Cnidarians turn evolutionary theory into jelly

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Phylum Cnidaria, which includes animals such as sea anemones, corals, hydras, and jellyfish, has interesting characteristics that impinge on the origins debate. According to evolution, cnidarians occupy a fairly basal position in the branch of the evolutionary tree that leads to animals with bilateral symmetry (the Bilateria). Several cnidarian species have been used to study the origins of several tissue types, including neural tissue, because of surprising similarities with vertebrates. It is paradoxical that such cellular structures, tissues, and organs would be conserved across the animal kingdom. In other words, many basic cell and tissue types, and the genes that control them, were already present in very early animal organisms, and barely changed or evolved over the supposed 700 Ma since the Precambrian. Cnidarians also have genes in common with vertebrates that are missing from insects and worms. Sensationally, these soft-bodied creatures have also been found as fossils, where modern species barely differ from fossilized ones. A characteristic cnidarian cell type is the nematocyst; a highly specialized cell that contains a spear-like structure used to capture prey, and which represents an irreducibly complex biological system. Cnidarians thwart evolution in a number of ways.

The position of Cnidaria within the animal kingdom

The main animal phyla are depicted in figure 1. Cnidarians are considered to be the first organisms after sponges (Porifera) to have real tissues. In some groups (including modern corals and the extinct tabulate and rugose corals) development even of the radially symmetric adult form occurs along bilateral lines. Yet, they are considered to still have radial symmetry, as opposed to animals with true bilateral body plans (Bilateria). The Bilateria are divided into two main groups, the protostomes and deuterostomes, depending on whether the blastopore, the first opening in the embryo, forms the mouth (protostomes) or the anus (deuterostomes). There are five classes within Phylum Cnidaria: Anthozoa (including corals and sea anemones), Cubozoa (box jellies), Scyphozoa (true jellyfish), Staurozoa (stalked jellyfish), and Hydrozoa (including hydra and Portuguese-man-o-war).[1,2] Cnidarians have been divided into two main subphyla, the Anthozoa and Medusozoa, which are thought to have separated early on in cnidarian evolution, 580 MYA at the latest. Anthozoa is held to be the more basal group, with Medusozoa, based on mitochondrial DNA structure and rRNA sequences. Interestingly enough, the split between these two groups is supposed to be as old as the split between protostomes and deuterostomes.[3,4]

Early organ and tissue complexity

One of the fascinating aspects of studying cnidarians, represented by the model organism, *Nematostella vectensis* (the starlet sea anemone), is that the gene repertoire of its body plan is close to that of vertebrates. Its genes code for relatively complex neural structures which are important for the development of further traits, such as mesoderm and bilaterality in the early stages of their lives.[5] This is supported by the fact that *N. vectensis* has 56 homeobox genes, which are responsible for delineating the limbs and body regions of higher organisms.[6] The current evolutionary genetic view is that the evolution of new body plans is often driven by changes in gene expression, controlled by homeobox genes, with cis-regulatory elements regulating gene expressions modularly.[2,7] A new theme in evolutionary biology is that all major body plans had originated quite early on in evolution, in the (hypothetical) common ancestor of all bilaterian animals called *Urbilateria*. Since then, there have been relatively few innovations. Moreover, many body plans are a result of gene loss, not gene acquisition.[8] Gene families for all basic body plans appeared miraculously at the beginning of the evolutionary process. Yet, for some unexplainable reason, however, evolution of newer gene families then ceased. A number of epigenetic and non-coding genetic elements are also conserved between cnidarians and vertebrates/bilaterians: chromatin marks, enhancer modifications, gene regulatory elements, and broad gene synteny.[9]

Triploblasty

According to some evolutionary views, early metazoans developed into mesodermate animals in a stepwise fashion with one, two, and then three germ layers. According to this view, cnidarians are a simpler group of organisms compared to bilaterian animals, which have three germ layers compared to the two layers of cnidarians. However, based on new discoveries, this view is now being overturned. Furthermore, diploblasty is seen by some to have evolved secondarily in cnidarian larvae and polyps.[10]

It turns out that cnidarians have been found to contain mesodermal and muscle tissues, along with myogenic regulatory genes.[11] A list of these genes can be seen in table 1.[10,12,13] These genes all have orthologs to bilaterian mesodermal or myogenic genes. Larval cnidarian cells, including gastrodermal and epithelial cells, also contain smooth muscle myofibre. A layer of cells is established at the beginning of the medusa stage, called the entocodon. In other species, an extracellular matrix wedged between the endoderm and ectoderm called the mesoglea also contains some scattered cells. The entocodon and mesoglea are considered by some to correspond to bilaterian mesoderm.[14] However, the mesenchymal entocodal mesoderm of hydromedusae have a separate three-dimensional structure. The bell of medusozoan jellyfish also contains mononucleated, non-fused striated muscle cells. Striated muscle originates from mesoderm-like primordia.

