; Kaboli et al. 2014; Tong et al. 2001, 2004). Of the 6200 *Saccharomyces cerevisiae* genes, about 5100 are non-essential for cell viability. In contrast, a study covering ~30% of the genome identified 10,000 synthetic lethal pairs, and it is estimated that *S. cerevisiae* contains over 200,000 synthetic lethal combinations, 200-fold more than the number of yeast essential genes (Baryshnikova et al. 2013; Costanzo et al. 2010). Third, not all essential genes are required for the survival of its host organisms at all growth conditions, i.e. some genes are only conditionally essential (Hillenmeyer et al. 2008; Ramani et al. 2012). For example, yeast genes involved in galactose metabolism are essential only when the sole carbon source of yeast is galactose. Thus, the exact list of essential genes for an organism may change depending on the experimental conditions. Normally, when determining what genes are essential for an organism, the organism is provided with an optimal growth environment with all necessary nutrients, a non-stressful situation that is least demanding for the organism. Thus, we will limit the essential gene lists to those required for the survival of organisms under their optimal growth conditions.

To determine whether there are TREGs, essential genes from several model organisms are grouped according to their taxonomic distribution, or apparent evolutionary age—the proposed “evolutionary origin of a gene, defined by the evolutionarily most distant species where homologs can be found” (Chen et al. 2012a; Wolf et al. 2009), based on the online gene essentiality database (OGEE, <http://ogeedb.embl.de>, [Chen et al. 2012a]) (figs. 1 and 2, table 1). For example, the *Escherichia coli* genes were divided into six groups: 1) Cellular organism group, which can be found in both bacteria and eukaryotes (note that archaea was not counted as a domain separate from bacteria in the analysis); 2) Bacteria group, which can be found in proteobacteria and some non-proteobacteria bacteria but not outside bacteria; 3) Proteobacteria group, which can be found in gammaproteobacteria and some non-

gammaproteobacteria proteobacteria but not outside proteobacteria; 4) Gammaproteobacteria group, which can be found in enterobacteriaceae and some non-enterobacteriaceae gammaproteobacteria but not outside gammaproteobacteria; 5) Enterobacteriaceae group, which can be found in *E. coli* and some non-*E. coli* enterobacteriaceae but not outside enterobacteriaceae; and 6) Not assigned group. The sixth group includes those genes of which no homologs could be found in other organisms at the time the OGEE database was generated. Some genes of this group are *E. coli* specific. Therefore, group one *E. coli* genes are shared between bacteria and eukaryotes; groups two to six are specific to the bacteria domain (fig. 1A, boxed with dash-dot-dot line); groups three to six are specific to the proteobacteria phylum (fig. 1A, boxed with dash-dot line); group four to six are specific to the gammaproteobacteria class (fig. 1A,



**Fig. 1.** Taxonomic distributions of the essential genes of different organisms. **(A)** Six bacteria. **(B)** Five eukaryotes. All genes are grouped according to their apparent evolutionary age. The groups labeled with red letters do not have homologs in any of the other organisms shown in the figure. All data are from the online gene essentiality database (OGEE, <http://ogeedb.embl.de>). The distributions of the various groups were obtained by running analyses of specific datasets with the feature “phyletic age” on the OGEE website. Detailed data can be found in Table 1, including dataset used, total genes analyzed, and criteria used to judge whether a gene is essential or not in each experiment.



**Fig. 2.** The vast majority of essential genes are taxonomically restricted, though differ at the taxonomic ranks of restriction. This graph was generated using the same data as those in Fig. 1, only presented as stacked columns. Bacteria-specific essential genes are boxed with dotted lines, while eukaryotic-specific ones boxed with dash-dotted lines. Letters in the columns are the first letters of taxonomic ranks.

boxed with dotted line); group five to six are specific to the enterobacteriaceae family. Note that a family-restricted TREG is also an order-restricted TREG, which is also a class-restricted TREG, which is also a phylum-restricted TREG, which is also a domain-restricted TREG.

Fig. 2 is generated with the same data as Fig. 1 but different groups are presented as stacked columns instead of clustered columns. Several conclusions can be drawn from the taxonomic distributions of essential genes in the six bacteria and five eukaryotes analyzed (figs. 1 and 2).

First, most of the essential genes are taxonomically restricted, for each of the organisms analyzed (fig. 2, compare the non-gray segments of each column with its gray segment). The TREGs differ in their taxonomic distribution; some of them are restricted to specific domains, some to specific phylum, some to specific order, some to specific family. Some are even restricted to specific species. For example, in the group of “not assigned” of *E. coli* and *S. cerevisiae* essential genes, I found two (b2450/access number P76550.2 and b1572/access number P29009.1) *E. coli* specific and two (YEL035C/access number AAS56770.1 and YPL124W/access number P33419.1) *S. cerevisiae* specific. Of the four *E. coli* or *S. cerevisiae* specific genes, only the function of YPL124W is known. It is a component of, and is required for, the duplication of the spindle pole body (<http://ogeedb.embl.de>).

Second, the vast majority (78.6%, table 2) of bacterial essential genes are bacterial domain specific (fig. 2, boxed with dotted lines) and even a higher percentage (95.5%) of eukaryotic essential genes is eukaryotic domain specific (fig. 2, boxed with dash-dotted lines). Some of these domain restricted essential genes are genes necessary for DNA replication, including bacterial *dnaA*, *dnaB*, *dnaC*, and *dnaE*, as well as all the subunits of eukaryotic DNA polymerase alpha ([Tan and Tomkins 2015a, b] and <http://ogeedb.embl.de>). When all the organisms analyzed are considered together, only a mere 9.1% of their essential genes are universal, having homologs in both bacteria and eukaryotes, and thus belong to the group of cellular organism genes (table 2, gray segments in fig. 2). It appears that the more complicated an organism is, the smaller the percentage of its universal essential genes becomes, from the 22.3% of *E. coli* essential genes, to 9.2% of yeast, to 2.8% of mice. Furthermore, many of the essential genes exist in only one phylum or one class or even one family.

The large number of the domain-restricted bacterial and eukaryotic essential genes (fig. 2, compare the boxed regions with the gray regions) suggests that life on earth is linked by at least two separated family trees, one for bacteria and another for eukaryotes. This is because, as mentioned earlier, an organism cannot survive unless all its essential genes are functional. Therefore, it is impossible for

**Table 1.** Taxonomic distribution of essential genes (EG), genes analyzed for essentiality (GA), and all genes encoded in the genomes (AG) of a few organisms

