

# The Cambrian Explosion: Biology's Big Bang

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## ***I. Introduction: Design without a Designer?***

Both Charles Darwin himself and contemporary neo-Darwinists such as Francisco Ayala, Richard Dawkins, and Richard Lewontin acknowledge that biological organisms appear to have been designed by an intelligence. Yet classical Darwinists and contemporary Darwinists alike have argued that what Francisco Ayala calls the “obvious design” of living things is only apparent. As Ayala, a former president of the American Association for the Advancement of Science, has explained: “The functional design of organisms and their features would therefore seem to argue for the existence of a designer. It was Darwin’s greatest accomplishment to show that the directive organization of living beings can be explained as the result of a natural process, natural selection, without any need to resort to a Creator or other external agent.”<sup>1</sup>

According to Darwin and his contemporary followers, the mechanism of natural selection acting on random variation is sufficient to explain the origin of those features of life that once seemed to require explanation by reference to an intelligent or purposeful designer. Thus, according to

Darwinists, the design hypothesis now represents an unnecessary and unparsimonious explanation for the complexity and apparent design of living organisms. On these as well as methodological grounds contemporary biologists have generally excluded the design hypothesis from consideration as an explanation for the origin of biological form.

Yet does Darwinism, in either its classical or contemporary versions, fully succeed in explaining the origin of biological form? Can it explain *all* evidence of apparent design? Most biologists now acknowledge that the Darwinian mechanism of natural selection acting on random variations can explain small-scale microevolutionary changes, such as cyclical variations in the size of the beaks of Galapagos finches or reversible changes in the expression of genes controlling color in English peppered moths.<sup>2</sup> But what about the large-scale innovations in the history of life? What about the origin of completely new organs, body plans, and structures—the macroevolutionary innovation to which the fossil record attests? Does Darwinism, or neo-Darwinism, or any other strictly materialistic model of evolutionary change explain the origin of the basic body plans or structural “designs” of animal life, without invoking actual (that is, purposive or intelligent) design?

In this essay, we will test the claims of neo-Darwinism and two other materialistic models of evolutionary theory: punctuated equilibrium and self-organization. We will do so by assessing how well these theories explain the main features of the Cambrian explosion—a term that refers to the geologically sudden appearance of numerous new animal forms (and their distinctive body plans) 530 million years ago. We shall show that the Cambrian fossil record contradicts the empirical expectations of both neo-Darwinism and punctuated equilibrium in several significant respects. We further show that neither neo-Darwinism’s selection/mutation mechanism nor more recent self-organizational models can account for the origin of the biological information necessary to produce the Cambrian animals and their distinctive body plans. Instead, we will argue that intelligent design explains both the pattern of the fossil record and the origin of new biological form and information better than the competing models of purposeless and undirected evolutionary change.

## ***II. The Cambrian Explosion***

The term *Cambrian explosion* describes the geologically sudden appearance of animals in the fossil record during the Cambrian period of geologic time. During this event, at least nineteen, and as many as thirty-five (of forty total), phyla made their first appearance on earth.<sup>3</sup> Phyla constitute the

highest biological categories in the animal kingdom, with each phylum exhibiting a unique architecture, blueprint, or structural body plan. Familiar examples of basic animal body plans are cnidarians (corals and jellyfish), mollusks (squids and shellfish), arthropods (crustaceans, insects, and trilobites), echinoderms (sea star and sea urchins), and the chordates, the phylum to which all vertebrates including humans belong. The fossils of the Cambrian explosion exhibit several distinctive features.

### A. Geologically Sudden Appearance and the Absence of Ancestral Precursors or Transitional Intermediates

First, as the name implies, the fossils of the Cambrian explosion appear suddenly or abruptly within a very brief period of geologic time (see figures 1 and 2). As recently as 1992, paleontologists thought the Cambrian period began 570 million years ago and ended 510 million years ago, with the Cambrian explosion itself occurring within a 20-to-40-million-year window during the lower Cambrian period. In 1993, radiometric dating of zircon crystals from formations just above and just below Cambrian strata in Siberia allowed for a precise recalibration of the age of Cambrian strata. Radiometric analyses of these crystals fixed the start of the Cambrian

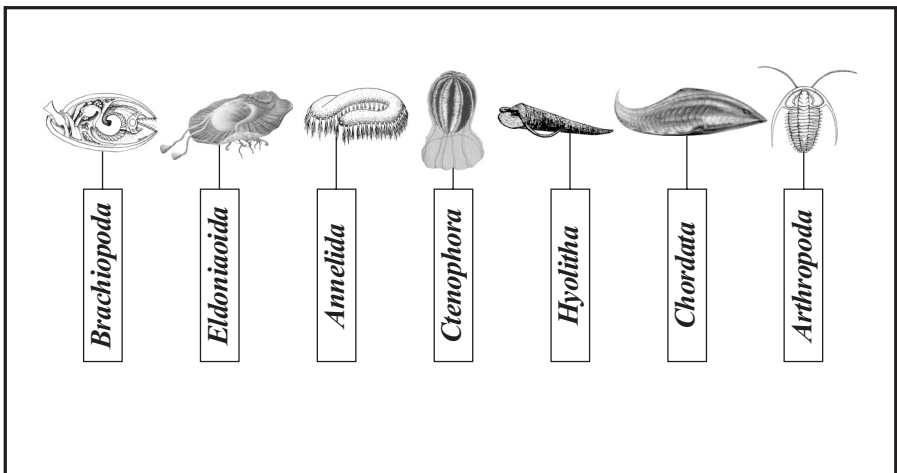


FIGURE 1. Some of the major animal groups (phyla) that first appeared in the Cambrian explosion. Artistic reconstructions of Cambrian fossils: *Brachiopoda* by Andrew Johnson, *Chordata* (*Myllokunmingia fengjiaoa*) courtesy of D. G. Shu, all other images courtesy of J. Y. Chen.

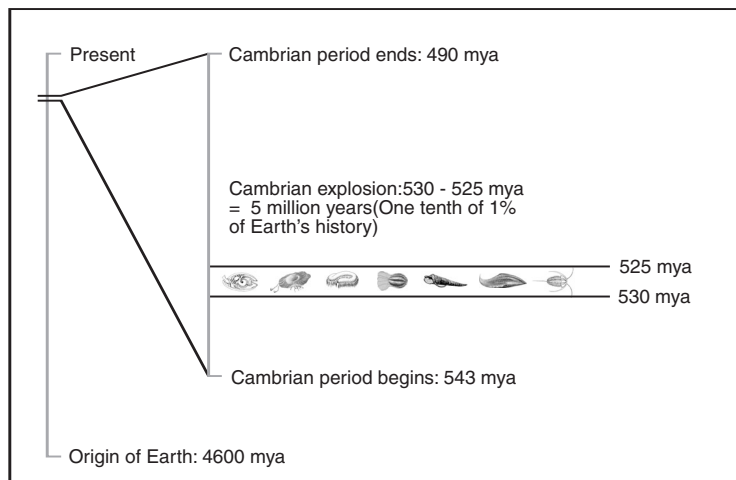


FIGURE 2. The Cambrian explosion occurred within a narrow window of geologic time. Artistic reconstructions of Cambrian fossils: *Brachiopoda* by Andrew Johnson, *Chordata* (*Mylokunmingia fengjiao*) courtesy of D. G. Shu, all other images courtesy of J. Y. Chen.

period at 543 million years ago and the beginning of the Cambrian explosion itself at 530 million years ago (see figure 2).<sup>4</sup> These studies also showed that the Cambrian explosion occurred within an exceedingly narrow window of geologic time, lasting no more than 5 million years. Geologically speaking, 5 million years represents a mere 0.11 percent of Earth's history. As Chinese paleontologist Jun-Yuan Chen has explained, "compared with the 3-plus-billion-year history of life on earth, the period [of the explosion] can be likened to one minute in 24 hours of one day."<sup>5</sup> Yet most of the innovations in the basic architecture of animal forms occurred abruptly within just such a small fraction of the earth's history during the Cambrian. Due to the suddenness of the appearance of animal life in the Cambrian, the Cambrian explosion has now earned titles such as "The Big Bang of Animal Evolution" (*Scientific American*), "Evolution's Big Bang" (*Science*), and the "Biological Big Bang" (*Science News*).<sup>6</sup>

To say that the fauna of the Cambrian period appeared in a geologically sudden manner also implies the absence of clear transitional intermediates connecting the complex Cambrian animals with those simpler living forms found in lower strata. Indeed, in almost all cases, the body plans and structures present in Cambrian period animals have no clear morphological antecedents in earlier strata. Some have argued that perhaps the (or

Venelian) fauna hold some hope in this regard, but as we will show below, those hopes now seem unfounded.

## B. Extensive Morphological Breadth and Representation of Phyla

Second, the Cambrian explosion exhibits an extraordinary morphological breadth and representation of the disparate animal phyla. Cambrian rocks display about half (or more) of the basic body plans or architectural designs of the animal kingdom. Representatives of nineteen of the forty known animal phyla definitely make their first appearance in the fossil record during the Cambrian explosion.<sup>7</sup> Three phyla appear in the Precambrian. Six animal phyla first appear in the fossil record after the Cambrian period, and twelve more are not represented in the fossil record. Nevertheless, for reasons described below, many paleontologists think that almost all of these additional eighteen phyla may well have originated during the Cambrian explosion. Some authorities even estimate that all animal phyla might have come into existence during the Cambrian explosion. As Valentine, Jablonski, and Erwin argue, "All living phyla may have originated by the end of the [Cambrian] explosion."<sup>8</sup>

An especially dramatic feature of the Cambrian explosion is the first appearance of all the invertebrate phyla (and subphyla) with mineralized exoskeletons, including the advanced metazoans such as Mollusca,

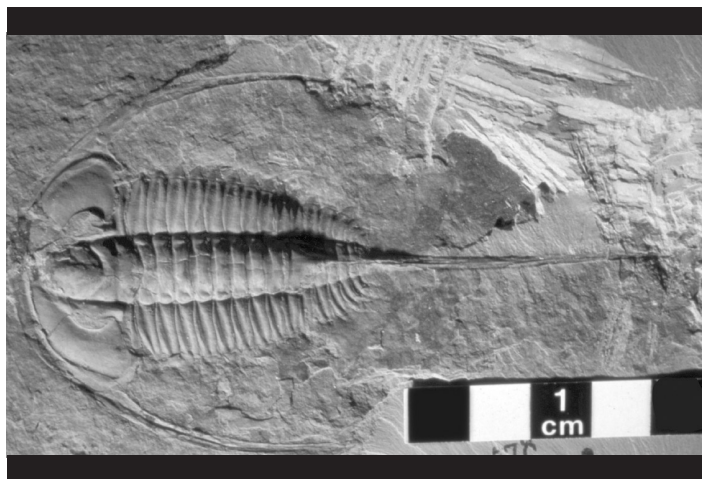


FIGURE 3. Fossil trilobite found in lower Cambrian strata near Chengjiang, China. Courtesy of J. Y. Chen.

Phylum: *Arthropoda*

Subphylum: *Trilobitomorpha*

Genus & species: *Eoredlichia intermedia*

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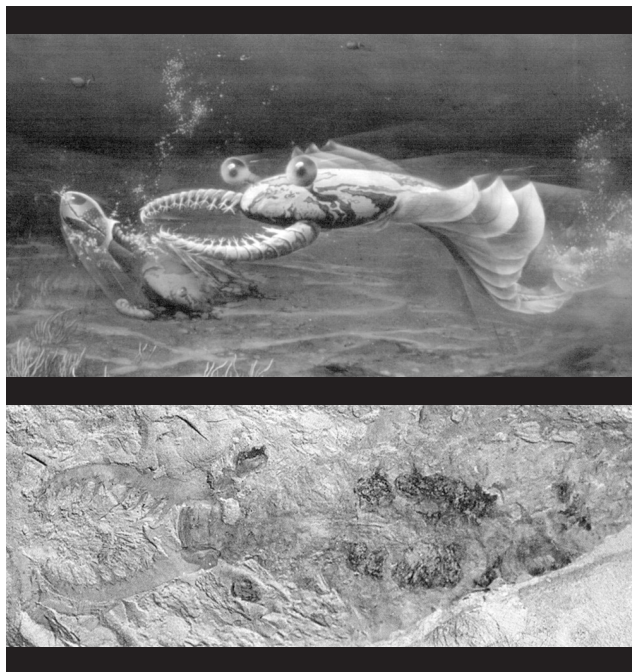


FIGURE 4. Artistic reconstruction and fossil specimen of an *Anomalocaris* found near Chengjiang China. Courtesy of J. Y. Chen.

Phylum: *Arthropoda*

Subphylum: *Anomalocarida*

Genus & species: *Anomalocaris saron*

Echinodermata, and Arthropoda. Trilobites (see figure 3), a subphylum of Arthropoda, were highly complex animals whose thoraxes comprised three lobes or sections (a medial axial ring and two lateral pleurae). The bodies of trilobites were covered by a shieldlike, keratinized exoskeleton called a carapace, which covered both the head and thorax of these animals. Like modern arthropods, trilobites grew by shedding their carapaces, and these cast-off carapaces help to account for the abundance of trilobite fossils. The Chengjiang fauna also contains a number of fossils of now-extinct, top-of-the-food-chain predators with exotic names such as *Anomalocaris* (up to six feet in length; see figure 4), which indicates the presence of a complex food web and a diverse ecological community.

Shelled animals leave a far more durable and extensive record than their soft-bodied counterparts. Nevertheless, Cambrian fossil discoveries from both the Burgess shale in the Canadian Rocky Mountains and from

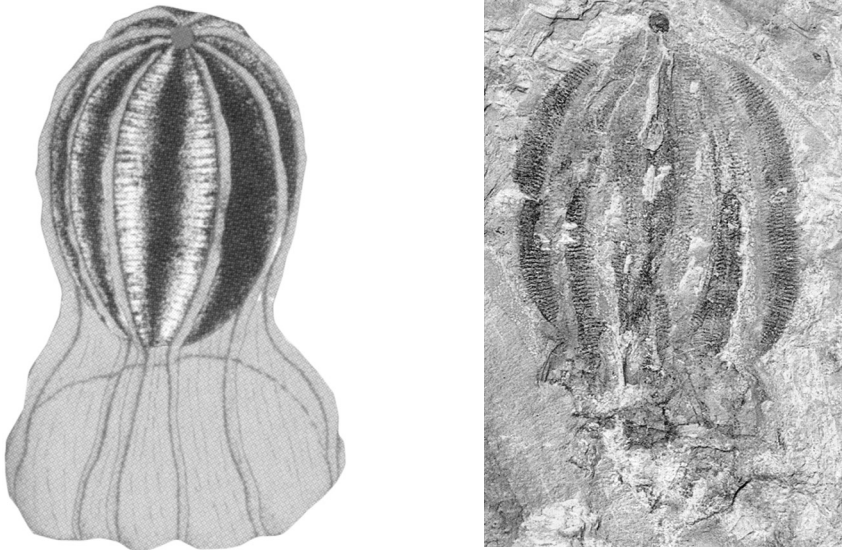


FIGURE 5. Artistic reconstruction and fossil specimen of a comb jelly found near Chengjiang, China. Courtesy of J. Y. Chen.