The cnidarian nervous system and sensory organs

Many genes are shared throughout the animal kingdom, and conserved genes and regulatory circuits are used differentially.[5,15,25] This is a roundabout way of saying that evolution didn't happen, since it is highly improbable that all major body plans would be conserved for all of evolutionary time. This is more consistent with creation, which states that all groups of organisms were created at the beginning of creation.

A prevailing evolutionary view of the cnidarian nervous system is that of a simple, diffuse neural network. However, this is based on the study of only a single freshwater *Hydra* species. Elements of the nervous system of more complex animals have been shown to be present in cnidarians. Such elements include mechanoreceptors, photoreceptors, chemoreceptors, neurotransmitters, motor neurons, and gangliar neurons. Homologous regulatory genes of the

nervous system are present in cnidarians and bilaterians.[16] For example, members of the *Pax* and *Six* gene families have been found to have similar structure and gene expression to their homologs in higher metazoans.[17,19]

The cnidarian nervous system is made up of pervasive nerve plexes that form linear or circular tracts, and can differentiate into several subsystems with separate functions and physiological properties. Synapses are also present between ganglion neurons and sensory cells and epithelial muscular cells. Neurons expressing neuropeptides are expressed in a polarized way relative to the body axis.[18] Visually guided behavioural patterns can also be quite complex, including navigation and courting.

On the genetic level, the Anthozoa and Hydrozoa have genes homologous with bilaterian genes involved in neurogenesis, neural network formation, synaptic structure formation and transmission, vesicle formation, and axon pathfinding. These genes also include conserved transcription factors such as bHLH factors, type B *Sox* genes, zinc-finger proteins, and neuron-specific RNA binding proteins. Neurotransmitters and their receptors such as acetylcholine, catecholamine, GABA, epinephrine, and dopamine are also present in cnidarians.[17]

Rhopalia are interesting sensory organs, which are responsible for gathering photic information as well as keeping the organism in balance. Light-sensing organs in cnidaris can be as complex as camera eyes complete with lens as in *Cladonema* or *Tripedalia cystophora*;[19] cubozoans even have a cornea and ciliated photoreceptor cells.[20] The PaxB gene in *T. cystophora* is expressed in the jellyfish lens, retina, and statocyst, and can also induce small, ectopic eyes in *Drosophila*. This gene is highly similar to the *Pax6* gene in more complex organisms, which is responsible for regulating eye development.[21] They are club-shaped bodies located on the bell of the medusa of
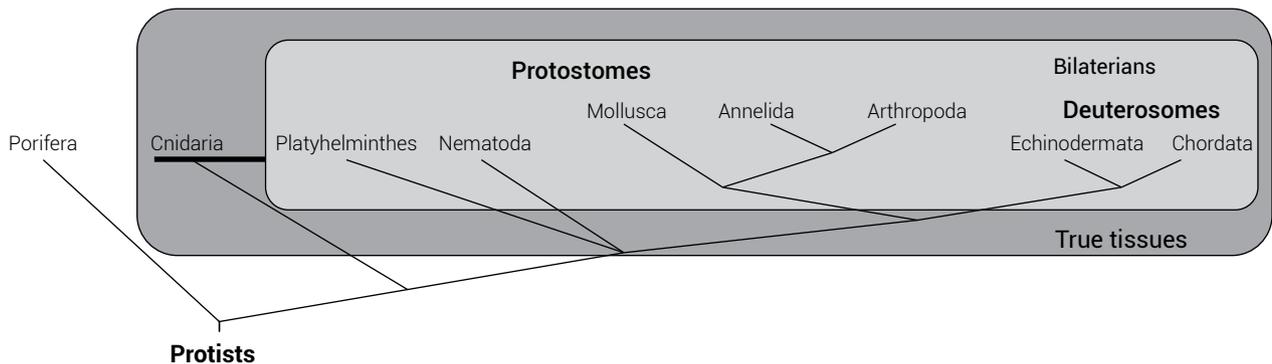

Figure 1. Phylogenetic tree depicting how evolutionists perceive the relationship between cnidarians and other animal phyla. Cnidarians are a sister group with bilaterians. They are deemed to have radial symmetry instead of two-sided symmetry. As compared to sponges (Porifera) they have true tissues (endoderm and ectoderm). This figure was reproduced based on figure I, from Technau *et al.*[39]. Choanoflagellates are not depicted, nor are the branch points for Urmetazoa, Ureumetazoa, and Urbilateria.