	Organisms	Percentage of different groups with apparent age of genes analyzed										Total gene number	Definition of essential genes	
		Cellular	Domain	Group	Kingdom	Phylum	Subdivision	Class	Order	Family	Not assigned			
Bacteria	<i>Mycoplasma genitalium</i> (357)	EG	23.9	23.6					12.3			40.2	381	Genes were asserted to be essential or nonessential based on the occurrence of transposon inserts within each ORF and the overall insertion density in the local environment.
		GA	22.1	21.5					12.6			43.8	475	
		AG	22.1	21.5					12.6			43.8	475	
	<i>Bacillus subtilis</i> 352	EG	33.8	41.2			7.5		6.6		5.3	5.7	228	
		GA	16.9	13.4			11.7		4.4		19.2	34.4	4176	
		AG	16.9	13.4			11.7		4.4		19.2	34.4	4176	
	<i>Helicobacter pylori</i> (356)	EG	13.6	19.0			9.3	4.2	21.1			32.8	332	
		GA	14.3	15.0			9.3	4.0	19.8			37.6	1467	
		AG	13.7	14.0			8.7	3.8	19.0			40.8	1573	
	<i>Acinetobacter</i> sp. ADP1 (351)	EG	23.2	36.5			14.7		8.2	5.1		12.3	293	
		GA	11.1	15.7			12.6		9.3	14.8		36.5	3195	
		AG	10.7	15.2			12.2		9.1	14.4		38.5	3307	
	<i>Haemophilus influenzae</i> (365)	EG	19.6	21.1			9.8		20.4		15.0	14.1	460	
		GA	19.7	17.7			10.5		21.5		15.7	15.0	974	
		AG	18.0	18.3			9.8		21.4		14.5	17.9	1657	
<i>Escherichia coli</i> K12 (367)	EG	20.0	20.5			10.1		9.1		30.1	10.1	604		
	GA	18.8	13.0			10.7		9.9		35.9	11.7	3527		
	AG	17.3	12.1			10.0		9.7		35.7	15.2	4145		
Eukarya	<i>Saccharomyces cerevisiae</i> (350)	EG	9.2	48.1	9.2	7.4	6.4		10.5			9.2	1049	Genes whose removal result in lethal phenotype (growth inhibition)
		GA	6.4	29.5	8.6	10.6	6.3		10.8			27.8	5635	
		AG	6.3	28.9	8.4	10.4	6.2		10.6			29.6	5868	
	<i>Drosophila melanogaster</i> (347)	EG	3.7	38.2	5.2	29.6			10.9			12.4	267	A z score signifies the severity or rank of specific RNAi phenotypes created by the authors; genes with z-scores higher than 3 are defined as essential.
		GA	3.0	24.8	6.0	26.8			16.6			22.8	13,781	
		AG	3.0	24.8	6.0	26.8			16.6			22.8	13,781	
	<i>Caenorhabditis elegans</i> (346)	EG	7.0	47.4	4.6	13.6			17.5			9.8	742	Genes whose removal result in lethal or infertile phenotype.
		GA	2.0	15.1	3.2	16.0			46.4			17.2	11,446	
		AG	2.0	15.1	3.2	16.4			43.6			19.8	20,426	
	<i>Mus musculus</i> (349)	EG	2.8	32.7	9.5	38.0	12.6		2.1			2.3	2618	Genes whose reduced expression by RNAi lead to inhibition of growth in any of the five tested cell lines.
		GA	2.6	27.3	7.7	36.1	16.9		6.7			2.8	6038	
		AG	2.2	22.9	5.3	23.2	20.6		8.7			17.0	23,041	
	<i>Homo sapiens</i> (348)	EG	3.1	48.5	4.3	21.4	13.6		5.2			3.8	1528	Genes whose reduced expression by RNAi lead to inhibition of growth in any of the five tested cell lines.
		GA	2.6	25.5	5.8	25.6	20.2		9.3			11.0	20,684	
		AG	2.6	25.5	5.8	25.6	20.2		9.3			11.0	20,684	

Note: EG: essential genes identified; GA: genes analyzed for essentiality; AG: all genes encoded in genome according to the online gene essentiality database (OGEE, <http://ogeedb.embl.de/>). Numbers in parentheses after the organism names are data set ID of OGEE.

organism “A” to evolve into another organism, “B”, unless they share the same essential genes, at least A should contain all the genes essential for B because B will not survive until it has all its essential genes, although these genes may not be necessary for the survival or propagation of organism A. Therefore, two lineages that differ in TREGs could not have shared and evolved from a simpler common ancestor. Thus, if each domain/phylum/class/order/family/genus contains phylum/class/order/family/genus-specific essential genes, then they could not have derived

naturally from the same simple ancestor, unless multiple new genes can pop up simultaneously via mutations, an unlikely process based on studies on spontaneous mutation and targeted mutagenesis that will be discussed later.

One may argue that the eukaryotes and prokaryotes separated a long time ago, and have evolved separately since then. The original split is long forgotten, and so are the genes that used to connect the two. So, we shouldn't expect homologs in many genes between eukaryotes and prokaryotes.

**Table 2.** Participation of genes between the cellular group and other groups in the prokaryotes and eukaryotes analyzed.

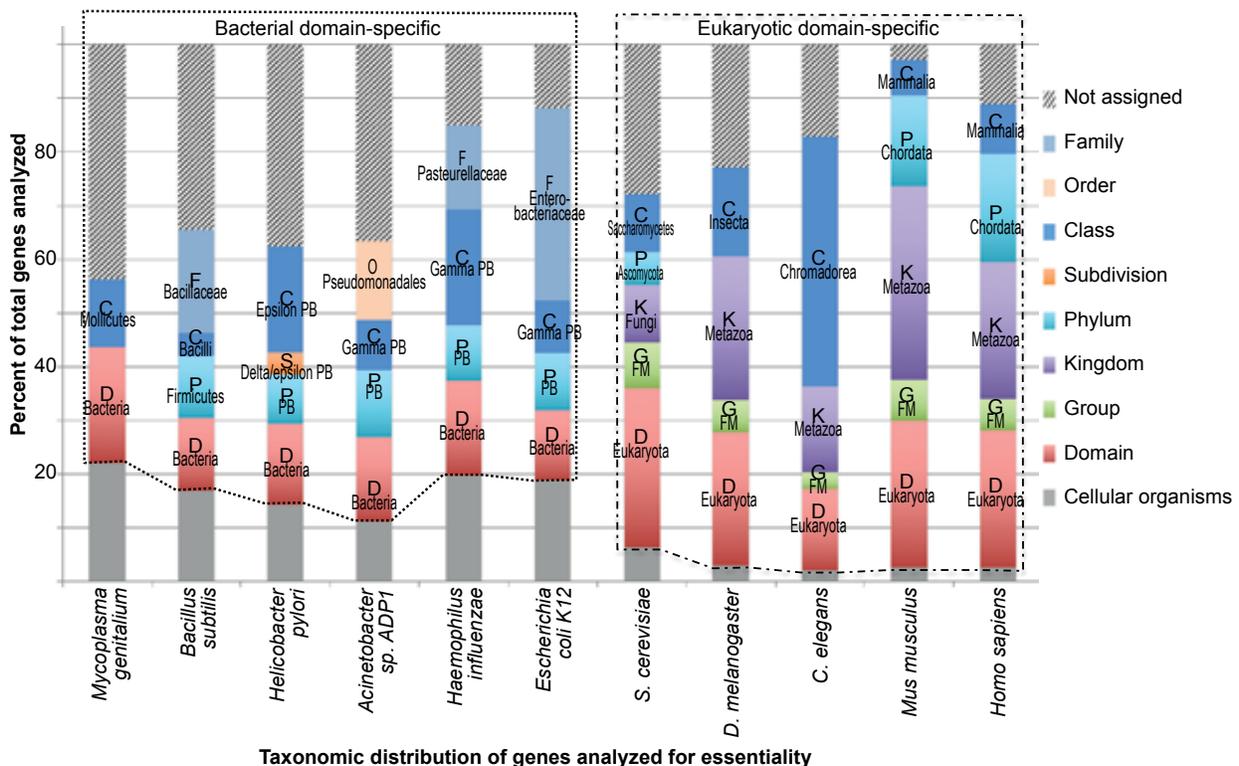
		Genes analyzed		Essential genes		All genes encoded	
		number	percentage	number	percentage	number	percentage
<b>All organisms analyzed</b>	cellular group	3918	5.5	771	9.1	4610	4.6
	other groups	67,480	94.5	7731	90.9	94,541	95.4
	total	71,398	100.0	8502	100.0	99,151	100.0
<b>Bacteria</b>	cellular group	2232	16.2	492	21.4	2396	15.6
	other groups	11,582	83.8	1806	78.6	12,937	84.4
	total	13,814	100.0	2298	100.0	15,333	100.0
<b>Eukaryotes</b>	cellular group	1686	2.9	279	4.5	2214	2.6
	other groups	55,898	97.1	5925	95.5	81,604	97.4
	total	57,584	100.0	6204	100.0	83,818	100.0

The argued scenario is unlikely what has happened in the history of life because, as will be discussed later, it is improbable that new genes just spring up into existence and gene loss cannot be the ultimate cause of biodiversity. Furthermore, once an organism is dead, it is unable to evolve into a different organism, new or old. A dead organism has but one fate: decay.