Phylum: *Ctenophora*

Genus & species: *Maotianoascus octonarius*

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the lower Cambrian Yuanshan Formation near Chengjiang, China, have also shown exquisitely preserved soft-bodied fauna. The Chengjiang fauna even show many excellent examples of well-preserved animals with soft tissue (animals lacking even a keratinized exoskeleton), including members of phyla such as Cnidaria, Ctenophora (see figure 5), Annelida, Onychophora, Phoronida (see figure 6), and Priapulida. Burgess Shale fossils from the middle Cambrian (515 million years ago) confirm that many of these Cambrian organisms were long-lived and geographically widespread.

The lower Cambrian sediments near Chengjiang have preserved fossils of such excellent quality that soft tissues and organs, such as eyes, intestines, stomachs, digestive glands, sensory organs, epidermis, bristles, mouths, and nerves, can be observed in detail. Even fossilized embryos of sponges are present in the Precambrian strata near Chengjiang.<sup>9</sup> Cambrian-level strata show the soft body parts of jellyfish-like organisms (known as *Eldonia*; see figure 7), such as radiating water canals and nerve rings. These fossils even include the gut contents of several different kinds of animals and undigested food residue in their stools.<sup>10</sup>

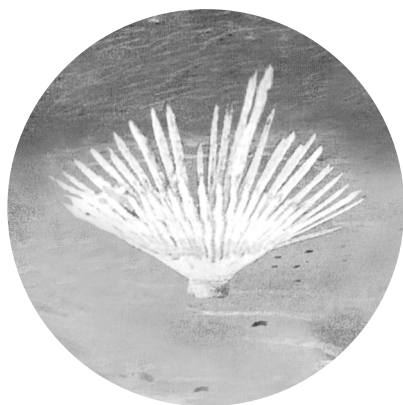


FIGURE 6. Artistic reconstruction and fossil specimen of a phoronid found near Chengjiang, China. Courtesy of J. Y. Chen.

Phylum: *Phoronida*

Genus & species: *Iotuba chengjiangensis*

The Chengjiang fauna also confirms the presence of animals from the phylum Chordata. *Yunnanozoon lividum* is a fusiform eel-shaped animal with, among other features, a digestive tract, branchial arches, and a large notochord. *Yunnanozoon* has been interpreted as a primitive chordate.<sup>11</sup> Two possible cephalochordates have been identified from Cambrian deposits in both China and Canada: Paleontologists have found a single specimen of a possible cephalochordate, *Cathaymyrus*, from the lower Cambrian Qiongzhusi Formation near Chengjiang.<sup>12</sup> Additionally, the cephalochordate *Pikaia* is known from the middle Cambrian Burgess Shale.<sup>13</sup>

More important, several recent discoveries from China have surprised (if not shocked) the paleontological community regarding early chordates. Chen, Huang, and Li have recently reported the discovery of a sophisticated craniate-like chordate called *Haikouella lanceolata* from the lower Cambrian Maotianshan Shale in China. According to Chen and his colleagues, *Haikouella* has many of the same features of the *Yunnanozoon lividum*, as well as several additional anatomical features including a “heart, ventral and dorsal aorta, an anterior branchial arterial, gill filaments, a caudal projection, a neural cord with a relatively large brain, a head with possible



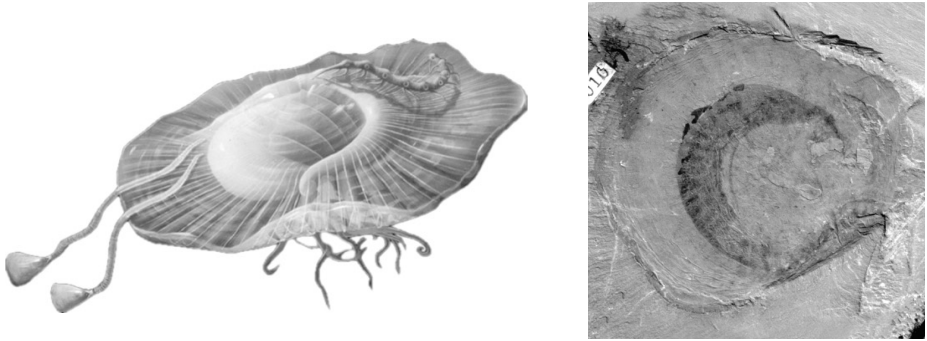


FIGURE 7. Artistic reconstruction and fossil specimen of an *Eldonia* found near Chengjiang, China. Courtesy of J. Y. Chen.

Phylum: *Eldoniaoidea* (contested designation)

Genus & species: *Eldonia eumorpha*

lateral eyes, and a ventrally situated buccal cavity with short tentacles.”<sup>14</sup> Also, D. G. Shu, Simon Conway Morris, and several Chinese colleagues have made a dramatic find of two small fish fossils, *Mylokunmingia fengjiaoa* and *Haikouichthys ercaicunensis* (see figures 8 and 9) suggesting a much earlier appearance for vertebrates than previously thought. Both of these taxa are jawless fish (agnathans) and are considered by Shu and his colleagues to be rather closely allied to lampreys.<sup>15</sup>

Lastly, a new paper by Shu and others reports the first convincing specimen of a urochordate (tunicate) from the Cambrian.<sup>16</sup> This specimen, *Cheungkongella ancestralis*, is likewise found from the early Cambrian shales (Qiongzhusi Formation) near Chengjiang. Remarkably, these recent finds now demonstrate that not only was the phylum Chordata present in the Cambrian but also that each one of the chordate subphyla (Cephalochordata, Craniata, and Urochordata) were present. Moreover, each of these chordate taxa displayed the morphological characteristics that place them securely within their respective subphyla. Indeed, many phyla such as arthropods, mollusks, and chordates include morphologically disparate subphyla that many paleontologists regard as separate body plans. If subphyla are included in the count of animal body plans, then at least thirty-two and possibly as many as forty-eight of fifty-six total body plans (57.1 to 85.7 percent) first appear on earth during the Cambrian explosion. Thus, depending on how one evaluates the data at either the phyla or



FIGURE 8. Artistic reconstruction and fossil specimen of a fish (similar to modern hagfish) found near Haikou, China. Courtesy of D. G. Shu.

Phylum: *Chordata*

Subphylum: *Vertebrata*

Genus & species: *Myllokunmingia fengjiaoa*

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FIGURE 9. Artistic reconstruction and fossil specimen of a fish (similar to modern lamprey) found near Haikou, China. Courtesy of D. G. Shu.

Phylum: *Chordata*

Subphylum: *Vertebrata*

Genus & species: *Haikouichthys ercaicunensis*

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subphyla level, the Cambrian strata document the abrupt appearance of between 47.5 and 85.7 percent of all the animal body plans that have ever existed on earth.

### **C. Persistent Morphological Disparity or Isolation**

A third feature of the Cambrian explosion (as well as the subsequent fossil record) bears mentioning. The major body plans that arise in the Cambrian period exhibit considerable morphological isolation from one another (or “disparity”) and then subsequent “stasis.” Though all Cambrian and subsequent animals fall clearly within one of a limited number of basic body plans, each of these body plans exhibits clear morphological differences (and thus disparity) from the others.<sup>17</sup> The animal body plans (as represented in the fossil record) do not grade imperceptibly one into another, either at a specific time in geological history or over the course of geological history. Instead, the body plans of the animals characterizing the separate phyla maintain their distinctive morphological and organizational features and thus their isolation from one another, over time. The body plans of animals exhibit what we are calling persistent morphological isolation or what others have called stasis (lack of directional change) during their time on earth.<sup>18</sup>

In one sense, of course, the stasis of the phylum as an abstract morphological unit is unremarkable, since phyla are defined for classificatory purposes by reference to an invariant set of anatomical characteristics. In another sense, however, body-plan stasis, as it finds expression in actual animals, is quite remarkable, precisely because actual animals naturally do fall within one, and only one, of a disparate but limited number of classificatory categories. While the phyla (as abstract classificatory units) must by definition exhibit stasis, the body plans of actual animals need not obey this definitional logic. As Jablonski has noted concerning the morphological disparity of the animal phyla, “[s]uch discordances are not simply an artifact of the greater inclusiveness of higher taxa . . . because similar patterns emerge from taxon-free analyses of multivariate morphological data.”<sup>19</sup> In other words, the morphological distance between the Cambrian animals persists whether one uses a classical Linnean method to describe them or a taxonomy-free method of description in morphological space—suggesting that the persistence of morphological distance between Cambrian animals is not an artifact of a classification system.<sup>20</sup>

### D. A “Quantum” or Discontinuous Increase in Specified Biological Information

Fourth, the sudden emergence of the various animals of the Cambrian explosion represents a dramatic discontinuous or “quantum” increase in the information content (or specified complexity) of the biological world. For 3 billion years, or five-sixths of the earth’s history, the biological realm included little more than unicellular bacteria and blue-green algae. During this time, some significant increases in complexity did occur. About 2.7 billion years ago, more complex eukaryotic cells (cells with nuclei) emerged after nearly 1 billion years of earth’s history in which only prokaryotic cells existed on the earth.<sup>21</sup> About 1 billion years ago, multicellular grade algae appeared. Then beginning about 565–570 million years ago in the late Precambrian (or Vendian), the first complex multicellular organisms appear in the rock record, including sponges, the peculiar Ediacaran biota, and perhaps some primitive worms or mollusks (see section IV.B; see figures 1 and 2). Forty million years later, the Cambrian explosion occurred. Relative to the rather modest increases in complexity that occurred between the origin of the first life (3.5 to 3.85 billion years ago) and the first appearance of multicellular algae (1 billion years ago), the emergence of the Vendian organisms (565–570 million years ago) and then, to a much greater extent, the Cambrian explosion (530 million years ago) represent steep climbs up the biological complexity gradient. Indeed, analyzed from an information-theoretic standpoint, the Cambrian explosion in particular represents a remarkable jump in the (specified) information content of the biological world.

Before proceeding, we must define the term *information* as used in biology. In classical Shannon information theory, the amount of information in a system is inversely related to the probability of the arrangement of constituents in a system or the characters along a communication channel.<sup>22</sup> The more improbable (or complex) the arrangement, the more Shannon information, or information-carrying capacity, a string or system possesses.

Since the 1960s, mathematical biologists have realized that Shannon’s theory could be applied to the analysis of DNA and proteins to measure their information-carrying capacity. Since DNA contains the assembly instructions for building proteins, the information processing system in the cell represents a kind of communication channel.<sup>23</sup> Further, DNA conveys information via specifically arranged sequences of four different chemicals—called nucleotide bases—that function as alphabetic or digital characters in

a linear array. Since each of the four bases has a roughly equiprobable chance of occurring at each site along the spine of the DNA molecule, biologists can calculate the probability, and thus the information-carrying capacity, of any particular sequence  $n$  bases long.

The ease with which information theory applies to molecular biology has created confusion about the type of information that DNA and proteins possess. Sequences of nucleotide bases in DNA, or amino acids in a protein, are highly improbable and thus have a large information-carrying capacity. But, like meaningful sentences or lines of computer code, genes and proteins are also *specified* with respect to function. Just as the meaning of a sentence depends upon the specific arrangement of the letters in the sentence, so, too, does the function of a gene sequence depend upon the specific arrangement of the nucleotide bases in the gene. Thus, as Sarkar points out, molecular biologists beginning with Francis Crick have equated *information* not only with complexity but also with "specificity," where specificity has meant "necessary to function."<sup>24</sup> Similarly, the Cambrian explosion represents not just an increase in complexity or Shannon information but an increase in the "specified complexity" or *specified* information of the biological world.

One way to measure the increase in specified information or specified complexity of the animals that appeared in the Cambrian is to assess the number of cell types that are required to build such animals and to compare that number with those creatures that went before.<sup>25</sup> Functionally more complex animal forms require more cell types to perform their more diverse functions. Compare, for example, a single-celled eukaryote and a trilobite or a mollusk. Although specialized internally, with a nucleus and various organelles, the single-celled eukaryote represents, obviously, a single type of cell. Not so with the trilobite or mollusk, where dozens of specific tissues and organs require "functionally dedicated," or specialized, cell types. But new cell types require many new and specialized proteins. For example, an epithelial cell lining a gut or intestine, which secretes a digestive enzyme, requires (minimally) structural proteins to modify its shape, regulatory enzymes to control the secretion of the digestive enzyme, and the digestive enzyme itself. New proteins in turn require new genetic information encoded in DNA. Thus, an increase in the number of cell types implies (at a minimum) a considerable increase in the amount of specified genetic information.

Molecular biologists have recently estimated that a minimally complex single-celled organism would require between 300 and 500 genes (or more

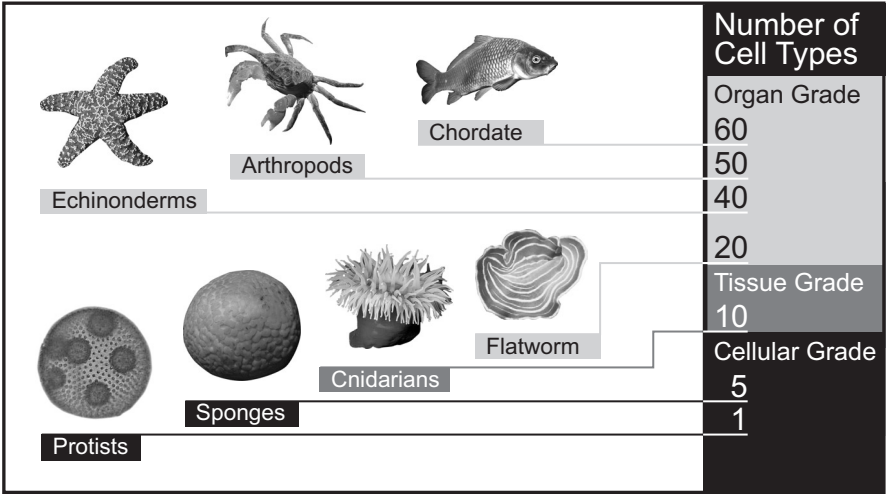


FIGURE 10. Biological Complexity Scale as measured by number of cell types per type of organism. Protist (Volvox) by John McWilliams, Flatworm by Wolfgang Seifarth, other images by Wernher Krutein.

precisely, between 318 and 562 kilobase pairs of DNA) to produce the proteins necessary to maintain life.<sup>26</sup> More complex single cells might require upward of 1 million base pairs. Yet to build the proteins necessary to sustain a complex animal would require orders of magnitude more coding instructions. For example, the genome size of the fly *Drosophila melanogaster* (an arthropod) is approximately 120 million base pairs.<sup>27</sup> Even *Caenorhabditis elegans*, a tiny worm about 1 millimeter long, has a genome of approximately 97 million base pairs.<sup>28</sup> Thus, transitions from a single cell to colonies of cells to complex animals represent significant (and in principle measurable) increases in specified complexity or information content.

The animal phyla represented in the top row of figure 10 (as depicted by modern representatives) first appeared in the Cambrian explosion. These highly complex animals typically had between forty and sixty different cell types. These new cell types would have required (at minimum) many new proteins and a correspondingly large complement of new genetic information encoded in DNA. Relative to the modest increases in specified complexity that occurred earlier in the Precambrian (see the bottom row of figure 10), the Cambrian explosion represents a steep climb up the biology complexity scale. Indeed, analyzed from an informational standpoint, the Cambrian explosion represents a remarkable jump in the specified information or specified complexity of the biological world.