Table 1. List of genes from certain cnidarian species which take part in mesoderm formation, neurogenesis, and myogenesis in cnidarians (from Martindale *et al.*[10] and Seipel and Schmid[12]). Note: just because the gene is not expressed in the mesoderm doesn't mean that it does not induce mesoderm development.

Gene	Tissue	Function
Ash	Endoderm nematboblasts, nematocytes	Nematocyte induction, HLH transcription factor
Ash 2	Endoderm secretory cells, myogenesis	HLH transcription factor
Atl1	Entocodon, proneural	Secretory cell, muscle differentiation
Bagpipe	Endoderm	Mesoderm patterning and differentiation
Brachyury	Entocodon	Myogenesis
Gata	Entocodon, muscles, mesoderm	Blastula development, zinc-finger transcription factor
Id	Endoderm, muscles	HLH transcription factor
Mef2	Entocodon	Nematocyte induction, MADS-box transcription factor
Mox	Endoderm	Mesoderm patterning and differentiation
MRF	Entocodon, muscles	HLH transcription factor
Msx	Entocodon, neuronal	Myogenesis
NK-2	Endoderm	Peduncle formation, homeobox protein
Otx	Entocodon, muscles	Homeobox transcription factor
Snail	Entocodon, muscles	Gastrulation, gastrodermis and pharynx development, C2H2 transcription factor
Tinman	Endoderm	Mesoderm patterning and differentiation
Twist	Endoderm	Induction of neurons in pharynx, HLH transcription factor

schypozoans and cubozoans. Each rhopalium consists of a lithocyst, otherwise known as a statocyst at its terminal end, covered by a layer of epithelium. Underneath this is a mass of subepidermal ectodermal pigmented sensory cells. Underneath this lies a touch plate consisting of thickened epidermal sensory cells, which synapse with the diffuse nervous system and the motor nerve net. When the jellyfish is tilted, the heavy rhopalium induces asymmetric muscle contraction to straighten up the jellyfish.[22]

The main genes responsible for the formation of rhopalia are in the *Otx* and *POU* gene families, which are conserved also in vertebrates and other bilaterians and perform similar functions.[23] In *Nematostella*, three Otx genes (Otx A, B, and C) play a role as homeodomain transcription factors in the aboral and pharyngeal endoderm, as well as the tentacles. However, expression patterns of *Otx* genes in the jellyfish *Podocoryne* do not correlate to those in bilaterians, which came about independently, as expected by the creation model. All three genes are expressed in endodermal tissues surrounding the mouth cavity, such as in the circum-oral nerve ring in the bilaterian nervous system.[19, 24] In vertebrates the *POU* gene family is known as the Brn3 gene family, which code for transcription factors, and takes part in the development of sensory cells related to vision, hearing, and olfaction.

The nematocyte

The nematocyte is an organelle inside the specialized cnidarian cnidocyte cell which play a role in predation, defence, and locomotion. They can vary in shape and size, from 5–100 μm and 25–30 basic types. They first develop in cells called nematoblasts and then migrate to battery cells, usually located in the tentacles. The nematocyte looks basically like a cylinder with a tubule located inside, adorned with spines or other appendages. An extreme osmotic pressure of 150 bar builds up inside and is used to launch the nematocyte. When activated by mechanical pressure at the operculum, the nematocyte shoots out at a phenomenal acceleration of more than 5 million g! The expanding tubule then punctures the surface or skin of the prey/attacker and injects toxins into its system, thereby subduing it.[26] Nematocyte venoms also exhibit additional effects, such as cytolysis, dermatonecrosis, proteolysis, and vasopermeation.