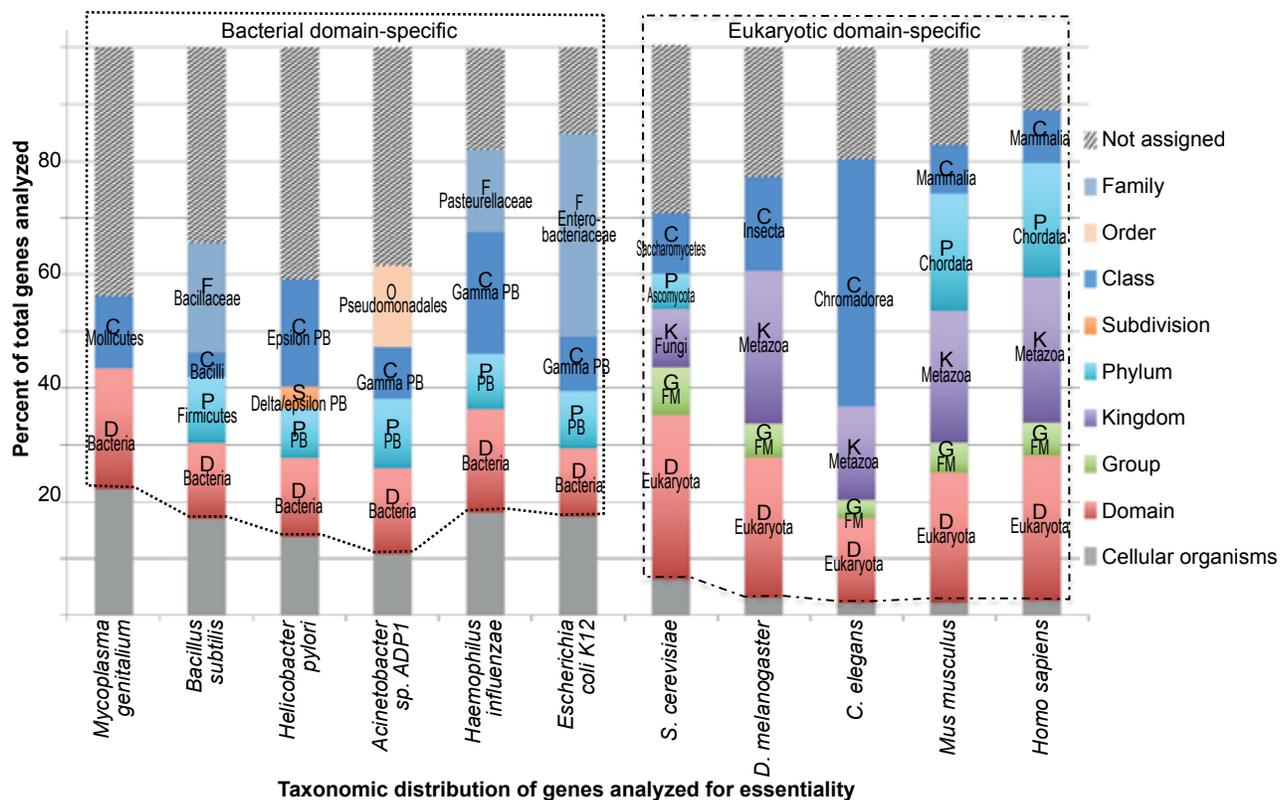
Note that the exact number of genes that belong to a specific group in an organism may change with the discovery of more genes in other currently uncharacterized organisms. However, it is unlikely that the new discoveries will alter the conclusion that most bacteria essential genes do not have eukaryotic homologs and that the vast majority of the eukaryotic essential genes are unique to the eukaryotic domain.

This is due to the fact that the pattern of taxonomic distribution of the essential genes is very similar to that of all the genes experimentally tested (fig. 3), or all the genes encoded in the genomes (fig. 4).

Consistently, *E. coli* TREGs restricted to the bacterial domain, or the proteobacteria phylum, or the gammaproteobacteria class, or the enterobacteriaceae family, have been identified via two independent methods, though not all TREGs identified are identical (fig. 5 [left] and table 3) (Baba et al. 2006; Chen et al. 2012a; Gerdes et al. 2003). One of the studies used single-gene deletion (Baba et al. 2006), the other used transposable element to disrupt gene function (Chen et al. 2012a; Gerdes et al. 2003). The latter is the source of the OGEE dataset used for *E. coli* in Fig. 1.



**Fig. 3.** Taxonomical distributions of all the genes tested for essentiality of the organisms analyzed in Fig. 1.



**Fig. 4.** Taxonomical distributions of all the genes encoded in the genomes of the organisms analyzed in Fig. 1.

Similarly, mouse TREGs restricted at different taxonomic ranks have been identified in two large-scale gene knockout studies, though not all TREGs identified are identical (fig. 5 [right] and table 4) (Chen et al. 2012a; Liao and Zhang 2007). Therefore, we can safely conclude that bacteria and eukaryotes belong to separate family trees.

Third, different bacteria have different TREGs, suggesting that not all bacteria can be connected by a single family tree. Of the six bacteria analyzed, *M. genitalium* and *Bacillus subtilis* belong to the phylum of Firmicutes, with the former a member of the Molicutes class and the latter the Bacilli class. *M. genitalium* and *B. subtilis* are separated from each other by their class-restricted TREGs, and together they are separated by phylum-restricted TREGs from

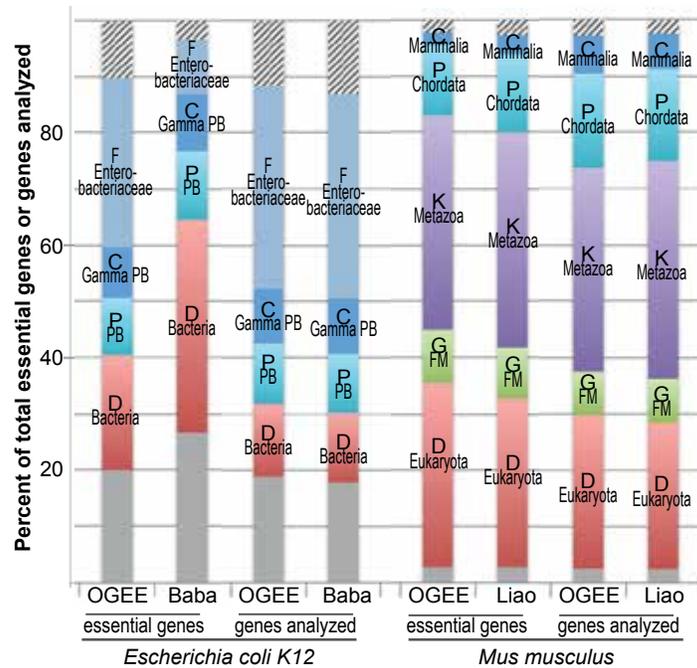
the other four analyzed bacteria, which belong to the phylum of Proteobacteria. Of these four, *Helicobacter pylori* is a member of the Epsilonproteobacteria class. *Haemophilus influenzae* (order: Pasteurellales, family: Pasteurellaceae), *Acinetobacter* (order: Pseudomonadales, family: Moraxellaceae), *E. coli* (order: Enterobacteriales, family: Enterobacteriaceae) are members of the Gammaproteobacteria class, within different orders and families. These four bacteria are separated from each other by class, or order, or family-restricted TREGs. Therefore, the six bacteria analyzed belong to six different family trees.

Fourth, different eukaryotes have different TREGs, suggesting that not all eukaryotes can be connected by a single family tree. Of the five eukaryotes analyzed, only *Mus musculus* and *Homo*

**Table 3.** Comparison of two studies of *E. coli* gene essentiality.

	Essential in Baba	Not essential in Baba	Analyzed in OGEE but not in Baba	Not found in Baba	Total in OGEE
<b>Essential in OGEE</b>	205	393	18	12	628
<b>Not essential in OGEE</b>	49	2939	87	152	3227
<b>Analyzed in Baba but not in OGEE</b>	46	576			
<b>Not found in OGEE</b>	4	192			
<b>Total in Baba</b>	304	4100			

Note: OGEE: <http://ogeedb.embl.de/>, Baba (Baba et al. 2006).



**Fig. 5.** Comparisons of essential genes identified in different experiments in *E. coli* (left) or in *Mus musculus* (right). The two experiments for *E. coli* use different methods to disrupt the functions of genes, the OGEE via transposable elements while the Baba via gene deletion. The two experiments for mice are both via knockout OGEE: <http://ogeedb.embl.de>, Baba: (Baba et al. 2006), Liao: (Liao and Zhang 2007).