### ***III. Testing Neo-Darwinism and Punctuated Equilibrium against the Cambrian Fossil Record***

In this section, we will test neo-Darwinism and punctuated equilibrium against the Cambrian fossil record. Both these theories envision mechanisms that produce biological change in a particular manner. As a result, both have implications for how life should develop over its history and what, therefore, the fossil record should generally look like. Further, both these theories, and neo-Darwinism in particular, purport to offer truly creative mechanisms of biological change. Since the Cambrian fossils attest not only to small-scale variations but also to large-scale innovations in basic body plans, the Cambrian data provide a key test to the efficacy of these mechanisms.

According to neo-Darwinism, biological change occurs as natural selection acts on small, random genetic changes and mutations (of various kinds), favoring those changes that enhance the survival of the organisms in which the changes occur. Over time, small-scale advantageous genetic changes accumulate, eventually resulting in large-scale changes in the morphology of organisms. Thus, according to neo-Darwinism, biological complexity should accumulate in a gradual bit-by-bit fashion over vast periods of geologic time.

A neo-Darwinian understanding of the mechanism that generates new biological structure generates three specific predictions or empirical expectations concerning the fossil record. Given the operation of the neo-Darwinian mechanism, the fossil record should show: (1) the gradual emergence of biological complexity and the existence of numerous transitional forms leading to new phylum-level body plans; (2) small-scale morphological diversity preceding the emergence of large-scale morphological disparity; and (3) a steady increase in the morphological distance between organic forms over time and, consequently, an overall steady increase in the number of phyla over time (taking into account factors such as extinction).

Alternatively, the theory of punctuated equilibrium envisions biological change occurring in larger, more discrete jumps as the result of natural selection acting primarily on whole species rather than on individuals within species. The theory of punctuated equilibrium, therefore, envisions a less gradual development of new living forms—it differs from neo-Darwinism in its understanding of the rate and mode of evolutionary development. Nevertheless, punctuated equilibrium implies that the fossil record should manifest many of the same general features that neo-Darwinism would predict. Thus,

we consider each of the main neo-Darwinian predictions or expectations in turn and then compare them to the Cambrian fossil record as a way of testing both neo-Darwinism (and where applicable) punctuated equilibrium.

### **A. Prediction 1: The Gradual Emergence of Biological Complexity and the Existence of Numerous Transitional Forms Leading to Phyla-Level Body Plans**

Charles Darwin regarded the sudden appearance of complex animals such as brachiopods and trilobites in the Cambrian strata (then called the Silurian) as a major challenge to his theory. Based on his theory, he “expected to find intervening strata showing fossils of increasing complexity until finally trilobites appeared.”<sup>29</sup> Darwin realized that building highly complex animals such as trilobites from single-celled organisms by natural selection operating on minute, step-by-step variations would require a multitude of transitional forms and failed biological experiments over vast amounts of geologic time. Accordingly, he made the following prediction: “if the theory be true, it is indisputable that before the lowest [Cambrian] stratum was deposited, long periods elapsed, as long as, or probably far longer than, the whole interval from the [Cambrian] age to the present day; and that during these vast, yet quite unknown periods of time, the world swarmed with living creatures.”<sup>30</sup>

Darwin’s prediction is significant because he recognized the amount of time that his theory required. Geologists in Darwin’s day employed relative dating methods. They did not yet have modern radiometric methods for determining the “absolute” date of rocks. Nevertheless, Darwin had a clear picture of what his postulated selection/variation mechanism implied about the history of life. On his theory, complex structures could only be built gradually, minute improvement by minute improvement. Thus, natural selection would require vast periods of time to create new biological forms and structures. Even in the nineteenth century, Darwin understood that this process would take many tens or hundreds of millions of years. Modern neo-Darwinists concur in this view. As noted above, neo-Darwinism envisions minute changes in gene sequences accumulating very slowly as the result of random mutations. Yet empirically derived estimates of mutation rates in extant organisms suggest that the kind of large-scale morphological changes that occurred in the Cambrian would have required far more time than the duration of the explosion (for further discussion, see section V.A.1).<sup>31</sup>



In addition to a pattern of gradual change, Darwinist theories anticipate a gradual increase in the complexity and morphological diversity of organisms over time. Clearly, the fossil record does (generally) show an overall increase in the complexity of organisms from Precambrian to Cambrian times. Nevertheless, the fossil record does not show that novel organisms arose gradually, nor does it document the existence of the many intermediate forms that Darwinian gradualism entails. Indeed, since the mutation/selection mechanism involves a trial and error process, both Darwinism and neo-Darwinism imply that the fossil record should show many transitional organisms and failed experiments (see figures 11 and

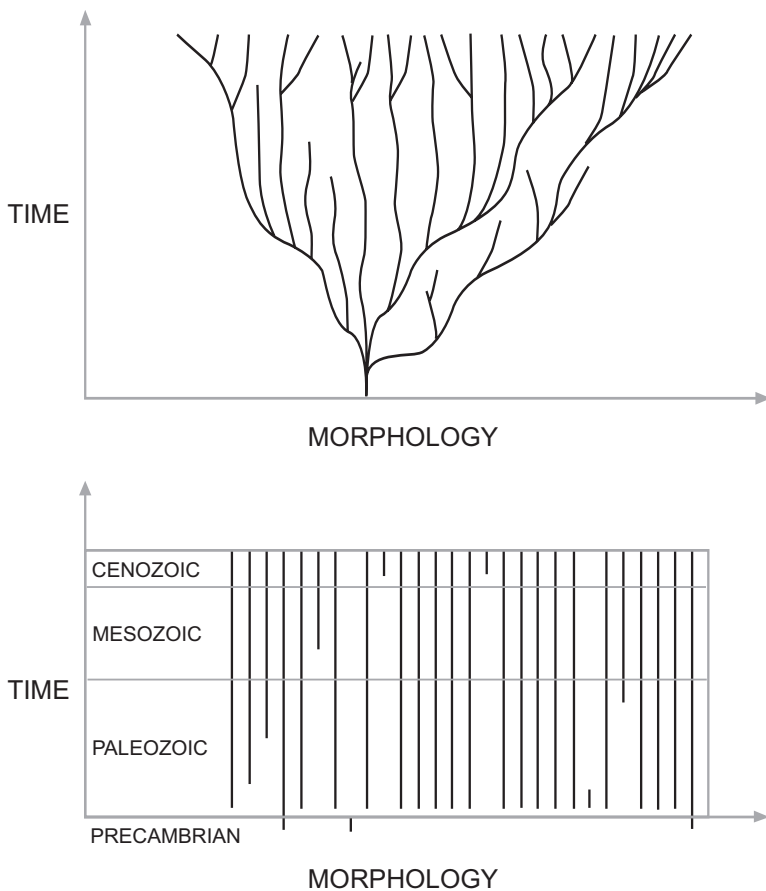


FIGURE 11. Origin of animal phyla: Neo-Darwinian theory (above) vs. fossil evidence (below).

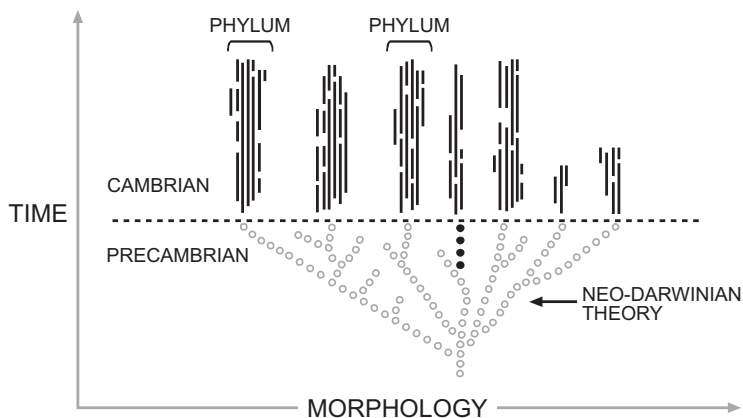


FIGURE 12. According to the theory of universal common descent (part of neo-Darwinian theory) the strata beneath the Cambrian rocks should evidence many ancestral and intermediate forms. Such forms have not been found for the vast majority of phyla. These anticipated and missing forms are represented by the gray circles. Lines and dark circles depict fossilized representatives of Phyla that have been found. Courtesy Art Battson.

12). Instead, organisms such as trilobites (phylum Arthropoda), with their articulated body plans, intricate nervous systems, and compound eyes, first appear fully formed at the beginning of the Cambrian explosion along with many other phyla of equal complexity. As Oxford zoologist Richard Dawkins acknowledges: “It is as though they [the invertebrate phyla] were just planted there, without any evolutionary history.”<sup>32</sup>

Darwin was, of course, well aware even in the nineteenth century of the problem that the Cambrian explosion presented for his theory. He stated: “The case at present must remain inexplicable; and may be truly urged as a valid argument against the views here entertained.”<sup>33</sup> Contrary to Darwin’s hope, however, in the 150 years since the publication of the *Origin*, discoveries in paleontology have only made the puzzle of the Cambrian explosion more acute. Not only have expected transitional forms not turned up, but the pattern of the sudden appearance of novel structure has become more pronounced. Massive new fossil discoveries in the rocks of the Burgess Shale in Canada and in the Yuanshan Formation near Chengjiang, China, have documented many previously unknown Cambrian phyla, thus only increasing the number of expected and missing transitional intermediates required on a Darwinian account of the emergence of new living forms.

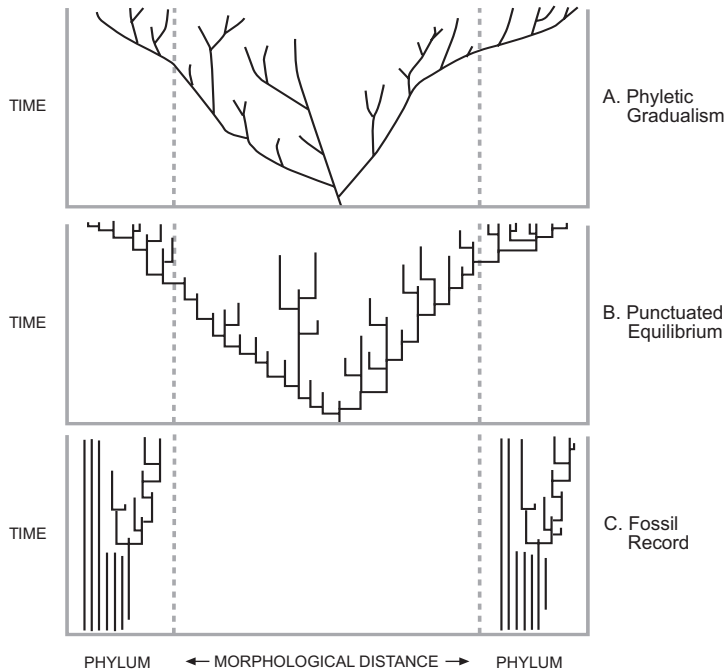


FIGURE 13. Origin of animal phyla. Two interpretations of the history of life compared with the fossil record.

The difficulty posed by the absence of transitional intermediates for both neo-Darwinism and, to a lesser but still significant extent, punctuationalist evolutionary theories is illustrated in figure 13. The diagrams depict morphological change versus time. The first diagram shows the Darwinian and neo-Darwinian expectation that changes in morphology should arise gradually as minute microevolutionary changes accumulate. This Darwinian commitment to gradual change via microevolution produces the classic representation of the history of life as a branching tree (figure 13A).

The second diagram (figure 13B) represents another model of strictly naturalistic evolutionary change as advanced by Niles Eldredge and Stephen J. Gould. This model, known as punctuated equilibrium, was developed during the late 1960s in an attempt to explain (or describe) more accurately the pattern of sudden appearance and stasis that paleontologists had long observed in the fossil record. According to the punctuationalists, evolutionary change occurs rapidly often after long periods of what they called stasis, periods in which organisms manifest no directional change in

their morphology. By repudiating Darwinian gradualism, this model specifically sought to account for the absence of transitional forms in the fossil record. Even so, insofar as this model maintained a commitment to the core Darwinian notion of common descent, it, too, implied that the fossil record should preserve many intermediate forms among higher-rank taxonomic levels. Figure 13B details how punctationalists conceive of evolutionary change and thus also their expectations for what the fossil record ought to show. According to many punctationalists, natural selection functions more as a mechanism for selecting the most fit species rather than the most fit individual among a species. Thus, morphological change should occur in larger, more discrete intervals than traditional Darwinism asserts. Nevertheless, as figure 13B shows, punctationalists still envision many transitional forms as a result of a series of rapid evolutionary changes (albeit representing larger jumps in morphology).

Figure 13C shows the relationship between time and morphology in the actual fossil record. Note that, contrary to the predicted patterns above, the Cambrian radiation and subsequent variation occur after but not before the basic body plans appear in the fossil record. The fossil record also shows a dearth of transitional intermediates between Cambrian and Precambrian fauna.

Since the late 1960s, paleontologists have recognized that the general absence of transitional forms contradicts the picture of the history of life that neo-Darwinism implies, given its commitment to a gradualistic mechanism of evolutionary change (see figure 11). Fewer have recognized, however, that the absence of transitional forms also represents a severe (though relatively lesser) difficulty for punctuated equilibrium. Note that both standard neo-Darwinian and more recent punctationalist versions of evolutionary theory predict (or expect) many more transitional intermediates than the fossil record actually preserves. This constitutes a particular difficulty because of the great number of new phyla represented in the Cambrian. At present, paleontologists lack clear ancestral precursors for the representatives of not just one new phylum but virtually all the phyla represented in Cambrian explosion (see section IV.B).