Just like the flagellum of the bacterium, *E. coli*, the nematocyte is truly an example of irreducible complexity, one of the fastest biomechanical events in nature. Hundreds of genes are involved in making up its structure. Nematocytes themselves contain thousands of proteins, all specific to cnidarians and many of them are species-specific venoms. Most surprisingly, however, Rachamim
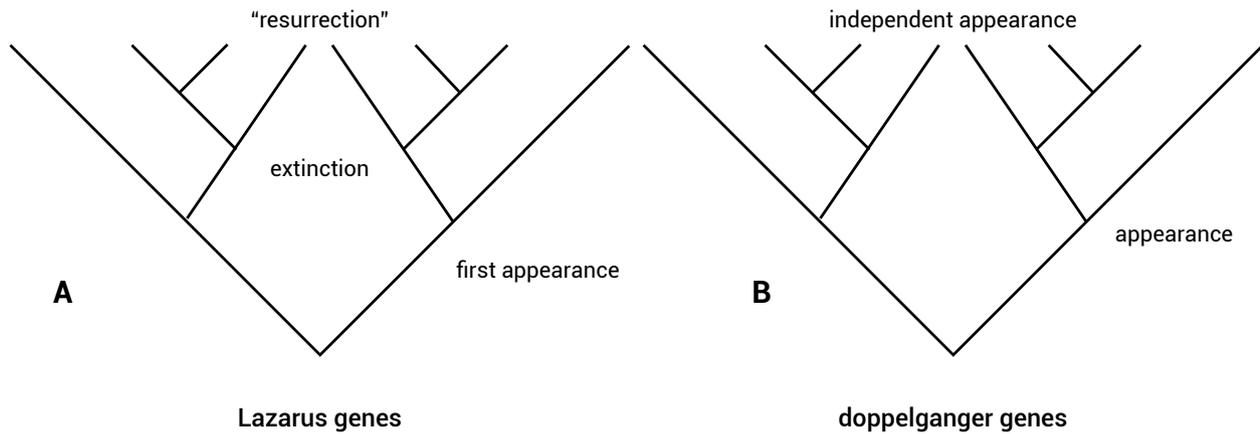
Figure 2. Phylogenetic trees depicting appearance of a hypothetical gene during evolution, followed by its extinction and 'resurrection' in Lazarus genes (part A). Two appearances of a hypothetical gene in two separate branches of the evolutionary tree, independently of each other. Such a gene may be slightly different in sequence or function in its two appearances.

et al. discovered that three diverse cnidarians (*Anemonia viridis*, *Aurelia aurita*, and *Hydra magnipapillata*) only have six proteins in common (see table 2).[27]

The picture presented of nematocyte development is surprising indeed, and definitely not expected if they arose through gradual genetic evolution. Many genes are specific to cnidarians,[28] which could only be explained by evolutionary theory if they arose through gene duplication followed by rapid successive divergence. Besides a lack of candidate ancestral genes from which these cnidarian genes have diverged—due to the nature of the genetic process involved, these newly cnidarian-specific genes must have been mutated beyond recognition— this process of duplication and divergence must also have happened on a grand scale, but specific only to cnidarians. It is much more simple to assume that duplication and divergence of so many cnidarian-specific genes actually did not take place, but that cnidarians, as a taxonomic group (an apobaramin[29]) were created separately from all other organisms. Such

taxonomically restricted genes are quite common in different species and defy evolutionary explanations.[30]

Fossil jellyfish

Recently fibres and cellular structures have been discovered in supposedly 75-Ma-old dinosaur specimens by Bertazzo *et al*.[31] The article states that until recently, it has been widely accepted that protein molecules cannot survive more than 1 Ma.[32] However, Bertazzo *et al*. write that since the dinosaur fossils do not show signs of exceptional preservation, the ultrastructure of putative collagen fibres can last for even 75 Ma.

Cartwright *et al*. have discovered several fossil jellyfish from the Middle Cambrian from Utah representing hydrozoans, scyphozoans, and cubozoans, all considered to be within modern cnidarian classes.[33] Tentacles and muscles have been shown to be preserved among these specimens. Modern cubozoans, such as *Tripedalia cystophora* have complex nervous systems, eye structures, and possess organs involved in sperm transfer called spermatophores. Complex medusae have appeared at the latest by the Late Carboniferous (290 Ma), but possibly as early as the Late Ediacaran (543 Ma), such as a conulariid from the genus *Paraconularia*, or the scyphozoan, *Corumbella werneri*. Evolutionists note that:

"One striking feature for all three classes, even when considering Palaeozoic forms, is *the general morphological similarity between fossil and living medusae; almost all well-preserved fossil medusae possess characters consistent with membership in extant groups* [emphasis added]."[34]

Many cnidarian groups can thus be considered to be living fossils. The natural consequence of this

Table 2. Six nematocyte proteins common to three cnidarian species (from Rachamim *et al*.[27])

Protein name	Function
Nematogalectin	Structural element of nematocyte tubule
Elongation Factor 1-alpha-like	Microtubule bundling and dissociation
Dickkopf	Neurotoxin; nematocyte differentiation
Heat Shock Protein 70	Protein folding for toxin proteins
Secreted protein	Unknown
Transmembrane protein	Unknown

statement is that cnidarians have not undergone significant evolution for hundreds of millions of years, since shortly after they were supposed to have evolved. In contrast, this fits in precisely with the creationist viewpoint which states that the cnidarian baramins were created and did not give rise to newer groups after their creation.