*sapiens* belong to the same class (Mammalia). These two organisms are separated from the other three organisms, *S. cerevisiae*, *Drosophila melanogaster*, *Caenorhabditis elegans*, which are separated from each other by their class-restricted essential genes. Thus, these five eukaryotes belong to at least four different family trees.

Do mice (*M. musculus*) and humans (*H. sapiens*) belong to one family tree or two family trees? The data analyzed in the OGEE database do not provide a definitive answer. Therefore, I performed additional studies to resolve the issue. Demuth and colleagues reported 870 primate protein families (with 689 human unique genes) that do not have homologs in rodents and 1773 rodent protein families that do not have homologs in primates (Demuth et al. 2006). Unfortunately, the identities of the genes cannot be retrieved due to the Ensembl protein family name changes and the authors' lack of a record of those genes (Matthew W. Hahn, personal communication). Thus, whether any of those genes are TREGs will remain unknown. In a more recent

study, Zhang and colleagues reported that 1828 human genes are primate specific (389 unique to humans) and 3111 mouse genes are rodent specific (1452 unique to mice) (Zhang et al. 2010). Eleven of the primate specific genes on their list are reported as essential in the OGEE database. A BLASTp search performed on 10/6/2015 in the NCBI non-redundant gene database confirmed that three of the 11 (ENSG00000143226, ENSG00000170848, ENSG00000179750) are primate specific. Two of the 11 are unique to humans according to Zhang and colleagues: ENSG00000182242, a testis specific protein that used to be called expressed 28 pseudogene 1 and is no longer listed as a gene in Ensembl, and ENSG00000185829, which encodes ADP-ribosylation factor-like 17A. A BLASTp search in the NCBI non-redundant gene database shows that neither is unique to human, nor to primates. Of the 3111 rodent specific genes reported by (Zhang et al. 2010), 14 (of which four belong to the mouse-specific group) were identified as essential by OGEE or by Liao et al. (<http://ogeedb.embl.de> and

**Table 4.** Comparison of two studies of mouse gene essentiality

	Essential in Liao	Not essential in Liao	Analyzed in OGEE but not in Liao	Total in OGEE
Essential in OGEE	1621	130	867	2618
Not essential in OGEE	421	1540	1459	3420
Analyzed in Liao but not in OGEE	68	35		
Total in Liao	2110	1705		

Note: OGEE: <http://ogeedb.embl.de/>, Liao: (Liao and Zhang 2007)

[Liao and Zhang 2007]. None of these are restricted in rodents based on the NCBI non-redundant gene database. A main reason for the failure of the reports on human or mouse specific genes in the Zhang study to remain true is that they only chose a few organisms for their study instead of using all the data available in the NCBI database (Zhang et al. 2010). More importantly, the list of human or mouse essential genes is far from complete. Only 6141 of mouse genes (26.6% of the 23,041 encoded) have been analyzed by gene knockout, while the essentiality of human genes was estimated from knockdown experiments in cell lines, not inside real human bodies in which a living cancer cell can lead to termination of its carrier (<http://ogeedb.embl.de> and [Liao and Zhang 2007]). Therefore, a thorough comparison of all of the human and mouse genes against genes of more organisms and a comprehensive investigation of the essentiality of the human and mouse genes are warranted. Nonetheless, the three primate-specific essential genes in the human genome suggest that mice and humans belong to two separate family trees. A conclusion confirmed by their taxonomically-restricted essential non-coding DNA sequences as described in the next section (Pikaard 2002; Tan and Tomkins 2015b).

#### D. Taxonomically-restricted Essential Non-coding DNA Sequences

In addition to genes, i.e. DNA sequences that code for proteins or RNAs as end products, all genomes contain non-coding DNA elements, including origins of replication that are required for DNA replication, enhancers and promoters that are necessary to determine when and where and how much a gene will be transcribed, introns (for eukaryotes), and sequences critical for maintaining the structure or stability of chromosomes or for chromosome segregation during cell division.

Many experiments have shown that prokaryotes and eukaryotes differ in their origin of DNA replication and gene regulatory sequences, including enhancers and promoters (Tan and Tomkins 2015b). Differences of regulatory sequences of ribosomal RNA genes in mice and humans render human cells unable to transcribe mouse ribosomal RNA genes, and vice versa (Pikaard 2002). Therefore, mouse protein producing machinery can only be generated in mice and human protein producing machinery can only be generated in humans. This incompatibility in the ribosomal biogenesis, a process vital for gene translation and survival of any organism, makes it impossible for mice and humans to share a common ancestor.

So far, a genome-wide, experimentally-tested, functional annotation of non-coding DNA sequences

has only been reported for the alphaproteobacteria *Caulobacter crescentus* (Christen et al. 2011). Consistent with the above conclusion about TREGs, 27% (129) of the 469 essential genes of *C. crescentus* (phylum: proteobacteria, class: alphaproteobacteria, order: caulobacterales) do not have homologs in *E. coli* and 46% (235) of the 512 essential genes of *E. coli* do not have homologs in *C. crescentus* (Christen et al. 2011), suggesting that *C. crescentus* and *E. coli* do not share a common ancestor. In addition, *C. crescentus* could not have shared a common ancestor with the other five bacteria analyzed in Fig. 1 due to their class restricted TREGs. Strikingly, of the 1012 essential DNA segments identified, the majority do not code for proteins. These non-coding DNAs include 402 regulatory sequences and 130 other non-coding elements. It is highly possible that other organisms also contain a large quantity of essential non-coding DNA sequences, as in *Caulobacter*. Knowledge of how organisms differ in their essential non-coding DNAs will be very useful in determining the origins and relationships of different life forms.

#### E. Gene Gain

Next I will address the question of whether two organisms with different TREGs belong to the same family tree by integrating results of experiments investigating, intentionally or unintentionally, where or how the TRGs arose or whether a TRG can be easily generated via mutation and selection. Keep in mind that, going back through the hypothetical evolutionary history, every gene was once a TRG and similar to no other genes. Therefore, to answer the question of the origin of TRGs is like to answer the question of the origin of life itself.

A variety of evolutionary mechanisms have been proposed to account for the emergence of new genes (Long et al. 2003):

1. Gene duplication followed by mutations and subfunctionalization or neofunctionalization;
2. Exon shuffling: combination of exons from different genes;
3. Retroposition: a new gene copy is created at a new genomic position;
4. Mobile element activity: part of a transposable element is incorporated into a gene;
5. Gene fusion/fission: two genes fuse into one or one gene splits into two;
6. Lateral gene transfer: horizontal, instead of vertical, transmission of genes;
7. De novo origination: a coding gene derived from non-coding DNA.

Of all the proposed mechanisms, only the de novo origination can generate a totally new gene that does not have homology to any other genes. The results of all others will be a homolog of the source gene(s).

Note that all these mechanisms are inferred from sequence comparison and have little empirical support. The assumption, normally unstated, is that we know the real family tree or the phylogeny of the life-forms and genes under consideration. The reality is that nobody has seen how a gene has come to be and that there are no labels on any organism or its coding genes telling people its parent(s). Furthermore, nobody is able to go back in time to investigate the issue. Of course, one can wish and claim that a non-coding DNA segment is on the way to becoming a gene, but such claims do not validate much unless he/she is able to prove that this non-coding DNA segment is not degeneration of a gene that used to be. In addition, it is more likely that this DNA segment has never been and will never be a gene—it just serves as a regulatory or structural sequence.

Is it possible that a new organism is born all together with all its organism-specific essential genes, which somehow derive from DNA segments that do not code for any genes in its parent(s)?

Though most people are satisfied with the idea that new genes or proteins somehow pop up in the history of life, and many claim gene gain, sometimes in the number of hundreds or thousands of genes at a time, based on mere sequence comparison and hypothetical pedigrees, e.g. (Demuth et al. 2006), some researchers made the painstaking efforts to experimentally test the possibility of generating new genes by accumulated mutation and selection. Some of them used the forward approach, while others the reverse approach. The former performed long-term culturing of different organisms—mutation accumulation experiments—and analyzed mutations accumulated. The latter artificially engineered mutations into known genes and estimated the possibility of finding a functional protein out of all the possible arrangements of the composing amino acids. I will examine the forward and reverse approaches in the next two subsections.