In a seminal paper titled "Interpreting Great Developmental Experiments: The Fossil Record" (after which figures 13A and 13B are patterned), paleontologists J. W. Valentine and D. H. Erwin question the sufficiency of both evolutionary models discussed above as explanations for the origin of body plans and higher-level taxa. They note that "transitional alliances are unknown or unconfirmed for any of the [Cambrian] phyla" and yet "the

evolutionary explosion near the beginning of Cambrian time was real and produced numerous [new] body plans." Clearly, neo-Darwinism does not explain this pattern. But as Valentine and Erwin point out, neither does punctuated equilibrium. They note that the proposed mechanism of punctuated evolutionary change simply would have lacked the raw material upon which to work. As Valentine and Erwin note, the fossil record fails to document a large pool of species prior to the Cambrian. Yet the proposed mechanism of species selection requires just such a pool of species upon which to act. Thus, they conclude that "the probability that species selection is a general solution to the origin of higher taxa is not great."<sup>34</sup>

Recent work on statistical paleontology by Michael Foote of the University of Chicago reinforces this point. Foote develops a method by which evolutionary models can be tested against several variables. Foote shows that "given estimates of [*a*] completeness [of the fossil record], [*b*] median species duration, [*c*] the time required for evolutionary transitions, and [*d*] the number of ordinal- or higher-level transitions, we could obtain an estimate of the number of major transitions we should expect to see in the fossil record." His method provides a way to evaluate, as he puts it, "whether the small number of documented major transitions provides strong evidence against evolution."<sup>35</sup> Because estimates of the completeness of the fossil record, median species duration, and the number of ordinal- or higher-level transitions are reasonably well established, the time required for plausible mechanisms to produce macroevolutionary transitions, stands as the crucial variable in any such analysis. If the time required to produce major evolutionary change is high, as it is for neo-Darwinian mechanisms of change, then given current estimates of the completeness of the fossil record, median species duration, and the number of ordinal- or higher-level transitions, neo-Darwinism fails to account for the data of the fossil record. Conversely, for punctuated equilibrium to succeed as an explanation for the data of the fossil record, the time required for plausible mechanisms to produce macroevolutionary transitions must be very low. In other words, the explanatory success of punctuated equilibrium depends upon the existence of a mechanism that can produce rapid macroevolutionary change. As Foote and Gould note elsewhere, the punctuationalist model of Cambrian evolution requires a mechanism of unusual "flexibility and speed."<sup>36</sup> As yet, however, neither Foote nor Gould nor anyone else has identified such a mechanism with any genetic or developmental plausibility. Thus, given the current empirical climate, the logic of Foote's statistical methodology tends to reinforce the earlier work of Valentine and

Erwin, who concluded that “neither of the contending theories of evolutionary change at the species level, phyletic gradualism or punctuated equilibrium, seem applicable to the origin of new body plans,” and thus we now require “a [new] theory for the evolution of novelty, not diversity.”<sup>37</sup>

## **B. Prediction 2: Diversity Precedes Morphological Disparity (contra Completeness and Morphological Breadth)**

The distinction between small-scale morphological diversity and large-scale morphological novelty (or what taxonomists call *disparity*) raises another key issue. Most biologists today believe that Darwinian mechanisms account for the great diversity of life, by which they often mean the vast numbers of different species in existence. Many fail to ask the question, “What produces novel morphology, and thus the *disparity* between forms, that we observe in the history of life?” By *disparity*, we mean the major differences in morphology, in contrast to minor variations. Specifically, paleontologists use the term *disparity* to measure the major morphological differences between the body plans that correspond to the higher-level taxonomic classifications, whereas they use *diversity* to describe the small-scale variations that correspond to lower-level taxonomic classifications such as species or genera. In other words, disparity refers to life’s basic morphological themes, whereas diversity refers to the variations on those themes.<sup>38</sup>

According to neo-Darwinism, morphological distance between evolving organisms will increase gradually over time as small-scale variations accumulate by natural selection to produce increasingly complex forms and structures (including, eventually, new body plans). Thus, given the neo-Darwinian mechanism, one would expect that small-scale differences or “diversity” between species should precede the emergence of morphological disparity between body plans and phyla (see figures 13A and 14). As Richard Dawkins expresses the point: “What had been distinct species within one genus become, in the fullness of time, distinct genera within one family. Later, families will be found to have diverged to the point where taxonomists (specialists in classification) prefer to call them orders, then classes, then phyla. . . . Ancestors of two different phyla, say vertebrates and mollusks, which we see as built upon utterly different ‘fundamental body plans’ were once just two species within a genus.”<sup>39</sup> Indeed, because the mutation/selection mechanism operates cumulatively and gradually, the novel body plans that define the different phyla must arise from numerous lower-level speciation events. For this reason, neo-

Darwinism expects a “cone of increasing diversity” in which large-scale morphological and taxonomic disparity results from the cumulative effects of many small-scale speciation events.

Darwin himself made this point in the *Origin*. Explaining his famous diagram (figure 14) illustrating the theory of common descent, Darwin described how higher taxa should emerge from lower taxa by the accumulation of numerous slight variations. As he said: “[T]he diagram illustrates the steps by which small differences distinguishing varieties are increased into larger differences distinguishing species. By continuing the process for a greater number of generations we get eight species.” He went on: “I see no reason to limit the process of modification, as now explained, to the formation of [species and] genera alone. These two groups of genera will thus form two distinct families, or orders, according to the amount of divergent modification supposed to be represented in the diagram.”<sup>40</sup> Thus, Darwin described small-scale variations producing new species, genera, and orders. This process would doubtless, on a Darwinian view, continue

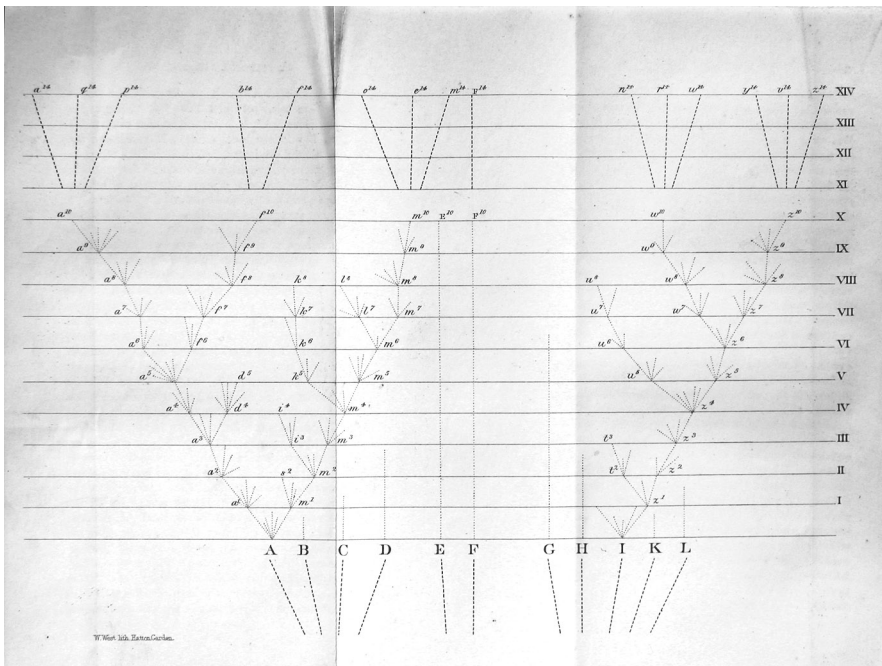


FIGURE 14. Darwin's theory of common descent illustrated here with his famous branching tree diagram, *Origin of Species*, 1859. Courtesy of the University of Oklahoma History of Science Collections.

until it produced new phyla as well. For both classical Darwinism and neo-Darwinism, diversity must precede disparity. Phyla-level differences in body plans must emerge, therefore, only after species-, genus-, and class-level differences appear.

Though advocates of punctuationalist change envision morphological distance arising in larger, more discrete intervals (due to species selection) than do classical neo-Darwinists, they, too, see phyla-level differences arising cumulatively starting from lower-level taxonomic differences between evolving forms. In other words, punctuated equilibrium also predicts morphological diversity preceding disparity (as figure 13B also shows). Thus, for both current evolutionary models, novel body plans are built “bottom-up” as the result of many smaller-scale genetic changes.

The actual pattern in the fossil record, however, contradicts this prediction (see figures 13C and 15). Instead of showing a gradual bottom-up origin of the basic body plans, where smaller-scale diversification or speciation precedes the advent of large-scale morphological disparity, disparity precedes diversity. Indeed, the fossil record shows a “top-down” pattern in which morphological disparity between many separate body plans emerges suddenly and prior to the occurrence of species-level (or higher) diversification on those basic themes. As science writer Roger Lewin has noted: “Several possible patterns exist for the establishment of higher taxa, the two most obvious of which are the bottom-up and the top-down approaches. In the first, evolutionary novelties emerge, bit by bit. The Cambrian explosion appears to conform to the second pattern, the top-down effect.”<sup>41</sup> Or as Erwin, Valentine, and Sepkoski observe in their study of well-skeletonized marine invertebrates: “Most higher taxa were built from the top down, rather than from the bottom up. The fossil record suggests that the major pulse of diversification of phyla occurs before that of classes, classes before that of orders, orders before that of families. The higher taxa do not seem to have diverged through an accumulation of lower taxa.”<sup>42</sup> In other words, instead of a multiplication of species and other representatives of lower-level taxa occurring first and the building to the disparity of higher taxa, the highest taxonomic differences such as those between phyla and classes appear first (instantiated by very few species-level representatives). Only later do lower-level taxonomic differences appear: different orders, families, genera, and so on. Yet we would not expect either the neo-Darwinian mechanism of natural selection acting on random genetic mutations or the mechanism of species selection to produce the top-down



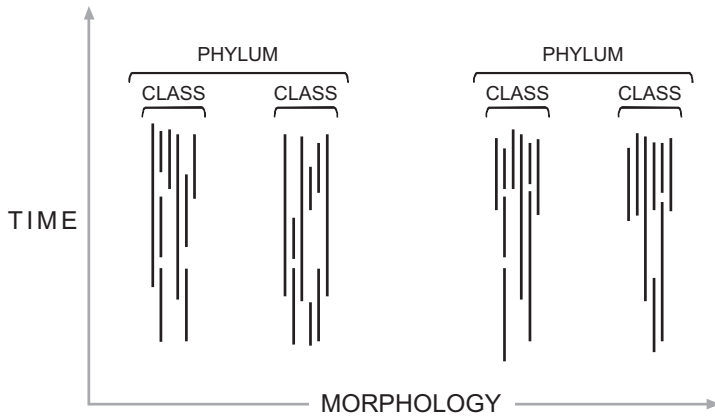


FIGURE 15. The top-down pattern of appearance in the fossil record: disparity precedes diversity.

pattern that we observe in the history of life following the Cambrian explosion.

### C. Prediction 3: The Morphological Distance between Organic Forms and thus the Number of Phyla Will Increase Gradually over Time

According to neo-Darwinism and punctuated equilibrium, the fossil record should exhibit another feature. As we have seen, the neo-Darwinian mechanism and the punctuationalist mechanism (of species selection) imply that the morphological distance between organisms will increase gradually over time. Thus, both these mechanisms should produce a steadily increasing number of new body plans, or phyla, over time. Borrowing from Darwin's predictions on the emergence of species (see above), we can express graphically the idealized expectation of the neo-Darwinian (and the punctuationalist) model concerning the appearance of phyla over time (see figure 16). For both these evolutionary models, the number of new phyla should increase in a steady logarithmic fashion as members of one phylum diversify and give rise to new phyla.

Figures 17A and 17B depict numerically the first appearance of all animal phyla over geological time. Figure 17A shows the first appearance of animal phyla based solely on the present body of paleontological evidence. Figure 17B shows the total number of phyla that are often thought to have

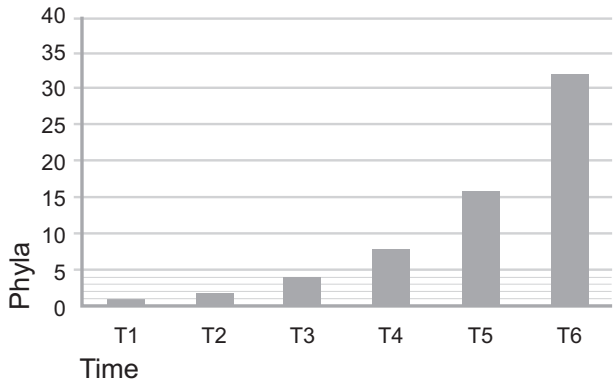


FIGURE 16. Animal phyla first appearances: idealized neo-Darwinism pattern.

made their first appearance in the Cambrian based on geological/environmental considerations as well as direct fossil evidence (see appendix E). Further, many of the phyla that first appear in the fossil record after the Cambrian are less complex than the phyla that first appear in the Cambrian. Since standard evolutionary reasoning assumes that complexity evolves from simplicity and not, generally, the reverse, both neo-Darwinists and punctualists often assumed that these simpler phyla must have been present in the Cambrian. Additionally, factors such as organism size, lifestyle, habitat, depositional environment, and the presence or absence of mineralized hard parts affect the likelihood of preservation. Many of the organisms representing phyla that first appear after the Cambrian, or those with no fossil record at all, have one or more of the above features that would have rendered their preservation unlikely, either in general or in specifically Cambrian conditions. Additionally, several phyla that do not appear in the fossil record—Dicymeda, Gastrotricha, Kinorhyncha, and Platyhelminthes—have members with known parasitic or symbiotic relationships with a wide suite of animals representing specific phyla that did first appear in the Cambrian. Many of these organisms are small parasites that lived within the digestive systems of larger animals and would not have been good candidates for preservation (or discovery) in the fossil record. Thus, their absence in the fossil record does not necessarily indicate a recent first appearance. Instead, it seems likely that these parasitic organisms themselves may have first appeared as far back as the Cambrian coincident with host organisms of Cambrian age. Thus, several factors suggest reasons, independent of evolutionary assumptions, for suspecting a Cambrian appearance

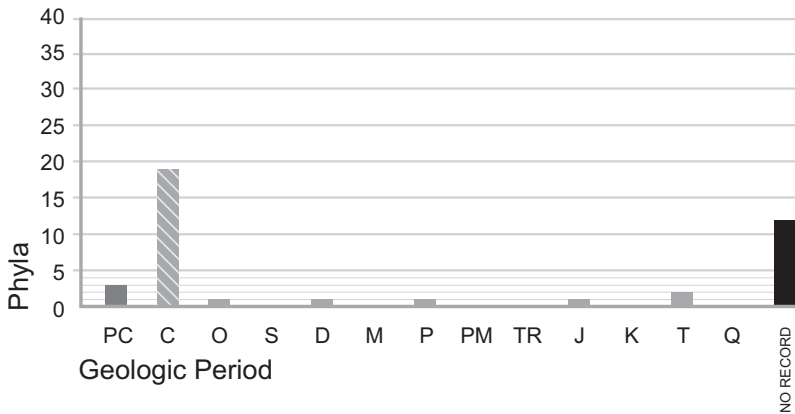


FIGURE 17A. Animal phyla first appearances: based on fossil data alone (see appendix C)

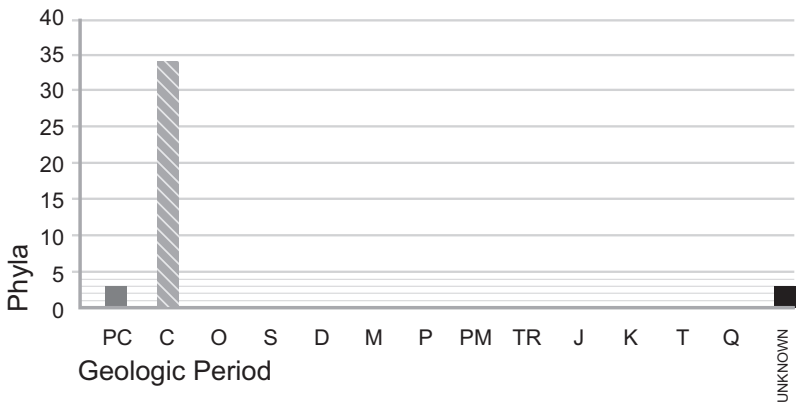


FIGURE 17B. Animal phyla first appearances: based on fossil data and other considerations (see appendix E)

for many of the eighteen phyla that either first appear in the fossil record after the Cambrian or that have no fossil record at all. Only three of these eighteen phyla can be excluded from a Cambrian first appearance given present knowledge (see the entries for Acanthocephala, Cycliophora, and Pentastoma in appendix E).<sup>43</sup>