Resurrecting Lazarus genes

In paleontology, 'Lazarus' species are named as such because there is a large gap in their extent in the geological record.[35] The distribution of fossils of Lazarus species can be due to local extinctions or sampling artefacts. However, the picture we see in genetics is different since we should be able to trace the existence or non-existence of genes within any organism or species throughout evolutionary time. *Alx* genes are present in *Nematostella*, and only 'resurface' later in vertebrates, a sub-branch of the Bilateria, during the hypothesized course of evolution.[36] Thus, the *Alx* gene could be termed a 'Lazarus gene' due to its 'resurrection' in species far removed from *Nematostella*.

This causes a great problem for evolutionary theory, since one of the basic assumptions is that no gene can evolve more than once. This is because the universe of possible gene sequences is simply so large ($4^{300} \sim 10^{180}$ possible combinations if an average gene is 300 bp long) that the same sequence occurring randomly, by chance, is practically impossible. According to evolution, organisms change so much over time that it is virtually impossible for two species to follow the exact same evolutionary trajectory, especially if evolution is a blind, unguided process, 'tinkering away' with

biological material, according to the famous evolutionist, François Jacob.[37] Figure 2, part A, depicts the appearance, extinction, and 'resurrection' of a hypothetical gene in a branch of the evolutionary tree.

Yet this is what we see in the case of a number of genes common to both *Nematostella* and vertebrates. Khalturin *et al.* write:

"EST (expressed sequence tag) and genome data from the sea anemone *Nematostella vectensis* and the anthozoan coral *Acropora millepora* (all Cnidarians) revealed that basal metazoans possess most of the gene families found in bilaterians and have retained many ancestral genes that have been lost from *Drosophila* and *[Caenorhabditis] elegans*. Cnidarians, therefore, are much more 'human-like' than flies and worms in terms of their gene content."[38]

This study talks about how cnidarians possess one of the most complex cell types in the animal kingdom; the cnidocyte, or nematocyte, or 'stinging cell', which is used by the animal to capture food. Technau *et al.* go so far as to comment, "One such possible interpretation of the counterintuitive complexity of cnidarians could be that they are actually highly derived deuterostomes,"[39] but remember that this is contradicted by other phylogenetic data. Putnam *et al.* found that nearly two thirds of all human genes (13,830) as well as 12,319 *Nematostella* genes have arisen from the ancestral eumetazoan gene set, whereas only 7,309 have arisen in *Drosophila* and 7,261 in *Caenorhabditis elegans*.[40] This raises the question, how can organisms such as the fruit fly and the roundworm remain viable organisms, if they lose

Table 3. List of some Lazarus and doppelganger genes found in cnidarians and other species

Gene symbol	Function	Species
Lazarus genes		
Alx-1, 3, 4	Aristaless-like; homeodomain protein	*N. vectensis*, vertebrates
Wnt-2, 3, 4, 8, 11		
Dickkopf	Wnt antagonist	*Cyanea, Hydra*
OR genes	Odorant receptors	*N. vectensis, Hydra magnipapillata*, cephalocordates, vertebrates
Cytovec	Cytoplasmic ADP-Intermediate filament protein	*N. vectensis*, vertebrates
Djnlg	Noggin homolog, induces neural tissue	*Dugesia japonica*, vertebrates
Doppelganger genes		
ADP-ribosyl cyclase	Intracellular calcium mobilizer, signal transduction	*Eudendrium racemosum, Euglena*
APX1	Ascorbate peroxidase	*Hydra* species, *Chlorella*
CaMKII	Long-term memory	*Dugesia japonica, Arabidopsis*, yeast
VDAC	Mitochondrial respiration; voltage-dependent anion channel	Yeast, Metazoa

so much of their genome? Genome decay produces only less viable species, as seen in bacterial genome decay.[41]