### E.1 Spontaneous Mutations

Generally, all the amino acid differences between two homologous proteins in two organisms are interpreted being generated by mutation with the allegedly less complicated organism representing the ancestor state and with the normally unstated presupposition that we know the pedigree/history of the compared organisms. In reality we barely know the deep-time history of any organism, so, it is formally possible that some of the differences were just standing genetic variation. For example, for sexually reproducing organisms, a two-egged twin may inherit two non-overlapping halves of the genomes of their parents. They would have many differences in their genomes and would appear that they have had experienced a long time of diverging at their birth.

To avoid the ambiguity of mutation designation based on hypothetical pedigrees, some try to investigate the power of naturally occurring mutations in the whole organism by culturing inbred lines at conditions of minimum selection so mutations can be accumulated and are allowed to drift to fixation. Such mutation accumulation experiments have been done in several organisms, including *S. cerevisiae*, *D. melanogaster*, *C. elegans*, *Chlamydomonas reinhardtii*, and *Arabidopsis thaliana* (Aquadro et al. 1990; Avila et al. 2006; Azevedo et al. 2002; Baer et al. 2005; Barrick et al. 2014; Bégin and Schoen 2006; Brito et al. 2010; Burch et al. 2007; Chavarrías, López-Fanjul, and García-Dorado 2001; Chen et al. 2012b; Chen and Zhang 2014; Clark, Wang, and Hulleberg 1995; Cooper 2014; Cooper, Bennett, and Lenski 2001; Cooper and Lenski 2000; Davidson, White, and Surette 2008; Deng, Li, and Li 1999; Denver et al. 2009; Denver et al. 2010; Denver et al. 2012; Domingo-Calap, Cuevas, and Sanjuán 2009; Downie 2003; Engström, Liljedahl, and Björklund 1992; Estes, Phillips, and Denver 2011; Fry 2004; Fry et al., 1999; García-Dorado and Caballero 2002; García-Dorado and Gallego 2003; Good and Desai 2015; Gray and Goddard 2012; Haag-Liautard et al. 2007; Hall et al. 2008, 2013; Heilbron et al. 2014; Houle and Nuzhdin 2004; Joseph and Hall 2004; Katju et al. 2015; Kavanaugh and Shaw 2005; Keightley and Caballero 1997; Keightley and Lynch 2003; Keightley et al. 2009; Kuzdzal-Fick et al. 2011; Lee and Marx 2012; Loewe, Textor, and Scherer 2003; Long et al. 2013; Lynch et al. 2008; Maklakov 2013; Maside, Assimacopoulos, and Charlesworth 2000; Matsuba et al. 2012; McGuigan, Petfield, and Blows 2011; Ness et al. 2012; Nishant et al. 2010; Ossowski et al. 2010; Pannebakker et al. 2008; Papaceit et al. 2007; Roles and Conner 2008; Rutter et al. 2012; Salgado et al. 2005; Saxer et al. 2012; Schrider et al. 2013; Schultz and Scofield 2009; Shabalina, Yampolsky, and Kondrashov 1997; Sousa et al. 2013; Sung et al. 2012a; Trindade, Perfeito, and Gordo 2010; Vassilieva, Hook, and Lynch 2000; Yampolsky et al. 2005; Zhu et al. 2014).

These mutation accumulation experiment studies show that the vast majority of the mutations decrease the fitness of the organisms (Domingo-Calap, Cuevas, and Sanjuán 2009; Heilbron et al. 2014; Katju et al. 2015; Leiby and Marx 2014; Mallet, Kimber, and Chippindale 2012; Morgan et al. 2014; Sharp and Agrawal 2013; Trindade, Perfeito, and Gordo 2010; Vassilieva, Hook, and Lynch 2000), especially in small size populations (Katju et al. 2015), not only the mutations located within protein coding regions but also those within the intergenic regions (Heilbron et al. 2014). In addition, the mutations that enhance the fitness of organisms in one growth condition tend

**Table 5.** Mutations identified in mutation accumulation experiments.

Organisms	Genome size	Number of generation	Small-sized mutations					Large-sized mutations			References
			Single base replacement <sup>a</sup>			insertion/deletion <sup>c</sup>	complex <sup>d</sup>	duplication <sup>e</sup>	insertion/deletion <sup>e</sup>	inversion	
			base substitution rate <sup>b</sup>	number	G/C to A/T biased?						
<b>Eukaryotes</b>											
<i>Arabidopsis thaliana</i>	125Mb	30	7.00E-09	99 (4/11)	yes	17 (1-15)			2 (610, 5445)	Ossowski et al. 2010	
<i>Armillaria gallica</i>	100Mb			12 (0/4)	n			1 (400)		Anderson and Catona 2014	
<i>Caenorhabditis briggsae</i>	100Mb	250	1.23E-09/1.44E-09 <sup>e</sup>	91+150 (6+12/14+23)	yes					Denver et al. 2012	
<i>Caenorhabditis elegans</i>	100Mb	250	1.33E-09/1.62E-09 <sup>e</sup>	108+99 (13+16/28+34)	yes					Denver et al. 2012	
		NA	2.7 E-09	391 (24/56)	yes					Denver et al. 2009	
<i>C. elegans N2 and LSJ1<sup>f</sup></i>	100Mb			877 (21/49)		311 (1-9)				Weber et al. 2010	
<i>Chlamydomonas reinhardtii</i>	121Mb	350	2.08E-10	9 (2/2)	yes	5 (1-3)				Ness et al. 2012	
		1730	6.76E-11	20 (0/1)	yes	13 (1-12)				Sung et al. 2012a	
<i>Daphnia pulex</i> (mitochondrion), asexual MA lines		116/81 <sup>f</sup>	4.3 E-08	3 (1/0)	n	8 (1-2)				Xu et al. 2012	
<i>Daphnia pulex</i> (mitochondrion), sexual MA lines		61	2.8 E-08	3 (0/3)	y	9 (1-2)				Xu et al. 2012	
<i>Drosophila melanogaster</i>	175Mb	262	3.5 E-09	174 (8/18)	y	7 (1-4)				Keightley et al. 2009	
		1	2.8 E-09	6		3 (4-13)				Keightley et al. 2014	
		145-149 <sup>h</sup>	5.5 E-09 <sup>h</sup>	732	y	60 (1-26)	7	7 (939-4285)	22 (26-2642)	Schrider et al. 2013	
<i>D. melanogaster</i> (mitochondrion)		200	6.20E-08	28 (1/23)	y	8(1-3)				Haag-Liautard et al. 2008	
<i>Mesoplasma florum</i>	0.79Mb	2351	9.78 E-09	527 (70/417)	y	101 (1-11)				Sung et al. 2012a	
<i>Paramecium tetraurelia</i>	72Mb	3300	1.94 E-11	29 (8/15)	y	5				Sung et al. 2012b	
<i>Saccharomyces cerevisiae</i>	12.05Mb	4800	3.3 E-10	33 (6/18)	y	2(1-3)		11 (74270-541056)	4 (6076-601163)	Lynch et al. 2008	
<i>S. cerevisiae</i> (mitochondrion)		4800	1.3 E-8	13	n	30 (1-6)				Lynch et al. 2008	
<b>Bacteria</b>											
<i>Bacillus subtilis</i>	4.15Mb	5080	3.28 E-10	350 (60/202)						Sung et al. 2015	
<i>B. subtilis mutS<sup>-1</sup></i>	4.15Mb	2000	3.31 E-8	5295 (1489/3247)	n					Sung et al. 2015	
<i>Escherichia coli</i> K12	4.64Mb	3080/6356 <sup>i</sup>	1.88 E-10/2.45 E-10	93/140 (55/124)	y	9/12 (1-4)				Lee et al. 2012	
		6356 <sup>k</sup>		154		19 (1-4)		3 (*50)	49 (*50)	1 (1829)	Barrick et al. 2014
<i>E. coli</i> K12, MutL <sup>-1</sup>	4.64Mb	375	3.26 E-8	1625 (482/930)	n	306 (1-4)				Lee et al. 2012	
<i>Mycobacterium tuberculosis</i>	4.0Mb	NA	2.01-3.03 E-10	24	y					Ford et al. 2011	