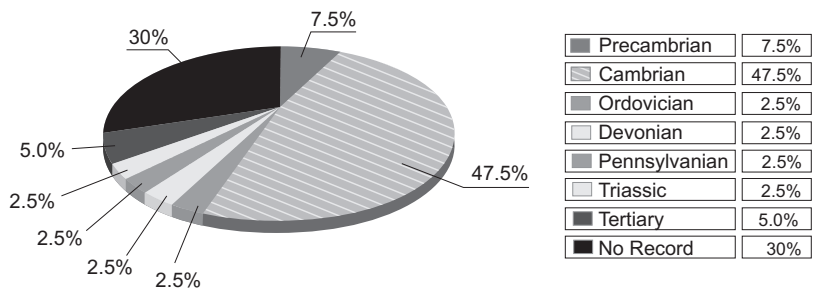


FIGURE 18A. Animal phyla first appearances: based on fossil data alone (see appendix C)

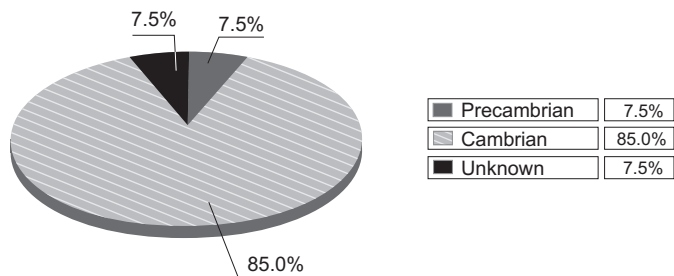


FIGURE 18B. Animal phyla first appearances: based on fossil data and other considerations (see appendix E)

Of course, how one weighs and assesses these various factors will result in differing estimates for the number of phyla or phyla-subphyla body plans that first appear during the Cambrian. Values ranging from 47.5 to 85.7 percent are consistent with existing data. Though we are skeptical of strictly presuppositionally driven arguments based on the theory of universal common descent, we do favor, on geological and environmental grounds, estimates in the middle of this range (see appendix E).<sup>44</sup> Nevertheless, Figures 18A and 18B (or 19B) show body plan first appearances at both extremes of this range in order to show that, however one assesses the various factors discussed above, the empirical expectations of neo-Darwinism and punctuated equilibrium do not conform to paleontological evidence concerning body plan first appearance. Indeed, rather than conforming to neo-Darwinian and punctuationalist expectations of a steadily

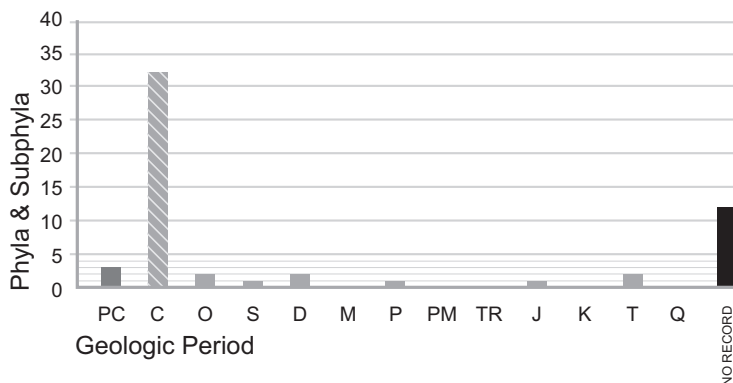


FIGURE 19A. Animal phyla and subphyla first appearances: based on fossil data alone (see appendix D)

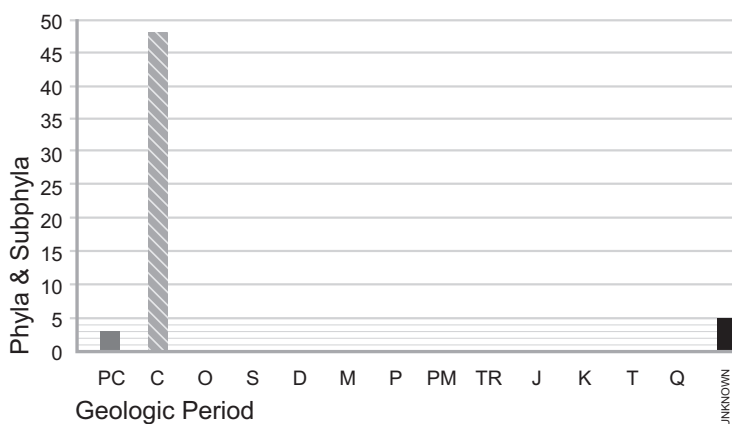


FIGURE 19B. Animal phyla and subphyla first appearances: based on fossil data and other considerations (see appendix E)

increasing number of phyla over geologic time, the fossil record shows a very different pattern; namely, a sudden burst of phyla first appearing in the Cambrian followed either by (as in 17A) a few small subsequent bursts or (as in 17B) a nearly complete absence of new phyla first appearing after the Cambrian.<sup>45</sup> Indeed, for 525 million years after the Cambrian explosion and for 3 billion years before it, the fossil record does not show anything like a steadily increasing number of new phyla. Nor does the sudden

explosive appearance of between nineteen and thirty-five new phyla within a 5-million-year window fit the pattern of steady increase that one would expect given either of the two main evolutionary pictures of the history of life.

We have provided two other graphs that reinforce these points. Several animal phyla may be subdivided into a number of subphyla. These subphyla represent major morphological divisions within their respective phyla (distinctions even greater than those seen between classes). Since many paleontologists regard subphyla as equivalent, or nearly equivalent, to phyla, we have also presented graphs (figures 19A and 19B) to show the stratigraphic first appearance and presumed first appearance not only for all the animal phyla but also for the twenty-two animal subphyla.<sup>46</sup> Figure 19A graphs the first appearance of the phyla and subphyla on strictly empirical grounds. Figure 19B graphs the presumed first appearance of the phyla and subphyla based upon the most favorable estimates of the number (of phyla and subphyla) that may have been present in the Cambrian taking the other considerations discussed above into account. Note that representing the data in this way poses an even more severe challenge to the neo-Darwinian picture of the history of life.

Even conservative estimates based strictly on existing fossil evidence show that at least 47.5 percent of all known animal phyla and 57.1 percent of the known phyla and subphyla combined have their first appearance in the Cambrian. Estimates based on an analysis of the factors discussed above can raise these measures to as high as 85.7 percent or more. As mentioned above, we favor values in the middle of this spectrum. Figure 20 provides additional support for this judgment. This figure shows that 67.8 percent of the phyla that do appear in the fossil record appear first in the Cambrian. In other words, if we exclude for the sake of analysis those phyla that do not appear in the fossil record at all and only analyze those phyla that definitely do appear in the record, we arrive at a value near the middle of the extremes (as depicted in figures 18A, 18B, and 19B). This value may represent a very realistic, and perhaps even a lower bound, estimate of the percentage of phyla that first appear in the Cambrian. In any case, we see that however we analyze the data, the pattern of first appearance of the phyla (and subphyla) contradicts that predicted by both the neo-Darwinian and punctuationalist models.

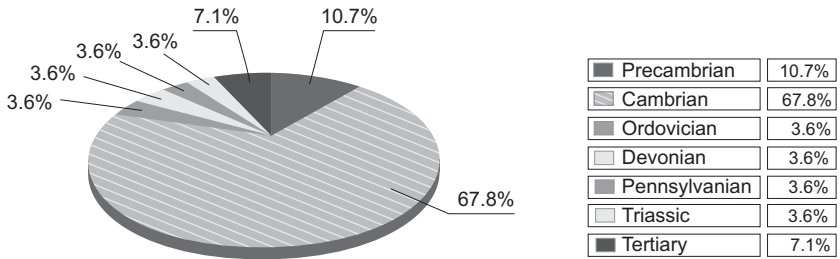


FIGURE 20. Animal phyla first appearances: analysis based on fossilized phyla alone

### D. Summary Assessment

When we compare the pattern of fossilization in the actual fossil record to the expected pattern given the neo-Darwinian mechanism, we encounter significant dissonance. Neither the pace nor the mode of evolutionary change match neo-Darwinian expectations. Indeed, the neo-Darwinism mechanism cannot explain the geologically sudden origin of the major body plans to which the term “the Cambrian explosion” principally refers. Further, the absence of plausible transitional organisms, the pattern of disparity preceding diversity, and the pattern of phyla first appearance all run counter to the neo-Darwinian predictions or expectations. Only the overall increase in complexity from the Precambrian to the Cambrian conforms to neo-Darwinian expectations. Although, as we have seen, the newer punctationalist model of evolutionary change appears more consonant with some aspects of the Cambrian/Precambrian fossil record, it, too, fails to account for the extreme absence of transitional intermediates, the top-down pattern of disparity preceding diversity, and the pattern of phylum first appearance. Furthermore, punctuated equilibrium lacks a sufficient mechanism to explain the origin of the major body plans that appear in the Cambrian strata.

These problems underscore a more significant theoretical difficulty for evolutionary theory generally, namely, the insufficiency of attempts to extrapolate microevolutionary mechanisms to explain macroevolutionary development. As developmental biologists Gilbert, Opitz, and Raff have noted: “The Modern Synthesis is a remarkable achievement. However, starting in the 1970s, many biologists began questioning its adequacy in explaining evolution. Genetics might be adequate for explaining microevolution, but microevolutionary changes in gene frequency were not seen as

able to turn a reptile into a mammal or to convert a fish into an amphibian. Microevolution looks at adaptations that concern only the survival of the fittest, not the arrival of the fittest."<sup>47</sup> Or as Roger Lewin stated in his summary of the historic Chicago "Macroevolution" conference in 1980: "The central question of the Chicago conference was whether the mechanisms underlying microevolution can be extrapolated to explain the phenomena of macroevolution. At the risk of doing violence to the position of some people at the meeting, the answer can be given as a clear, No."<sup>48</sup>

The origin of major innovations and complexity is increasingly recognized as an unsolved problem for all fully naturalistic versions of evolutionary theory, and biologists, especially developmental biologists, are beginning an intensive search for solutions.<sup>49</sup> Before considering whether the theory of intelligent design should be considered in this search, we will consider some objections to the paleontological arguments that we have marshaled against the adequacy of neo-Darwinism and punctuated equilibrium.

## **IV. Objections**

### **A. The Artifact Hypothesis: Is the Cambrian Explosion Real?**

Many have argued that absence of Precambrian transitional intermediates does not disconfirm neo-Darwinian predictions but instead testifies only to the incompleteness of the fossil record. The difference between what the fossil record shows and what neo-Darwinism implies that it should show has led many to question not the neo-Darwinian mechanism or its picture of the history of life but the completeness of the fossil record.

Initially, however, Darwinists adopted a different approach. For many decades after the publication of the *Origin*, paleontologists sympathetic to Darwin's theory sought to find the missing ancestors of the Cambrian animals. The search for the missing fossils in Precambrian formations all over the world resulted in universal disappointment. Maintaining Darwin's theory, therefore, eventually required formulating ad hoc hypotheses to account for the absence of ancestral and transitional forms. Various so-called artifact hypotheses have been proposed to explain the missing ancestors. Artifact hypotheses hold that the fossil ancestors existed but for various reasons were not preserved in an "imperfect and biased" fossil record. On this view, the absence of the fossil ancestors represents "an artifact" of



incomplete sampling of the fossil record and not an accurate representation of the history of life. Gaps in the fossil record are apparent, not real.

A popular version of the artifact hypothesis was proposed by the prominent American geologist Charles Walcott in the early 1900s. Taking his lead from Darwin, Walcott proposed a so-called Liplian interval. According to Walcott, the ancestors of the trilobites first lived and evolved at a time when the Precambrian seas had receded from the land masses. Then, at the beginning of the Cambrian, the seas again rose, covering the continents and depositing recently evolved trilobites. According to Walcott, ancestral trilobites did exist but were not fossilized in terrestrial sediments until the beginning of the Cambrian. Before the Cambrian, during a period of recession of seas, trilobites (and their ancestral forms) were being deposited only in deep-sea sediments.<sup>50</sup> Thus, Walcott argued that paleontologists should not expect to find fossilized trilobites in terrestrial strata but only in the marine sediments that were, in Walcott's time, inaccessible to paleontology. The Liplian interval hypothesis had the advantage of accounting for the sudden appearance of the trilobites and the absence of ancestral and transitional forms. Moreover, it could be tested, at least once offshore drilling technology advanced to allow for the sampling of the buried offshore Precambrian sedimentary rocks.

Walcott's Liplian interval hypothesis ultimately failed for two reasons. First, offshore drilling technology has now been developed, and offshore drilling cores have repeatedly failed to verify the existence of Walcott's predicted fossils in marine sediments.<sup>51</sup> Second, and more fundamentally, even if trilobite fossils had been found in the marine sediments, such fossils would not have confirmed the existence of Precambrian trilobite ancestors because Walcott incorrectly assumed that the oceanic crust included Precambrian sediments. At the time that Walcott proposed his version of the artifact hypothesis, geologists considered the oceanic and continental plates to be essentially stable and fixed with respect to one another. Mountain building, faulting, and other geologic events were thought to be caused by changes in eustasy (or other mechanisms favored at the time). The idea that lithospheric plates actually moved, recycling themselves through the process of plate tectonics, had not yet been proposed. According to modern estimations, the oldest section of oceanic crust is Jurassic (between 145 and 210 million years ago), far too young to contain the Precambrian fossil ancestors of the trilobites. Thus, the Liplian interval was discarded (as a non-starter) once geologists had accepted plate tectonic theory. Paleontologists today do not expect to find any Precambrian ancestors to the trilobites in

oceanic sediments, since there are no Precambrian rocks in the ocean basins. Instead, if Precambrian ancestors of the trilobites (or any other Cambrian animals) did exist, then they would have to be found within Precambrian sedimentary rocks retained on the continental crust. Yet such Precambrian fossils have not been found.

Over the years, paleontologists have proposed various “missing strata” hypotheses to explain the missing ancestors. Some have suggested that rocks containing Precambrian transitional fossils were metamorphosed or melted beyond recognition. Others claimed that major evolutionary innovation occurred during periods in which sedimentary deposition had ceased. Advocates of these hypotheses abandoned them, however, once geologists began to uncover extensive Precambrian sedimentary deposits that again failed to document the existence of plausible ancestors for the complex Cambrian animals.<sup>52</sup>

Proponents of the artifact hypothesis have advanced other explanations. One asserts that the Precambrian ancestors of the Cambrian animals lacked hard parts such as shells and exoskeletons. Thus, according to this version of the artifact hypothesis, we should not expect to find remains of ancestral forms in the Precambrian fossil record since soft-bodied animals do not leave fossil remains.

Yet this idea has also met with difficulty. While clearly the fossil record does not preserve soft body parts of organisms as frequently as hard body parts, it has preserved enough soft-bodied animals and organs to render this version of the artifact hypothesis suspect. Indeed, entirely soft-bodied representatives of several phyla have been identified in the Cambrian.<sup>53</sup> Soft-bodied organisms are also preserved in Precambrian strata around the world. Even so, these Precambrian organisms do not represent plausible transitional intermediates to representatives of the Cambrian phyla. In each case, the jump in complexity (as measured by the number of cell types, for example) and the morphological disparity between the Precambrian and Cambrian organisms appear far too great (see section IV.B).