Indeed, besides *Alx*, hundreds of other Lazarus genes exist in cnidarians and other species at the base of the evolutionary tree. Miller and Ball report that genes in common between *Nematostella* and humans are nearly twice as numerous as between fly, worm, and human.[42,43] Observable 'ancient complexity' does not make sense in the light of evolution, yet makes perfect sense in the light of creation theory: each created kind, or baramin, was created with inherent genetic and morphological complexity, with subsequent gene loss over time, as a result of devolutionary processes due to the Fall. For an overview of some of these genes, see table 3. Indeed, Technau *et al.* report some 318 genes from *Nematostella*, and 196 from *Acropora* which have been detected in vertebrates at an e-score level of 10^{-10}, but did not even score 10^{-4} in ecdyzoans (arthropods and nematodes).[39] Other such examples include the *Wnt* gene family, where five members (*Wnt*-2, 3, 4, 8, and 11) occur in *Nematostella* but not in ecdyzoans (a subset of the protostomes).[44,45] Examples of vertebrate genes in other cnidarian species include the *Wnt* antagonist, *Dickkopf*, present in the jellyfish, *Cyanea capillata*,[46] and the bone morphogenic protein (*BMP*) antagonist in invertebrate species, such as the sponge *Suberites*.[47] *OR* genes also occur in cephalocordates, vertebrates, and the hydrozoan *Hydra magnipapillata* and the cnidarian *N. vectensis*. *OR* genes play a role in cellular migration in several invertebrate species.[48] A lamin gene called *cytovec* occurs in *N. vectensis* and in vertebrates, and plays a role in cytoskeleton formation. The *cytovec* gene is the most similar to intermediate filament genes from another cnidarian, *Clytia hemispherica*, and a *nematocilin* A and B from *Hydra vulgaris*.[49]

Doppelganger genes

Even more interesting are genes which occur in cnidarians and non-metazoans, such as plant species. Whereas Lazarus genes are supposedly 'resurrected' in later species in the lineage of species derived from cnidarians, *doppelganger* genes occur in completely different domains of life. Here again, the probability of the same gene arising twice through random evolutionary tinkering is beyond possibility. Figure 2, part B, depicts how a hypothetical gene arises by chance in two separate regions of the evolutionary tree, independently from one another. Such genes might be slightly different in sequence or in function.

For example, the ADP-ribosyl cyclase gene occurs in *Euglena*, where it undergoes light-induced regulation. In sponges, along with ABA it mediates temperature signalling. In the hydra *Eudendrium racemosum* it induces regeneration in the dark. *ABA* is also present in mammals and may induce cell proliferation.[50] Another doppelganger gene, *HvAPX1* functions as an ascorbate peroxidase, which plays a protectant role during oogenesis in *Hydra*.[51] Evolutionary theory states that this gene was transferred to *Hydra* via horizontal gene transfer from an ancient endosymbiont. This, however, is contradicted by the fact that the *APX1* gene in plants contains introns, whereas *HvAPX1* is intronless. Since the two genes have a different structure, they must also have separate origins. Further intriguing is the presence of *APX* genes in trypanosomes, which are more similar to plant sequences than animal sequences.[52] Since trypanosomes are single-celled parasites, they cannot contain plant endosymbionts. Thus the chance of horizontal gene transfer is negligible. This study is just one of many phylogenetic analyses which show that the topology of the eukaryotic phylogenetic tree is inconsistent. A full 26% of human and *Nematostella* introns are conserved with *Arabidopsis thaliana* (a plant) and 24% with *Cryptococcus* (a fungi). Interestingly, a number of genes involved in the central nervous system have been discovered not only in the planarian, *Dugesia japonica*, and vertebrates, but also in yeast and *Arabidopsis*, which are organisms without any kind of nervous system! These genes include the planarian homolog of *noggin*, *Djnlg*, as well as *CaMKII*, which is essential for long-term memory in animals.[53] In order for evolution to be even remotely possible, these genes must have had a meaningful function in single-celled organisms, and then stay conserved for 1,700 Ma. Of course, long-term memory in single-celled organisms is simply meaningless. The nervous system deals with signals transmitted over a range of different kinds of neurons; single-celled organisms do not have any other cell to transmit any kind of signal to.

Figure 3 shows a multiple alignment of the 265 aa long protein kinase domain common to five species which have the *CaMKII* gene. The high homology of doppelganger genes might pertain only to individual domains. Here the average amino acid identity between these five species for this protein is 54%. Koonin *et al.*[54] state for example that 80% identity between two sequences over 100 aa is very high homology. Yet, even a 43% identity in the lysozyme protein between goose and mouse is also high enough to recognize homology.