Organisms	Genome size	Number of generation	Small-sized mutations					Large-sized mutations			References
			Single base replacement <sup>a</sup>			insertion/deletion <sup>c</sup>	complex <sup>d</sup>	duplication <sup>e</sup>	insertion/deletion <sup>e</sup>	inversion	
			base substitution rate <sup>b</sup>	number	G/C to A/T biased?						
<i>Pseudomonas aeruginosa</i> PAO1Δ <i>mutS</i> <sup>i</sup>	6.26Mb	644	2.95 E-8	778 (202/495)	y	164 (<10)		1	1 (1880)	Heilbron et al. 2014	
<i>Salmonella typhimurium</i>	4.95Mb	5000		943 (230/566)	y					Lind and Andersson 2008	
<b>Phage</b>											
bacteriophage PhiX174	5.4kb		1.0 E-6	7 (0/7)	n					Cuevas, Duffy, and Sanjuan 2009	
DNA and RNA bacteriophages	3.6-6.4kb			303 (89/202)	n					Domingo-Calap, Cuevas, and Sanjuan 2009	
phage Qβ			9.1 E-6	41 (9/32)	n	4 (1)				Garcia-Villada and Drake, 2012	
<b>Population genomics</b>											
<i>Arabidopsis thaliana</i>	161-184Mb <sup>m</sup>			4,540,000				600,000		Long et al. 2013	
<i>Drosophila melanogaster</i>	169.7-192.8Mb <sup>n</sup>			4,853,802				1,296,080		Huang et al. 2014	
<i>Homo sapiens</i>	3300Mb			5,907,699 (60,157/69,434) <sup>o</sup>		650,000 (1-50)		14,000		Abecasis et al. 2010	
				9,243,994				17,601		Schuster et al. 2010	
<i>Apis mellifera</i>	236Mb			8,282,459						Wallberg et al. 2014	
				12,041,303						Harpur et al. 2014	

## Note:

- Numbers in parentheses are numbers of synonymous/nonsynonymous mutations when the mutations are in exons. Nonsynonymous mutations include changes of amino acids and stop codon mutations.
- Unit: per base per generation.
- Numbers in parentheses indicate the range of the numbers of bases inserted or deleted.
- Replace a segment of DNA with another stretch of seemingly random nucleotides that differs in length.
- Two genotypes were studied.
- Two lines, N2 and LSJ1, are compared. These two lines were derived from the same progenitor and were separately domesticated from 1956.
- Two lines were studied.
- Two genotypes, eight sublines, were studied. The average base substitution rate of one subline is 7.71 E-09, two times more that of the other subline (3.27 E-09).
- A key enzyme *mutS* involved in mismatch repair is deleted.
- Two time points.
- Reanalysis of the same data from 6356 generation mutation accumulation experiment.
- A key enzyme *mutL* involved in mismatch repair is deleted.
- Genome size variance 14%.
- Genome size variance 14%. 6637 potentially damaging variants (15% of all *D. melanogaster* genes) were identified that affecting splicing, reading frame, or translation starting or stopping; each line contains ~136 such genes.
- Most mutations may be somatic or cell line mutations. It was "estimated that an individual typically differs from the reference human genome sequence at 10,000–11,000 non-synonymous sites ... in addition to 10,000–12,000 synonymous sites ... 190–210 in-frame indels, 80–100 premature stop codons, 40–50 splice-site-disrupting variants and 220–250 deletions that shift reading frame"(Abecasis et al. 2010).

to render them less competitive in other conditions (Cooper and Lenski 2000; Leiby and Marx 2014; Rutter et al. 2012). Furthermore, some recent studies suggest that many natural mutations are not random after all, but context dependent (Lee et al. 2012; Sung et al. 2015).

Table 5 lists mutations that have been identified in some of the mutation accumulation experiments where the genetic mutations have been determined by sequencing. Some mutations are located within genes and some in the intergenic regions. For those point mutations located within genes, the ones causing amino acid changes are called nonsynonymous mutations, while those not causing amino acid changes are called synonymous mutations.

No birth of novel genes has been found to result from these accumulated mutations; most experimentally-identified spontaneous mutations are single base substitutions and small (<13 base pairs) indels (deletions/insertions) (table 5, also see [Wei et al. 2014] and references wherein). In contrast, a common phenomenon that emerges from the multiple mutation accumulation experiments is that genes that are not used tend to degenerate—mutate to a non-functional gene, or get lost—be deleted totally (Cooper and Lenski 2000; Lee and Marx 2012; Leiby and Marx 2014; Raeside et al. 2014; Rau et al. 2012). This conclusion is confirmed by studies of genomic changes of symbiotic organisms (Lee and Marx 2012; Rau et al. 2012) and the unintended mutation accumulation in the balancer chromosomes of *Drosophila* (Araye and Sawamura 2013).

The most celebrated gain of novel function mutation discovered from the famous Lenski long-term *E. coli* evolution experiment is the acquired ability of *E. coli*, which uses citrate as carbon source only in anaerobic conditions, to use citrate as carbon source at aerobic atmosphere (Blount et al. 2008). A detailed analysis showed that the reason the mutant *E. coli* is able to use the citrate in the aerobic environment is not due to a gain of new genes but is caused by a tandem duplication. The resultant duplicated citrate transporter is positioned next to an aerobically expressed promoter, leading to the citrate transporter that normally is only expressed in the absence of oxygen being ectopically expressed in the presence of oxygen (Blount et al. 2012). Such misregulations of gene expression have been reported previously with the consequence of cancer formation, e.g. ectopic expression of Wnt1 gene caused by mouse mammary tumor virus integrations (Nusse 2005; Tekmal and Keshava 1997).

The fate of unused genes from both the mutation accumulation experiments of various organisms in artificial laboratorial environments and from the symbiotic organisms in natural hosts demonstrate

that it is highly unlikely, if not totally impossible, for an organism-specific gene to arise naturally. This is because before the organism-specific novel gene—a gene without homologs—could come to be, it would be a useless stretch of DNA, a burden for the organism carrying it, and would likely be deleted as an organism normally does to an unused gene. In fact, all the alleged births of new genes are based on sequence comparison of an organism with its theoretical or hypothetical ancestral organism (Demuth et al. 2006; Kaessmann 2010; Long et al. 2003; Tautz and Domazet-Lošo 2011).

## E.2 Engineered Mutations

Instead of waiting for spontaneous mutations, another group of researchers use the reverse approach to determine the frequency of finding a functional protein enzyme in the possible sequence space (Axe 2004; Gauger et al. 2010; Reidharr-Olson and Sauer 1990; Taylor et al. 2001). They found that to make a polypeptide, i.e. linking amino acids together with peptide bonds is one thing, while it is totally another thing to make a functional polypeptide—a protein enzyme—that folds like a natural protein and catalyzes a chemical reaction like a natural enzyme in the cell, albeit with less efficiency.

For a 153 amino acid long  $\beta$ -lactamase domain, a typical protein domain with  $\alpha$  helices,  $\beta$  sheets, and loops, the possibility of finding a polypeptide that functions is one in  $10^{77}$  (Axe 2004). The human genome contains 23,000~30,000 protein coding genes, with a median length of 375 amino acids (Broccieri and Karlin 2005; Wijaya et al. 2013). If we scale according to the length of the protein, the possibility of a 375 amino acid long polypeptide functions as a natural protein is one in  $10^{189}$  ( $=10^{77(375/153)}$ ). To put this number in perspective, the estimated total mass of the visible universe is  $10^{80}$  hydrogen atoms ([Davies 2006] and [http://en.wikipedia.org/wiki/Observable\\_universe](http://en.wikipedia.org/wiki/Observable_universe)). The maximum number of events that could have happened since the birth of the universe are approximately  $10^{140}$ , assuming the universe started at the big bang 14.6 billion years ( $10^{17}$  seconds) ago:

$$\frac{\text{Total Matter (M)} \times \text{Total Time (T)}}{\text{Planck Time (P)}} \approx \frac{10^{80} \times 10^{17}}{10^{-43}}$$

T: the longest estimated history of the universe, P: The shortest time in which any physical effect can occur ( $10^{-43}$  seconds) (Meyer 2009).