Furthermore, the postulation of exclusively soft-bodied ancestors for hard-bodied Cambrian organisms seems implausible on anatomical grounds.<sup>54</sup> Many phyla such as brachiopods and arthropods could have not evolved their soft parts first and then added shells later, since their survival depends in large part upon their ability to protect their soft parts from hostile environmental forces. Instead, soft and hard parts had to arise together.<sup>55</sup> As Valentine notes in the case of brachiopods, “the brachiopod

*Baupläne* cannot function without a durable skeleton.”<sup>56</sup> To admit that hard-bodied Cambrian animals had not yet evolved their hard-bodied parts in the Precambrian effectively concedes that credible precursor animals themselves had not yet evolved.<sup>57</sup> As Chen and Zhou explain: “[A]nimals such as brachiopods and most echinoderms and mollusks cannot exist without a mineralized skeleton. Arthropods bear jointed appendages and likewise require a hard, organic or mineralized outer covering. Therefore the existence of these organisms in the distant past should be recorded either by fossil tracks and trails or remains of skeletons. The observation that such fossils are absent in Precambrian strata proves that these phyla arose in the Cambrian.”<sup>58</sup>

Others have explained the absence of transitional organisms as the result of their putatively tiny size. Some have even suggested that transitionals only existed in the larval stage.<sup>59</sup> While possible perhaps, it should be noted that cells of filamentous microorganisms (interpreted as cyanobacteria) have been discovered and documented in the Warrawoona Group strata of western Australia. These microfossils, found in bedded carbonaceous cherts, are estimated to be between 3.3 billion to 3.5 billion years old.<sup>60</sup> Species of single-celled algae and the appearance of cells with a nucleus about 2.7 billion years ago have been well documented in the fossil record.<sup>61</sup> If paleontologists can find minuscule single cells in formations that are far older (and therefore far more rare due to the greater likelihood of tectonic destruction), it would seem that the allegedly tiny fossil precursors of the Cambrian animals should have been found somewhere in the over 500 million years of sedimentary strata below the Cambrian. Moreover, as already noted, the Precambrian rocks in China beneath the Chengjiang Cambrian biota reveal the presence of tiny sponge embryos at the very earliest stages of cell division.<sup>62</sup> If the fossil record has preserved such tiny organisms in Precambrian strata, why has it not preserved any of the allegedly miniature or soft-bodied ancestral forms of the animals that first appear in the Cambrian? If these strata can preserve embryos, then they should be able to preserve the ancestral animals to the new forms that arise in the Cambrian. But they do not.

Of course, there are conditions under which fossils are unlikely to be preserved. Nevertheless, the factors that generally make preservation unlikely do not help to account for the specific absence of Precambrian ancestral forms. We know, for example, that nearshore sands do not favor preservation of detail, let alone the fine detail of very small organisms a millimeter or less in length. Similarly, paleontologists rarely find the

remains of parasites that live in the soft tissues of other organisms (indeed, parasitic organisms represent several of the phyla that have no fossil record).<sup>63</sup> Even so, such considerations do little to bolster the artifact hypothesis. The carbonates, phosphorates, and shales of the Precambrian strata beneath the Chengjiang fauna, for example, would have provided moderate to very favorable depositional environments in Precambrian times. Yet these strata do not preserve plausible ancestral forms for any of the animals in the Cambrian beds of the Chengjiang. Advocates of the artifact hypothesis need to show not just that certain factors discourage preservation in general (which is not disputed) but that these factors were ubiquitous in Precambrian depositional environments worldwide. If nearshore sands characterized all Precambrian sedimentary deposits, then paleontologists would not expect to find any ancestral, or at least any tiny ancestral, forms for the Cambrian animals. Yet clearly this is not the case. Precambrian strata include many types of sediments that can preserve—and in the case of sponge embryos, have preserved—animal remains in fine detail. Yet no forms plausibly intermediate to the metazoan animals have been found in such beds.

The implausibility of the artifact hypotheses in its various manifestations has been reinforced by recent work in statistical paleontology. Michael Foote has shown that new fossil discoveries have repeatedly fallen into existing taxonomic groups. This pattern of discovery suggests that the fossil record is, at best, curiously selective in its incompleteness. Though the record amply documents the organisms corresponding to the branches on the Darwinian tree of life, it inexplicably (from a neo-Darwinian point of view) fails to preserve the organisms required to connect the branches (that is, those corresponding to the nodes). As more and more fossil finds fall within existing higher taxonomic groups, it seems less and less likely that the absence of morphologically intermediate forms reflects a bias in sampling. In other words, Foote's analysis suggests the extreme improbability of discovering enough fossils representing previously unrepresented taxonomic categories to close the morphological distance between the Cambrian forms. Instead, based on sampling theory, Foote argues that "we have a representative sample of morphological diversity and therefore we can rely on patterns documented in the fossil record." As he concludes, "although we have much to learn about the evolution of form, in many respects our view of the history of biological diversity is mature."<sup>64</sup>

## B. The Vendian Radiation

As we have seen above, some have attempted to defend neo-Darwinism by questioning the completeness of the fossil record. Nevertheless, others accept the testimony of the fossil record but then defend neo-Darwinism by suggesting that the fossil record does indeed document some of the transitional intermediate forms required by the theory and (to a lesser extent) by the theory of punctuated equilibrium. In particular, it has been suggested that a group of late Precambrian (Vendian) multicellular organisms might represent transitional intermediates to the Cambrian animals.

Paleontologists have made discoveries of Vendian fossils in England, Newfoundland, the White Sea in northwestern Russia, and the Namibian desert in southern Africa. While these fossils were originally dated at between 700 million and 640 million years old, volcanic ash beds both below and above the Namibian site have recently provided more accurate radiometric dates. These studies fix the date for the first appearance of the Vendian fossils at 565–570 million years ago and their last appearance at the Cambrian boundary about 543 million years ago.<sup>65</sup>

There are four types of Vendian fossils, all of which first appeared between 570 and 543 million years ago. The first includes the strange Ediacaran fauna named for their most notable locale in the Ediacara Hills in the outback of southwestern Australia. These include the flat, air mattress-like *Dickinsonia* and the enigmatic *Spriggina*, with its elongate and segmented body and possible head shield. These organisms are at least mostly soft bodied and large enough to identify with the naked eye. The second group consists of the Precambrian sponges, primitive animals that first arose 565–570 million years ago. The third group includes trace fossils (the possible remains of animal activity) such as tracks, burrows, and fecal pellets. These may represent the remains of primitive wormlike creatures or primitive mollusks. The fourth group of fossils may actually represent body fossils of primitive mollusks. Indeed, a recent discovery in the cliffs along the White Sea in northwest Russia provides support for the existence of mollusks in the Vendian. There, scientists have discovered thirty-five distinctive specimens of *Kimberella*, a simple animal form. These new White Sea specimens, dated at 550 million years ago, suggest that *Kimberella* “had a strong, limpet like shell, crept along the sea floor, and resembled a mollusk.” Paleontologist Douglas Erwin of the Smithsonian Institution has commented that “it’s the first animal that you can convincingly demonstrate is more complicated than a flatworm.” Radula-style sea-floor tracks from Precambrian sediments in both Canada and Australia have been

attributed to mollusks, and *Kimberella* may well be the track maker.<sup>66</sup> The authors of the original descriptive paper in *Nature*, Mikhail Fedonkin and Benjamin Waggoner, conclude on the basis of their finds that at least “‘molluscan-grade bilaterians,’ began to diversify before the beginning of the Cambrian.”<sup>67</sup>

Though fascinating, the late Precambrian fossil record does not significantly diminish the difficulty of accounting for the Cambrian explosion on either a neo-Darwinian or punctuationalist model. First, with the exception of *Kimberella*, the body plans of visibly fossilized organisms (as opposed to trace fossils) bear no clear relationship to any of the new organisms that appear in the Cambrian explosion (or thereafter).<sup>68</sup> The Ediacaran organisms such as *Dickinsonia* and *Springinna* do not have eyes, mouths, or anuses. For this reason, many paleontologists doubt that these organisms even belong in the animal kingdom.<sup>69</sup> As Erwin, Valentine, and Jablonski have noted:

Although the soft-bodied fossils that appear about 565 million years ago are animal-like, their classifications are hotly debated. In just the past few years these [Ediacaran] fossils have been viewed as protozoans; as lichens; as close relatives of the cnidarians; as a sister group to cnidarians plus all other animals; as representatives of more advanced, extinct phyla; and as representatives of a new kingdom entirely separate from the animals. Still other specialists have parceled the fauna out among living phyla, with some assigned to the Cnidaria and others to the flatworms, annelids, arthropods and echinoderms. *This confusing state of affairs arose because these body fossils do not tend to share definitive anatomical details with modern groups, and thus the assignments must be based on vague similarities of overall shape and form, a method that has frequently proved misleading in other cases* [emphasis added].<sup>70</sup>

Second, the late Precambrian strata document very few types of animals, three or at most four phyla (Cnidaria, Porifera, and possibly Mollusca and a worm phylum), even granting the most optimistic estimates of the significance of Vendian body and trace fossils.<sup>71</sup> Precambrian strata do reveal trace fossils consisting of surface tracks and burrows, along with fecal pellets. Though small, these could only have been made by organisms of a relatively high degree of differentiation. Thus, some have argued that these trace fossils suggest the existence of organisms with a head and tail, nervous systems, a muscular body wall allowing creeping or burrowing, and a gut with mouth and anus.<sup>72</sup> These inferred physical characteristics would indicate organisms of “organ grade” complexity, above that of flatworms. Some paleobiologists have, therefore, speculated that the tracks, burrows,

and feeding trails indicate the existence of two (probably Mollusca and a worm phylum) or so types of animals prior to the Cambrian.<sup>73</sup>

Nevertheless, even on the most optimistic interpretation of these remains, Precambrian strata account for no more than four animal body plans (including some of largely unknown characteristics). Thus, neither the peculiar Ediacaran fauna nor the Precambrian fossil record taken as a whole establishes the existence of the wide variety of transitional intermediates that neo-Darwinism and punctuated equilibrium require. The Cambrian explosion attests to the first appearance of organisms representing at least nineteen phyla. Yet, Vendian organisms represent ancestral forms for, at most, four Cambrian phyla (granting ancestral status to a worm phylum and *Kimberella* as a mollusk). This leaves between 80 and 90 percent of the Cambrian phyla with no ancestors in the Precambrian rocks. Further, even if one grants that representatives of four phyla existed in the Precambrian, it does not follow that these forms were actually transitional intermediates. Some were, or may have been, representatives of known Cambrian phyla such as sponges (phylum Porifera), thus demonstrating not a gradual transformation but instead only the earlier appearance of a previously known phyla.

There is another reason that late Precambrian (or Vendian) fossils do not make it easier for neo-Darwinism to explain the pattern of appearance in the fossil record. The Vendian fossils themselves evidence a puzzling discontinuous increase in specified biological complexity, though not one nearly great enough (or of the right kind) to account for the Cambrian explosion. Prior to the appearance of organisms such as *Kimberella*, *Dickinsonia*, and sponges, the only living forms documented in the fossil record for over 3 billion years are single-celled organisms and colonial algae. The emergence of primitive mollusks, the two-dimensional animal-like *Dickinsonia*, sponges, and worms (as attested by trace fossils) represents, therefore, a significant discontinuous increase in the information content or specified complexity of the biological world, not unlike that evidenced in the Cambrian explosion itself (though of a much lesser degree).

Thus, the Ediacaran and other organisms in the Vendian may attest to a separate sudden increase in specified biological complexity within a short window of geological time (about 20 million years) following roughly 3 billion years in which only bacteria and algae inhabited the earth. The complexity jump required by the appearance of these organisms in this short period of time would seem to exceed the explanatory resources of either the selection/mutation or the species/selection mechanisms (see

further discussion in section V.A). Thus, the appearance of the Vendian fossils does not solve the problem of the sudden increase in biological complexity during the Cambrian; at best it constitutes another, though lesser, manifestation of the same problem in older Precambrian strata.

Indeed, even if one regards the appearance of the Vendian fossils as evidence of a kind of “fuse” on the Cambrian explosion, the total time encompassed by the Vendian and Cambrian radiations still remains exceedingly brief relative to neo-Darwinian expectations and requirements.<sup>74</sup> Only 40–45 million years elapsed between the beginning of the Vendian radiation (565–570 million years ago) and the end of the Cambrian explosion (525 million years ago). This represents about 7 percent of the time that modern neo-Darwinists expect for the development of complex animals from their alleged common ancestor (see discussion of deep divergence in section IV.C) and, by nearly all accounts, far less time than the mutation/selection mechanism would require (see section V.A). Until recently, radiometric studies had estimated the duration of the Cambrian radiation itself at 40 million years, a period of time so brief, geologically speaking, that paleontologists had dubbed it an “explosion.” The relative suddenness of this event, even on the earlier measure of its duration, had already raised serious questions about the adequacy of the neo-Darwinian mechanism. Treating the Vendian and the Cambrian radiations as one continuous evolutionary event (itself a dubious assumption) only returns the problem to its earlier (pre-Zircon redating) status—hardly a positive state of affairs for advocates of neo-Darwinism.

### C. The Deep Divergence Hypothesis

Recently, evolutionary biologists have attempted to defend neo-Darwinism against the evidential challenge of the fossil record in another way. Some evolutionary biologists have denied the explosive character of the Cambrian radiation and postulated a long period of undetected or cryptic evolution in the Precambrian, beginning from a common ancestor, some 1.2 billion years ago. To support such claims, these biologists have asserted the primacy of molecular data over the evidence of the fossil record itself. In particular, a recent study of molecular sequence data by Wray, Levinton, and Shapiro, entitled “Molecular Evidence for Deep Precambrian Divergences among Metazoan Phyla,” purports to provide compelling molecular evidence for a common ancestor of the Cambrian phyla dating from 1.2 billion years ago (or nearly 700 million years before the Cambrian radiation).<sup>75</sup> Wray, Levinton, and Shapiro suggest that the evolution of the



Cambrian phyla continued at a steady pace for nearly 700 million years from this "deep divergence" point until the Cambrian animals first appeared in the fossil record 530 million years ago. They then explain the absence of ancestral forms using a version of the artifact hypothesis, namely, that Precambrian ancestors existed in an exclusively soft-bodied form until the Cambrian explosion occurred.

Wray, Levinton, and Shapiro support their fundamental claim about the deep divergence of animal evolution 1.2 billion years ago on the basis of molecular sequence comparisons. Specifically, they compared the degree of difference between the amino acid sequences of seven proteins (ATP-ase, cytochrome c, cytochrome oxidase I and II, alpha and beta hemoglobin, and NADH I) derived from several different modern animals representing five Cambrian phyla (annelids, arthropods, mollusks, chordates, and echinoderms). They also compared the nucleotide base sequences of a ribosomal RNA (18S rRNA) from the same animal representatives of the same five phyla. Assuming that the degree of difference in sequencing reflects the amount of time that has elapsed since the ancestors of different animals began to diverge from each other, Wray, Levinton, and Shapiro determine a date for the common ancestor from which the evolution of the Cambrian animals began. Their analysis places the common ancestor from which all animal forms diverged at nearly 700 million years before the Cambrian explosion. Their analysis implies a very ancient or (stratigraphically) "deep" divergence of the animal forms, in opposition to those who claim that the Cambrian animals appeared suddenly. Indeed, a major purpose of their study was to disconfirm the traditional view "that the animal phyla diverged in an 'explosion' near the beginning of the Cambrian period." They argue instead that "all mean divergence time estimates between these four phyla and chordates, based on all seven genes, substantially predate the beginning of the Cambrian period." And they conclude, "Our results cast doubt on the prevailing notion that the animal phyla diverged explosively during the Cambrian or late Vendian, and instead suggest that there was an extended period of divergence during the mid-Proterozoic, commencing about a billion years ago."<sup>76</sup>

From a neo-Darwinian point of view, the results of Wray, Levinton, and Shapiro's study seem almost axiomatic, since the neo-Darwinian mechanism requires extensive amounts of time to produce the new form present in the Cambrian strata. As Andrew Knoll, a Harvard paleontologist, has stated, "The idea that animals should have originated much earlier than we see them in the fossil record is almost inescapable."<sup>77</sup>

Nevertheless, the “deep divergence” hypothesis suffers from several severe difficulties.