Non-coding doppelganger genetic elements

Lazarus elements are also present in non-coding regions of the genome, for example micro-RNA (miRNA). According to evolutionists, miRNA elements had independent origin in plants, animals, and fungi.[55] No recognizable miRNAs exist in Placozoans, which are simple organisms with only a few different types of cells, and only several cell layers thick. The sizes of miRNA elements are also different between cnidarians, poriferans, and
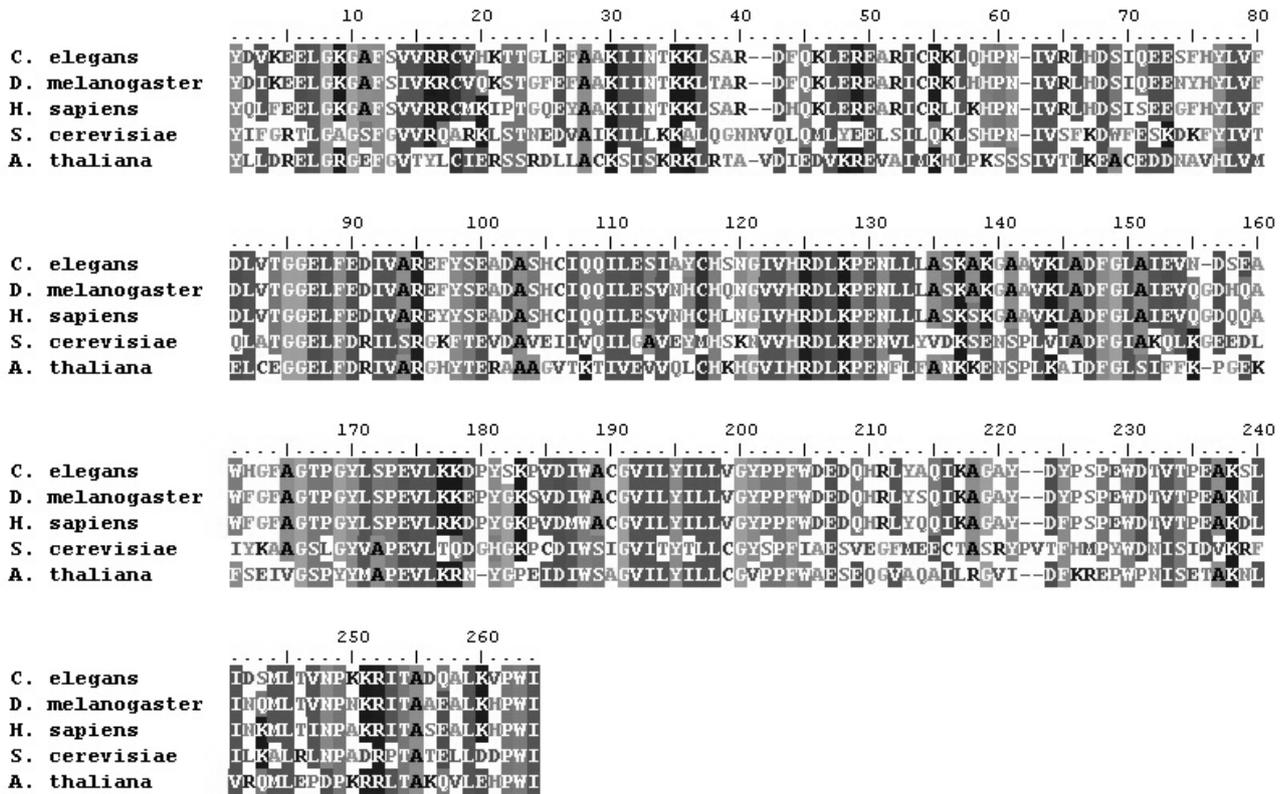
Figure 3. Multiple alignment of the protein kinase domain from the CaMKII (calcium/calmodulin-dependent protein kinase type II) gene from *Caenorhabditis elegans* (O62305.2), *Drosophila melanogaster* (Q00168.1), human (Q13557.3), *Saccharomyces cerevisiae* (P22517.2), and *Arabidopsis thaliana* (Q8W4I7.2).

bilaterians, implying discontinuity between these separate apobaramins. *Nematostella* miRNAs also direct splicing of their mRNA targets, which is different from bilaterian miRNAs.[56] Evolution would posit that miRNAs thus had evolved independently in Cnidaria and Bilateria,[57] yet the extreme improbability of this happening gives more support to separate creation of these apobaramins.