Starting with a shorter and structurally simpler enzyme, the 93 amino acids long chorismate mutase (CM), which has three  $\alpha$  helices connected with two short loops, Taylor and his colleagues gave a more optimistic estimate (Taylor et al. 2001): one in  $10^{24}$  polypeptides that have the same hydrophobic pattern

of the natural CM would have some enzymatic activities. Accordingly, for an average human protein of 375 amino acids having the desired hydrophobicity, one in  $10^{97}$  ( $=10^{24(375/93)}$ ) may function as the native protein. To account for the foldability based on hydrophobic constraints alone (maximum: one in  $10^{10}$ ) (Lau and Dill 1990) and the percentage of correctly folded polypeptides to perform a particular function (assuming one in  $10^3$ ) (Axe 2004), that number becomes  $10^{110}$ , i.e.  $10^{30}$  less likely than finding a specific hydrogen atom in the whole visible universe, assuming all the mass in the universe were made of hydrogen.

A more shocking observation of Taylor and colleagues (Taylor et al. 2001) is that two beneficial and functional mutations often cancel each other's effects. Briefly, they generated and screened two libraries of CM mutants, library one (lib1) partially randomized helix H1 and library two (lib2) partially randomized H2 and H3 of the three  $\alpha$  helices of CM. They found ~99.99% of their mutants were not functional, i.e. only one in  $10^4$  maintained some enzymatic function. The big surprise arose when they combined those functional mutants from lib1 and lib2. The vast majority (~99.99%) of the combinations did not function at all as a CM. Thus, instead of increases, the second mutation normally counteracts the beneficial effect introduced by the first mutation, though the second mutation is functional by itself. Furthermore, the chance of finding a functional mutant is not increased with the knowledge of the functionality of the individual mutations. Such phenomenon is later termed "sign epistasis," a fancy way of stating that two beneficial mutations work against each other (Schenk et al. 2013; Weinreich et al. 2006).

In other words, a mutation is much more likely to disrupt than to improve the function of a protein. For each constructive path to a functional protein, there are many disruptive sidetracks. These sidetracks may prevent the cells from taking a constructive path, however beneficial it might be theoretically. This is experimentally demonstrated by Gauger and colleagues (Gauger et al. 2010).

### E.3 Route Possible and Route Actual

To determine what an organism would naturally do when given the choice of a potential long-term beneficial path that is a short-term burden, a scenario very similar to making a new gene from a no-gene, Gauger and colleagues directly analyzed the likelihood of *E. coli* taking a two-step, theoretically highly beneficial path—restoring function to a nonfunctional *trpA* gene with two point mutations (Gauger et al. 2010). One of the two, *trpA*<sub>E49V</sub> is a complete loss of function mutation, while the

other, *trpA*<sub>D60N</sub> a partial loss of function mutation. Both mutations, individually, revert readily to functional *trpA*<sup>+</sup> (three to seven revertants from an overnight culture of about  $10^9$  colony-forming units). They combined the two mutations and overexpressed the double mutant in *E. coli* whose endogenous *trpA* gene was deleted. They screened for revertants of the double mutation under three tryptophan-limiting conditions: in liquid cultures, in solid cultures, as well as in a mutator strain that increased the reversion rate of the *trpA*<sub>E49V</sub> and *trpA*<sub>D60N</sub> five-fold and twenty-fold, respectively. No double mutants reverted to full Trp<sup>+</sup> phenotype, although some serial cultures have been propagated for 9300 generations. They also routinely plated batch and serial cultures of the mutant strains to tryptophan-free agar to look for the presence of weak Trp<sup>+</sup> revertants and found one weak Trp<sup>+</sup> colony this way. This mutant had the *trpA*<sub>D60N</sub> genotype. Unfortunately, this revertant failed to compete with its coevolving siblings to survive and propagate to become fixed in the population, thus, failed to generate a full Trp<sup>+</sup> phenotype. The failure for the double mutants to revert is not due to the inability of the long-term cultures to adapt; their growth rate doubled within 500 generations. The failure resulted from sidetracking, including deletion of the non-functional *TrpA* gene and expression-reducing insertions, point mutations, and rearrangements.

Four conclusions can be drawn from the experiments on mutation and natural selection: 1) Out of all the possible sequences of amino acids in a polypeptide, only a tiny fraction can function as proteins—1 in  $10^{77}$  for a 153 amino acid long polypeptide (Axe 2004); 2) Most spontaneous mutations are small and deleterious; 3) A gene not used tends to be lost; 4) A long-term beneficial path can be easily sidetracked by short-term metabolic cost cuts. Thus, it is highly unlikely, if not totally impossible, to generate a novel protein by accumulated mutation and natural selection.

### F. Gene Loss

The above discussion makes natural gene gain highly improbable, even if theoretically possible. Next, I will discuss the opposite, gene loss, regarding the possibility that the organism B specific essential genes were in its ancestor organism A but were lost because they were not required for the survival of the ancestor.

Indeed, as mentioned above, a gene that is not used tends to degenerate or be totally deleted. However, gene loss cannot be the ultimate cause of the diverse life forms on earth for two reasons. First, all the mutations studied with model organisms,

including virus, bacteria, yeast, worms, flies, and mice, have only made them abnormal or dead or have no observable phenotypes; the mutations have not changed one species into another. Second, gene loss as a mechanism to generate biodiversity requires the ancestors to be more complicated and contain more genes than the extant organisms. This will only create an even bigger question of how or where those ancestors came from.

For instance, considering six simple hypothetical organisms (fig. 6), when only organisms A and B (each contains four genes) are analyzed and the rest are unknown or not analyzed, genes X2, X3, X4, and X6 would be identified as organism specific. Suppose that X2 and X3 are essential genes, while X4 and X6 are not. Because A and B each contains its own organism specific essential gene, they could not evolve from each other. However, they could share a common ancestor that contains genes X2, X3, X4, and X6. Note that even though both A and B could be generated by gene loss from their common ancestor (CA), it is unlikely either A or B could become the CA because it requires gene gain. In other words, CA has to be the parent but not a transitional intermediate. Furthermore, genes X2 and X3 would perform a redundant function in the ancestor; they would be synthetic lethal for the ancestor. Therefore, loss of function of either gene X2 or X3 may have no visible phenotype in the ancestor but loss of both would be lethal. With the discovery of organisms C to E, we will find that an organism has to have either X2 or

X3 or both (fig. 6C to E). On the other hand genes X4 and X6 may be involved in functions that do not threaten the survival of their carrier organisms in the experimental conditions, although may do so in other conditions.

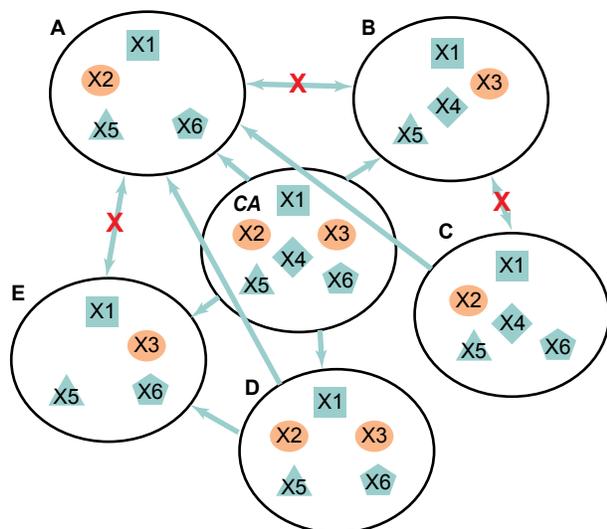
Yeast strains that have either one of two genes that are synthetic lethal deleted have been generated in laboratories, though the resultant strains remain being yeast, instead of becoming a new species (Ooi et al. 2006; Zinovyev et al. 2013). It is formally possible that such mutations occur naturally. Only comparison of the genome sequences of various individuals within a species could allow us to know whether such complementary gene loss occur naturally, and if so, the frequency of the occurrence.