First, the postulation of an extensive 700-million-year period of undetectable evolution remains highly problematic from a paleontological point of view. The preservation of numerous soft-bodied Cambrian animals, as well as Precambrian sponge embryos and microorganisms, severely challenges those versions of the artifact hypothesis that invoke an extensive period of undetected soft-bodied evolution in the Precambrian. Further, the postulation of exclusively soft-bodied ancestors for hard-bodied Cambrian forms remains anatomically implausible, as noted earlier. A brachiopod cannot survive without its shell. Nor can an arthropod exist without its exoskeleton. Any plausible ancestor to such organisms would have needed hard body parts that could have been fossilized, yet none have been found in the Precambrian.

Second, Wray, Levinton, and Shapiro’s results vary dramatically from other similar sequence comparisons. In a more recent publication, Ayala, Rzhetsky, and Ayala have recalculated the divergence times, using the same protein-coding genes as Wray, Levinton, and Shapiro (but eliminating 18S rRNA, an RNA-coding gene, because of problems with obtaining a reliable alignment) and adding an additional twelve protein-coding genes. Correcting what they argue are “a host of statistical problems” in the Wray, Levinton, and Shapiro study, Ayala, Rzhetsky, and Ayala found that their own estimates “are consistent with paleontological estimates”—not with the deep divergence hypothesis. “Extrapolating to distant times from molecular evolutionary rates estimated within confined data-sets,” note Ayala and his colleagues, “are fraught with danger.”<sup>78</sup> Nevertheless, to the extent that such estimates can be made, they contend, their results correspond with the standard paleontological estimates.

Third, Wray, Levinton, and Shapiro rely on the molecular clock data to estimate the point of deep divergence. Yet unlike radiometric clocks, molecular clocks depend upon a whole host of contingent factors, both biological and environmental, that render them unreliable. As Valentine, Jablonski, and Erwin note: “different genes in different clades evolve at different rates, different parts of genes evolve at different rates and, most importantly, rates within clades have changed over time.”<sup>79</sup> Moreover, many environmental factors influence mutation rates, including catastrophic events that have often punctuated the geologic record. The mutation rate can greatly increase during the collapse of the magnetic field or following mass extinctions when new ecological niches open up. Further, mutations

depend upon active biological processes that occur at different stages of genomic and embryological developmental. They do not depend upon the physics of constant radiometric decay. In any case, without evidence from the fossil record (older than 565 million years ago) with which to calibrate the molecular clock, its reliability in dating the origin of the Cambrian animal phyla (at between 1 and 1.2 billion years ago) remains highly questionable. Thus, Valentine, Jablonski, and Erwin argue that "the accuracy of the molecular clock is still problematical, at least for phylum divergences, for the estimates vary by some 800 million years depending upon the techniques and or the molecules used . . . it is not clear that molecular clock dates can ever be applied reliably to such geologically remote events as Neoproterozoic branchings within the Metazoa."<sup>80</sup> Thus, as Simon Conway Morris concludes, "a deep history extending to an origination in excess of 1,000 Myr is very unlikely."<sup>81</sup>

Fourth, the basic housekeeping proteins (and ribosomal RNAs) that Wray, Levinton, and Shapiro analyzed would, in any case, have had little role in the origin of novel body plans. Nearly all of the proteins analyzed by Wray, Levinton, and Shapiro are found in any organism, from the simplest one-celled prokaryotes or protists (eukaryotes) to multicellular animals. Any evolution that these proteins might have undergone (over whatever duration of time) could not have caused higher-level body plans to differentiate, since such differentiation involves, at the very least, morphological regulator proteins (such as DNA binding proteins) that Wray, Levinton, and Shapiro did not analyze. As Johns and Miklos have noted elsewhere, "changes in . . . structural genes are unlikely to have anything to do with the production of [major] morphological change."<sup>82</sup> The kinds of proteins that Wray, Levinton, and Shapiro did analyze simply do not suffice to explain body-plan formation. Yet they use their analyses of the differences between these molecules to make, in effect, a claim about the time at which body plans began to diverge.

Finally, all analyses of sequence data make assumptions that raise serious questions about their reliability as indicators of very ancient common ancestors. All sequence analyses assume, rather than demonstrate, the doctrine of universal common descent. By assuming that sequence differences reflect the amount of time that has passed since different animals began to diverge from a common ancestor, molecular studies clearly presuppose that some such ancestor existed. Sequence analyses calculate how long ago a common ancestor for two (or more) organisms might have existed—if *one assumes* that some such organism must have existed. But

whether the Cambrian animals had a common ancestor is part of the point at issue, or should be.<sup>83</sup> The fossil record taken at face value certainly provides no evidential basis for this claim. To invoke molecular analyses that presuppose a common ancestor as evidence for the existence of such an entity only begs the question. Perhaps the Precambrian rocks do not record transitional intermediates and ancestors for Cambrian animals because none existed. Citing sequence analyses that tacitly assume the existence of a common ancestor does not provide evidential support for the existence of such an ancestor. Certainly, it provides no reason for privileging molecular analyses over fossil evidence.

### ***V. Evidence of Design?***

Our discussion to this point has suggested that neither neo-Darwinism nor the theory of punctuated equilibrium adequately accounts for the pattern of fossil evidence surrounding the Cambrian explosion. Instead, both these theories rely on mechanisms that should produce new forms of life in a manner quite different than that evident in the Precambrian/Cambrian fossil record. In this section, we will now expand our critique by further challenging the efficacy of various undirected mechanisms of evolutionary change and by proposing an alternative causal explanation for both the origin of the new information that arises in the Cambrian and the other specific features of the explosion as described above.

Studies in the history and philosophy of science have shown that many scientific theories, particularly in the historical sciences, are formulated and justified as inferences to the best explanation.<sup>84</sup> Historical scientists, in particular, assess competing hypotheses by evaluating which hypothesis would, if true, provide the best explanation for some set of relevant data. Those with greater explanatory power are typically judged to be better, more probably true, theories. Darwin himself used this method of reasoning in defending his theory of universal common descent.<sup>85</sup> Moreover, contemporary studies on the method of inference to the best explanation have shown that determining which among a set of competing possible explanations constitutes the best depends upon judgments about the causal adequacy, or causal powers, of the competing explanatory entities.<sup>86</sup> Historical scientists reasoning in accord with uniformitarian canons of method judge the plausibility of causal explanations of past events against their knowledge of present cause-and-effect relationships—that is, against their knowledge of the present causal powers of various entities or processes.

In what follows, we shall make a case for intelligent design as the best—most causally adequate—explanation of the features of the Cambrian explosion. To do so, we will show that, in addition to the difficulties described above, the main materialistic mechanisms of evolutionary change are not sufficient to produce the new information and body plans that arise in the Cambrian. Yet we will not infer the activity of an intelligent designer just because known natural processes or mechanisms cannot explain the origin of the main features of the Cambrian explosion. Instead, we will show that intelligent agents possess precisely those causal powers that are needed to produce the unique features of the Cambrian explosion. In other words, we will show that the Cambrian explosion manifests hallmarks or positive indicators of intelligently designed systems—features that in any other realm of experience would trigger the recognition of purposive or intelligent activity. We now consider these features (in roughly the reverse order as they were discussed in Part II).

### **A. The “Quantum” Increase in Specified Biological Information**

How can we best explain such a discontinuous or “quantum” increase in biological information that emerges during the Cambrian? Meyer argued, in a previous essay about the origin of life, that intelligent design provides a sufficient causal explanation for the origin of large amounts of information, since we have considerable experience of intelligent agents generating informational configurations of matter. To quote information theorist Henry Quastler, the “creation of new information is habitually associated with conscious activity.”<sup>87</sup> Yet whether intelligent design constitutes a necessary or best causal explanation for the biological information that arises in the Cambrian depends upon whether other causally adequate explanations exist. In Meyer’s previous discussion of the origin of genetic information in a prebiotic context, he argued against the sufficiency of three broad classes of naturalistic explanation for the origin of the genetic information required to make a cell in the first place. He argued that neither chance nor prebiotic natural selection acting on random variations nor physical-chemical necessity (that is, self-organization) can account for the origin of biological information starting from simple chemistry. Since only intelligent design is sufficient as a causal explanation for the origin of information, he concluded that intelligent design represents the best explanation for the origin of the information necessary to build the first living cell.

Nevertheless, the origin of information in the Cambrian fossils presents a different situation. Clearly, the amount of information represented by the many novel genes, proteins, and morphological structures that arise in the Cambrian defies the explanatory resources of chance, especially given the limited time involved in the explosion. Nevertheless, neo-Darwinists would argue that in a biological as opposed to a prebiotic context, the neo-Darwinian mechanism of natural selection acting on random variation does play a significant role in generating novel information. Further, self-organizational models for the origin of the Cambrian information explosion have been proposed.<sup>88</sup> Thus, for intelligent design to stand as *the best*, rather than just *a plausible*, explanation for the origin of the biological information that arises in the Cambrian, one must show the implausibility of both the neo-Darwinian and self-organizational mechanisms as explanations for the origin of the biological information that arises in the Cambrian. We shall do so below. (The theory of punctuated equilibrium offers no special mechanism for the origin of novel biological information beyond an appeal to macromutations. Since we critique this approach in our discussion of the neo-Darwinian and self-organizational mechanisms, we will offer no further critique of punctuated equilibrium.)

## 1. NATURAL SELECTION, GENES, AND PROTEINS

As noted above, one useful metric of complexity is number of cell types (see figure 10).<sup>89</sup> To build an animal requires, at a minimum, building many new types of cells. But cell types themselves require specialized proteins, and novel proteins require novel gene sequences—that is, new genetic information. The organisms that suddenly appeared in the Cambrian had many more novel and specialized cell types (and thus many more novel and specialized proteins) than the much more simple organisms found in the Precambrian. Hence, they would have required (at minimum) a vast amount of new genetic information. How did this information arise?

According to neo-Darwinism, novel genes and proteins arise as the result of natural selection acting on random variations or mutations in the genetic material of organisms. Yet since the 1960s a number of scientists and mathematicians have questioned the ability of mutation and selection to generate information in the form of novel genes and proteins. Their skepticism has derived from consideration of the extreme improbability (and specificity) of functional genes and proteins.

A typical gene contains over 1,000 precisely arranged bases. Yet for any specific arrangement of four nucleotide bases of length  $n$ , there are a

corresponding number of  $4^n$  possible arrangements of bases. For any protein, there are  $20^n$  possible arrangements of protein-forming amino acids. A gene of 999 bases in length represents one of  $4^{999}$  possible nucleotide sequences; a protein of 333 amino acids one of  $20^{333}$  possibilities.

Since the 1960s, biologists have generally thought functional proteins to be rare among the set of possible amino acid sequences (of corresponding length). Some have used an analogy with human language to illustrate why. Michael Denton, for example, has shown that meaningful words or sentences are extremely rare among the set of possible combinations of English letters, especially as sequence length grows. (The ratio of meaningful 12-letter words to 12-letter sequences is  $1/10^{14}$ ; the ratio of 100-letter sentences to possible 100-letter strings is  $1/10^{100}$ ). Further, Denton shows that most meaningful sentences are *highly isolated* from one another in the space of possible combinations such that random substitutions of letters will, after a very few changes, inevitably degrade meaning. Apart from a few closely clustered sentences accessible by random substitution, the overwhelming majority of meaningful sentences lie, probabilistically speaking, beyond the reach of random search.

Denton and others have argued that similar constraints apply to genes. They have questioned, therefore, whether an undirected search via mutation/selection would have a reasonable chance of locating new islands of function—representing fundamentally new genes or proteins—within available time.<sup>90</sup> Some have also argued that alterations in sequencing would likely result in loss of protein function before fundamentally new function could arise. Nevertheless, neither the sensitivity of genes and proteins to functional loss as the result of sequence change nor the extent to which functional proteins are isolated within sequence space has been fully known.

Recently, experiments in molecular biology have shed light on these questions. A variety of “mutagenesis” techniques have shown that proteins (and thus the genes that produce them) are indeed highly specified relative to biological function.<sup>91</sup> Mutagenesis research tests the sensitivity of proteins (and, by implication, DNA) to functional loss as a result of alterations in sequencing. This research has shown that, though many proteins do tolerate a variety of amino acids at some sites without loss of function, amino acid residues at many key active sites cannot vary at all without functional loss.<sup>92</sup> Moreover, whereas proteins will admit some variation at some sites, even in these cases only a limited set of the twenty protein-forming residues will preserve function—that is, even at sites that admit variation

not just any amino acid will do. Further, multiple as opposed to single amino acid substitutions generally result in rapid loss of protein function, even when these changes occur at sites that allow variation when altered in isolation.<sup>93</sup> Cumulatively, these constraints imply that proteins are highly sensitive to functional loss as a result of alterations in the sequencing and that functional proteins represent highly isolated and improbable arrangements of amino acids—arrangements that are far more improbable in fact than would be likely to arise by chance, even given our multibillion-year-old universe.<sup>94</sup>

Of course, neo-Darwinists do not envision a completely random search through the space of possible nucleotide sequences. They see natural selection acting to preserve small advantageous variations in genetic sequences and their corresponding protein products. Richard Dawkins, for example, likens an organism to a high mountain peak.<sup>95</sup> He compares climbing the sheer precipice up the front side of the mountain to building a new organism by chance. He acknowledges that this approach up “Mount Improbable” will not succeed. Nevertheless, he suggests that there is a gradual slope up the backside of the mountain that could be climbed in small, incremental steps. In his analogy, the backside up Mount Improbable corresponds to the process of natural selection acting on random changes in the genetic text. What chance alone cannot accomplish blindly or in one leap, selection (acting on mutations) can accomplish through the cumulative effect of many slight successive steps.

Yet the extreme specificity and complexity of proteins present a difficulty not only for the chance origin of specified biological information (that is, for random mutations acting alone) but also for selection and mutation acting in concert. Indeed, mutagenesis experiments cast doubt on each of the two scenarios by which neo-Darwinists envision new information arising by the mutation/selection mechanism. According to Neo-Darwinists, either new functional genes arise from noncoding sections in the genome or functional genes arise from preexisting genes. Both scenarios are problematic.

In the first scenario, neo-Darwinists envision new genetic information arising from those sections of the genetic text that can presumably vary freely without consequence to the organism. According to this scenario, noncoding sections of the genome, or duplicated sections of coding regions, can experience a protracted period of “neutral evolution” in which alterations in nucleotide sequences have no discernible effect on the function of the organism. Eventually, however, a new gene sequence will arise that



can code for a novel protein. At that point, natural selection can favor the new gene and its functional protein product, thus securing the preservation and heritability of both.