In cnidarians, along with a large part of their genes, miRNAs are highly taxonomically restricted. *N. vectensis* has only one of its 40 miRNAs in common with Bilateria, miR-100 (which even has different gene targets), whereas none of the 126 miRNAs of *Hydra magnipapillata* are in common with bilaterians. Although not all elements of the miRNA processing pathway are present in cnidarians, core elements are present, such as *Drosha*, *Pasha*, and *Dicer*, the last one of which is present in multiple copies. Moran *et al.* even report from a study of 87 *Nematostella* miRNAs that only two of them are conserved across the Cnidaria itself.[58–60]

An example of a doppelganger gene involved in miRNA biogenesis is *HYL1*. It was previously thought only to occur in plants, but recently its homolog was discovered in cnidarians and other non-bilaterians, as well as fungi.[48,49]

The phenomenon of trans-splicing

Another case of Lazarus elements appearing in several animal phyla is that of trans-splicing of genes. As opposed to regular cis-splicing where exons are differentially excised out of a single gene, trans-splicing involves joining sequences from different locations, forming a hybrid mRNA molecule. Genes which are trans-spliced contain a characteristic SL sequence. Trans-splicing involves most of the regular splicing machinery, except for the *U1 snRNP*, and also uses similar splice donor and acceptor sites, making cis-splicing and trans-splicing closely related.[61] Indeed, evolutionists argue that trans-splicing could have arisen quite easily during evolution. The process would involve changing a few bases to form a new acceptor/donor splice site, which occurs rather quickly.[53]

However, the phylogenetic distribution of trans-splicing argues against the evolution of these genetic elements. Despite the possibility of quick evolution, trans-splicing has only been recognized in a smaller number of organisms: euglenazoans, dinoflagellates, hydrozoan cnidarians, nematodes, flatworms, bdelloid rotifers, chaetognaths, and urochordates. Interestingly, in trypanosomes, all mRNAs undergo trans-splicing.[62,63] Genes evolving in pairs as a functional unit make the scenario more difficult

for evolution, since it would have to explain how genes coordinate their evolution with each other, similar to the problem of how bidirectional promoters (which are promoter sequences nested in between two genes on opposite strands) came about.

The emergence of trans-splicing is fast, evolutionarily speaking, yet it is restricted to only a few animal groups, from single-celled organisms to urochordates. It is supposed to have arisen separately in Lazarus-like fashion, according to EST data matching the SL motif (in ctenophores, hydrozoans, urochordates, and some protostomes).[55] One would expect that if trans-splicing is such a rapid evolutionary process, lower organisms would have more trans-spliced mRNAs, compared to higher organisms, which would have proportionately less, according to their complexity. Rapid processes present in only a few entities correlate with younger ages of those entities, and not evolutionarily long ages.

Conclusion

Cnidarians are wonderful creations of God. Despite evolutionary assumptions, these organisms are relatively complex, both morphologically and genetically. Genetic complexity has traditionally been assumed to have arisen much later in animal evolution, but is now considered to be an ancestral feature.[17] Thus, animal diversity is largely based on differential use of conserved genes and regulatory circuits. Conservation of genes responsible for the basic body plan of organisms throughout evolution actually disproves it.[64] The long-held view that cnidarians are also simple, diploblastic organisms is also being overturned, as these organisms have been shown to have mesoderm and also a relatively complex nervous system.

Moreover, not only genes but their cis-regulatory elements are also very similar in cnidarians and bilaterians.[9] Thus the picture seems to be that different organismal phenotypes are fundamentally defined by the genetic context that the genes are in. Cnidarians also defy evolution by the preservation of their soft tissue over periods of time longer than the dinosaurs. Preservation of jellyfish tissue over such supposed long periods of time is thus highly improbable. Fossil medusae are also very similar in morphology to extant species, implying that no evolution took place over hundreds of millions of years, and include many 'living fossil' species.

Furthermore, the genetics of cnidarians is also fascinating. The evolutionarily impossible event of hundreds of genes (called Lazarus and doppelganger genes) appearing, disappearing, then reappearing over the course of eons and innumerable genetic steps disproves evolution on strictly Darwinian terms. Evolution dogmatically states that thousands of homologous genes are common to

Nematostella and vertebrates, yet are missing from flies and worms (ecdyzoans). It is much simpler to state (via Occam's razor) that these genes didn't actually disappear from ecdyzoans, but rather that separate and distinct sets of genes are responsible for the morphology of different groups (apobaramins) of animals (cnidarians, flies, worms, and vertebrates).

All of these considerations present a picture much more compatible with creation rather than evolution.

Materials and methods

Figure 1 was made with the Phylodendron tree-making software at iubio.bio.indiana.edu/treeapp/treeprint-sample1.html. Tree data for animal phyla was entered in Newick format. Figure 3 was made in BioEdit.[65]

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