### G. A Potential Problem and Possible Solutions

If indeed complementary gene loss does occur naturally, would this negate the above argument on using TREGs to determine whether two organisms can belong to the same family tree? I think this unlikely. However, it does raise an issue that we need to be cautioned about when using the TREGs to determine whether two organisms belong to the same family tree. The conclusion needs to be checked with the following three considerations.

First, the similarity of the shared genes and of non-coding DNA elements between the two organisms compared needs to be considered. The shared genes or non-coding DNA elements of two organisms of the same species with unequal essential gene lists, such as the engineered yeast strains that contain one or the other of a pair of synthetic lethal genes, should be identical or nearly identical. They should contain only small differences, such as single base changes, small indels, or rearrangement of segments, including inversions, translocations, or copy number variations. By copy number variations, I exclude the difference between zero copy and non-zero copy or copies. In addition, as shown in the hypothetical example of Fig. 6, sequencing of diverse members of the same species will likely reveal that each of these members has at least one of the two synthetic lethal genes.

Second, the scale is important. Since the mutation accumulation experiments show that most observed mutations are single base mutations or small indels, gene loss should be a rare event. The number of TREGs between organisms that belong to separate family trees should be much larger than the number of TREGs between organisms that belong to the same family tree. How much larger the difference should be needs to be determined by population genomics. Currently, genome sequences of most organisms are based on the sequences of a single individual or a single culture. Consequently, we do not know how many mutations a species can hold,



**Fig. 6.** A hypothetical group of six organisms. X1 through X6 represent genes. X2 and X3 are essential genes for organisms A, B, C, and E but not for organisms D and CA. X2 and X3 are synthetic lethal for organisms D and CA. Potential ancestor-offspring pairs are linked with arrows pointing from ancestors to offspring. Red Xs indicate that it is impossible for A and B, or A and E, or B and C to evolve from each other.

or the extent of genetic diversity between individuals in the same species. To estimate the whole gene pool of a species, it is necessary to sequence multiple diverse individuals (for large animals or large plants) or populations (for micro-organisms). Several studies have sequenced the genomes of humans from different locations around the world (Abecasis et al. 2010, 2012; Ball et al. 2012; Rasmussen et al. 2011; Schuster et al. 2010). It will be interesting to have a detailed comparison of these human genomes to determine the extent of homozygous or heterozygous gene loss within the *Homo sapiens* species.

Finally, the knowledge of gene networks is important. Genes never work alone but function with other genes in signal transduction pathways and other elaborate regulatory networks. It is more likely that one gene or a small number of genes of a pathway be lost than all members of the whole pathway. Fig. 7 summarizes in a flowchart the steps to determine whether two organisms can belong to the same family tree.

### Conclusions and Discussions

TREGs can be used as a means to determine whether two organisms can belong to the same family tree for two reasons. First, each TREG of an organism is necessary for the survival of that organism. Second, it is improbable for a new gene to be generated naturally, de novo, via accumulated mutation and selection. This is experimentally demonstrated by the failure of mutation accumulation experiments

to generate any new genes, the extreme rarity of functional sequences of all the possible arrangements of the composing amino acids, the high possibility of a mutation to disrupt the function of a protein, the tendency of two beneficial mutations to work against each other, and the readiness of an organism's choosing a route that provides short term metabolic cost cuts instead of a route that provides long term beneficial gains. The large number of TREGs in the diverse, though few, organisms analyzed in Figs. 1 and 2 indicate that no two of these organisms could have shared a common ancestor. This suggests that life on earth is represented by a forest of family trees, instead of one family tree.

The data shown in Figs. 1 and 2 are limited in several ways:

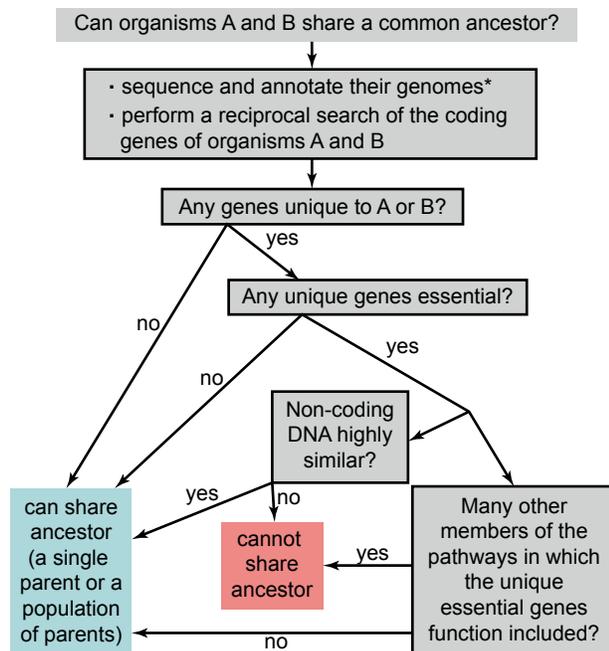
1. Not many organisms are analyzed.
2. Genes are not grouped in the same taxonomic ranks.
3. Not all essential genes are known and/or analyzed for each organism.
4. Data reliability has not been analyzed by an independent, second research group.
5. Data are not updated with new findings.

To address these limitations, the following needs to be done:

1. Analyze as many organisms as possible, starting from one member from each phylum, then expand to one member per order, then to one per family, then to one per genus.
2. Group all genes from different organisms according to the same taxonomic ranks, including domain, phylum, class, order, family, genus, and species.
3. Identify all essential genes for each organism, starting with model organisms and the species-specific genes, then to genus-specific, to family-specific, moving up the taxonomic rank.
4. Cross-check the reliability of the data by different persons and different experimental approaches.
5. Update with new findings.

In order to fully and reliably determine how all life forms are related to each other, we need to do the following:

1. Sequence and annotate at least one genome in each phylum, class, order, or family.
2. Identify TRGs and taxonomically restricted non-coding DNA sequences.
3. Determine whether the TRGs and the taxonomically restricted non-coding DNA sequences are necessary for the viability or propagation of their carrier organisms.
4. Continue to experimentally investigate the power of mutation.
5. Cross-check the accuracy of the sequences and annotations of genomes and other data and data analyses.



**Fig. 7.** A flowchart to determine whether two organisms can belong to the same family tree. \*: For sexually reproducing organisms, the genomes of both sexes should be included.

Currently, the bottleneck is not obtaining genome sequences but their analyses, especially with regard to the differences between organisms. Furthermore, the limited analyses available were mostly done with the presumption of all organisms being linked via a big phylogenetic tree, an idea that I have argued against above and that has also been challenged by many others (Baptiste et al. 2013; Criswell 2009; Jeanson 2013; Koonin 2007; Koonin, Puigbò, and Wolf 2011; Koonin and Wolf 2009; Koonin, Wolf, and Puigbò 2009; Puigbò, Wolf, and Koonin 2009, 2012, 2013; Suárez-Díaz and Anaya-Muñoz 2008; Tan and Tomkins 2015a, b; Tomkins 2013; Tomkins and Bergman 2013). Thus, data analyses with the idea of a forest of family trees will be not only informative but also necessary and will be fruitful.

The emergent need is to build an information processing pipeline that is based on the framework of a forest of family trees, or an orchard of life (Frair 2000; Tomkins and Bergman 2013; Wise 1990; Wood 2006; Wood et al. 2003). The pipeline should streamline retrieving of sequence data, integrating multiple sequence datasets and phenotypic analyses datasets. It should distinguish functions inferred from mere sequence alignments and those from real wet experiments. Ideally, the pipeline will allow automatic updating yet with proper quality control.

Though the work is demanding, both in labor and in funds, it is exciting and rewarding. At the end, we will find the work worthwhile because it will help everybody to find a truly scientifically satisfactory answer to the fundamental question of life and the origin of life.

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