This scenario has the advantage of allowing the genome to vary through many generations as mutations “search” the space of possible base sequences. The scenario has an overriding problem, however: the size of the combinatorial space and the extreme rarity of the functional sequences within that space of possibilities. Since natural selection can do nothing to help *generate* new functional sequences but rather can only preserve such sequences once they have arisen, chance alone—random variation—must do the work of information generation—that is, of finding rare functional sequences within a universe of combinatorial possibilities. Yet the probability of randomly assembling (or “finding,” in the previous sense) a functional sequence is vanishingly small even on a scale of billions of years. Robert Sauer’s mutagenesis experiments imply that the probability of attaining (at random) the correct sequencing for a short protein 100 amino acids long is about 1 chance in  $10^{65}$ .<sup>96</sup> More recent mutagenesis research suggests that Sauer’s methods imply probability measures that are, if anything, too optimistic.<sup>97</sup>

Other considerations imply additional improbabilities. First, new Cambrian animals would require proteins much longer than 100 residues to perform necessary specialized functions. Susumu Ohno has noted that Cambrian animals would have required complex proteins such as lysyl oxidase in order to support their stout body structures.<sup>98</sup> Lysyl oxidase molecules in extant organisms comprise over 400 amino acids. These molecules represent highly complex (nonrepetitive) and tightly specified arrangements of matter. Reasonable extrapolation from mutagenesis experiments done on shorter protein molecules suggests that the probability of producing functionally sequenced proteins of this length at random is far smaller than 1 chance in  $10^{150}$ —the point at which, according to Dembski’s calculation of the Universal Probability Bound, appeals to chance become absurd given the time and other probabilistic resources of the entire universe.<sup>99</sup> Second, the Cambrian explosion took far less time ( $5 \times 10^6$  years) than the duration of the universe as a whole ( $2 \times 10^{10}$  years) that Dembski assumes in his calculation. Third, DNA mutation rates are far too slow to generate the novel genes and proteins necessary to building the Cambrian animals given the duration of the explosion. As Ohno has explained: “Assuming a spontaneous mutation rate to be a generous  $10^{-9}$  per base pair per year and also assuming no negative interference by natural

selection, it still takes 10 million years to undergo 1% change in DNA base sequences. It follows that 6–10 million years in the evolutionary time scale is but a blink of an eye. The Cambrian explosion denoting the almost simultaneous emergence of nearly all the extant phyla . . . within the time span of 6–10 million years can't possibly be explained by mutational divergence of individual gene functions."<sup>100</sup>

The mutation/selection mechanism faces another probabilistic obstacle. The animals that arise in the Cambrian exhibit structures that suggest many new *types* of cells, each of which would require many novel proteins to perform their specialized functions. Further, new cell types require *systems* of proteins that must, as a condition of function, act in close coordination with one another. The unit of selection in such systems ascends to the system as a whole. Natural selection selects for functional advantage. But new cell types require whole systems of proteins to perform their distinctive functions. In such cases, natural selection cannot contribute to the process of information generation until *after* the information necessary to build the requisite *system* of proteins has arisen. Thus, random variations must, again, do the work of information generation—and now not simply for one protein but for many proteins arising at nearly the same time. Yet the odds of this occurring by chance are far smaller than the odds of the chance origin of a single gene or protein (see above).

Richard Dawkins has acknowledged that “we can accept a certain amount of luck in our explanations, but not too much.”<sup>101</sup> The neutral theory of evolution, which, by its own logic, prevents natural selection from playing a role in generating genetic information until after the fact, relies on entirely “too much luck.” The sensitivity of proteins to functional loss, the need for long proteins to build new cell types and animals, the need for whole new *systems* of proteins to service new cell types, the brevity of the Cambrian explosion relative to mutation rates—all these factors suggest that the sequencing in many novel genes and proteins is too improbable (and tightly specified) to have a realistic chance of arising by chance unassisted by natural selection.

Yet the neutral theory requires novel genes and proteins to arise—essentially—by random mutation alone. Adaptive advantage accrues *after* the generation of new functional genes and proteins. Thus, natural selection cannot play a role *until* new information-bearing molecules have independently arisen. Thus, the neutral theory envisions the need to scale the steep face of a Dawkins-style precipice in which there is *no* gradually

sloping backside—a situation that, by Dawkins's own logic, is probabilistically untenable.

In the second scenario, neo-Darwinists envision novel genes and proteins arising by numerous successive mutations in a preexisting genetic text that codes for proteins. To adapt Dawkins's metaphor slightly, this scenario envisions gradually climbing down one functional peak and then ascending another. Yet mutagenesis experiments again suggest a difficulty. Recent experiments performed by Douglas Axe at Cambridge University show that, even when exploring a region of sequence space populated by proteins of a single function, most multiple position changes quickly lead to loss of function.<sup>102</sup> Yet to turn one protein into another with *a completely novel* function requires vastly more changes than are typically sufficient to degrade function. Axe's results imply that, in all probability, random searches for novel proteins (through sequence space) will result in functional loss long before any novel functional protein will emerge.

Francisco Blanco at the European Molecular Biology laboratory has come to a similar conclusion. Using directed mutagenesis, his team has found that the sequence space between two natural protein domains is not populated by folded or functional confirmations (that is, proteins). Instead, mutant sequences "lack a well defined three-dimensional structure." They conclude: "The results obtained here show that both the hydrophobic core residues and the surface residues are important in determining the structure of the proteins, and suggest that the appearance of a completely new fold from an existing one *is unlikely to occur by evolution through a route of folded intermediate sequences*" (emphasis added).<sup>103</sup>

Thus, although this second neo-Darwinian scenario has the advantage of starting with functional genes and proteins, it also has a lethal disadvantage: any process of random mutation or rearrangement in the genome will almost inevitably generate nonfunctional intermediate sequences before any fundamentally new functional gene and protein would arise (see figure 21). Such sequences would thus confer no survival advantage on their host organisms. Yet natural selection favors *only* functional advantage. It cannot select or favor nucleotide sequences or polypeptide chains that do not yet perform biological functions, still less will it favor sequences that efface or destroy preexisting function.

Evolving genes and proteins must range through a series of nonfunctional intermediate sequences that natural selection will not favor or preserve but will, in all probability, eliminate.<sup>104</sup> When this happens,

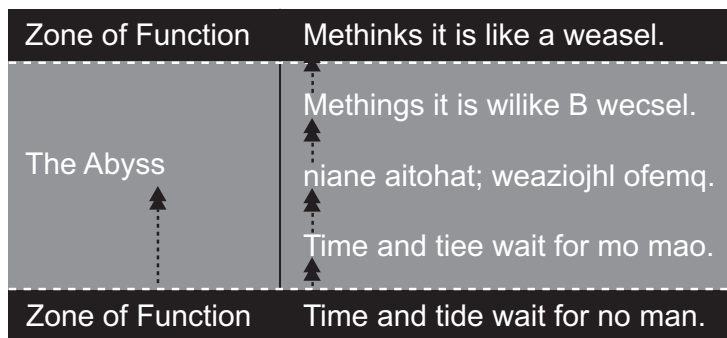


FIGURE 21. This diagram shows that multiple changes in the sequencing of letters in an English sentence inevitably degrade meaning before new meaning arises. A similar problem applies to sequence specific genes and proteins.

selection-driven evolution will cease. At this point, neutral evolution of the genome (unhinged from selective pressure) may ensue, but, as we have already seen, such a process faces immense probabilistic hurdles to generating new functional sequences even granting a cosmic time scale.

Thus, whether one envisions the evolutionary process beginning with a noncoding region of the genome or a preexisting functional gene, the functional specificity and complexity of proteins impose very stringent limitations on the efficacy of mutation and selection. In the first case, function must arise first before natural selection can act to favor a novel variation. In the second case, function must be continuously maintained to prevent deleterious (or lethal) consequences to the organism and to allow for the possibility of further evolution. Yet the complexity and functional specificity of proteins imply that both these conditions will be extremely difficult to meet. Therefore, the neo-Darwinian mechanism appears inadequate to generate the new information present in the novel genes and proteins that arise with the Cambrian animals.

## 2. NATURAL SELECTION AND NOVEL BODY PLANS

Problems with the neo-Darwinian mechanism run deeper still. To explain the origin of the Cambrian animals, one must account not only for new proteins and cell types but also for the origin of new body plans. Within the past decade, developmental biology has dramatically advanced

understanding of how body plans are built during ontogeny. In the process, it has also uncovered a profound difficulty cutting to the core of neo-Darwinism.

To create significant changes in the form of organisms requires attention to timing. Mutations in genetic material that are expressed late in the development of an organism will not affect the body plan. Mutations expressed early in development, however, could conceivably produce gross changes in the morphology of an organism.<sup>105</sup> Thus, events expressed early in the development of organisms have the only realistic chance of producing large-scale macroevolutionary change.<sup>106</sup> As Miklos and Johns explain, macroevolutionary change requires changes in “very early embryogenesis.”<sup>107</sup>

Yet recent studies in developmental biology make clear that mutations expressed early in development typically have deleterious (or at best neutral) effects, including mutations in the crucially important “master regulator,” or *hox*, genes. For example, when early-acting body-plan molecules, or morphogens, such as *bicoid* (which helps set up the anterior-posterior head-to-tail axis in the fly *Drosophila*) are perturbed, development shuts down.<sup>108</sup> The resulting embryos die. Moreover, there is a good reason for this. If an engineer modifies the length of the piston rods in an internal combustion engine without modifying the crankshaft accordingly, the engine won't start. Similarly, processes of development are so tightly integrated spatially and temporally that changes early in development will require a host of other coordinated changes in separate but functionally interrelated developmental processes downstream. For this reason, as Stuart Kauffman explains, “A mutation disrupting formation of a spinal column and cord is more likely to be lethal than one affecting the number of fingers.”<sup>109</sup>

This tight functional integration helps explain why mutations early in development inevitably result in embryonic death and why even mutations that are expressed somewhat later leave organisms crippled. For example, a regulative mutation in the *bithorax* gene (expressed midway in the development of a fly) does produce an extra pair of wings on a normally two-winged creature. Nevertheless, this “innovation” produces a cripple that cannot fly because it lacks, among other things, a musculature to support the use of its new wings. Since the developmental mutation was not accompanied by the many other coordinated developmental changes that would have been necessary to ensure the production of muscles at the

appropriate place on the fly's body, the original mutation did not lead to a positive morphological change but to a strikingly deleterious one.

This problem has led to what geneticist John F. McDonald has called "a great Darwinian paradox." He notes that genes that vary within natural populations seem to affect only minor aspects of form and function—while genes that govern major changes, the very stuff of macroevolution, apparently do not vary or vary only to the detriment of the organism. As he puts it, "those [genetic] *loci* that are obviously variable within natural populations do not seem to lie at the basis of many major adaptive changes, while those *loci* that seemingly do constitute the foundation of many if not most major adaptive changes are not variable."<sup>110</sup> In other words, the kind of mutations that macroevolution needs (namely, *beneficial* regulatory or *Bau-pläne* mutations expressed during early development) don't occur; the kind it doesn't need (namely, viable genetic mutations in DNA expressed late in development) do occur, if infrequently.

Darwin wrote that "nothing can be effected" by natural selection "unless favorable variations occur."<sup>111</sup> Yet discoveries about the genetic regulation of development suggest that the kind of variations required by neo-Darwinism—favorable mutations that generate new body plans—do not occur.

Developmental biology has raised another formidable problem for the mutation/selection mechanism. Embryological evidence has long shown that DNA does not wholly determine morphological form, suggesting that mutations in DNA alone cannot account for the morphological changes required to build a new body plan.<sup>112</sup>

DNA directs protein synthesis. It also helps regulate the timing and expression of the synthesis of various proteins within cells. Nevertheless, DNA alone does not determine how individual proteins assemble themselves into larger systems of proteins, still less does it alone determine how cell types, tissue types, and organs arrange themselves into body plans.<sup>113</sup> Instead, other factors—such as the structure and organization of the cell membrane and cytoskeleton—play important roles in determining developmental pathways that determine body-plan formation during embryogenesis.

For example, the shape and location of microtubules in the cytoskeleton influence the "patterning" of embryos. Arrays of microtubules help distribute the essential proteins used during development to their correct location in the cell.<sup>114</sup> Of course, microtubules themselves are made of many protein subunits. Nevertheless, the protein subunits in the cell's microtubules are identical to one another. Neither they nor the genes that produce them

account for the different shapes and locations of microtubule arrays that distinguish different kinds of embryos and developmental pathways. As Jonathan Wells explains, "What matters in development is the shape and location of microtubule arrays, and the shape and location of a microtubule array is not determined by its units."<sup>115</sup>

Two analogies may help. At a building site, builders will make use of many materials: lumber, wires, nails, drywall, piping, and windows. Yet building materials do not determine the floor plan of the house or the arrangement of houses in a neighborhood. Similarly, electronic circuits are composed of many components, such as resistors, capacitors, and transistors. But such lower-level components do not determine their own arrangement in an integrated circuit. Biological systems also depend on hierarchical arrangements of parts. Genes and proteins are made from simple building blocks—nucleotide bases and amino acids—arranged in specific ways. Cell types are made of, among other things, systems of specialized proteins. Organs are made of specialized arrangements of cell types and tissues. And body plans comprise specific arrangements of organs. Yet clearly the properties of individual proteins (or indeed the lower-level parts in the hierarchy generally) do not determine the organization of the higher-level structures and organizational patterns.<sup>116</sup> It follows, therefore, that the genetic information that codes for proteins does not determine these higher-level structures either.

These considerations pose another challenge to the sufficiency of the neo-Darwinian mechanism. Neo-Darwinism seeks to explain the origin of new information, form, and structure as the result of selection acting on randomly arising variation at a very low level within the biological hierarchy, namely, within the genetic text. Yet major morphological innovations depend on a specificity of arrangement at a much higher level of the organizational hierarchy that DNA alone does not determine. If DNA is not wholly responsible for body-plan morphogenesis, then DNA sequences can mutate indefinitely, without regard to realistic probabilistic limits, and still not produce a new body plan. Thus, the mechanism of natural selection acting on random mutations in DNA cannot *in principle* generate novel body plans, including those that first arose in the Cambrian explosion.

### 3. SELF-ORGANIZATIONAL MODELS AND NOVEL GENES AND PROTEINS

Of course, neo-Darwinism is not the only evolutionary model for explaining the origin of novel biological form in an undirected fashion. Stuart

Kauffman, for example, has recently advanced a self-organizational model to account for the emergence of form and presumably the information necessary to generate it. Whereas neo-Darwinism attempts to explain new form as the consequence of selection acting on random mutation, Kauffman suggests that selection acts not mainly on random variations but on emergent patterns of order that self-organize via the laws of nature.

Kauffman illustrates how this might work with various model systems in a computer environment. In one, he conceives a system of buttons connected by strings. Buttons represent novel genes or gene products, strings the lawlike forces of interaction that obtain between gene products—that is, proteins. Kauffman suggests that when the complexity of the system (as represented by the number of connected buttons and strings) reaches a critical threshold, new modes of organization can arise in the system “for free”—that is, without intelligent guidance—after the manner of a phase transition in chemistry. He explains that, “as clusters get larger, they begin to become cross-connected. Now the magic! As the ratio of threads to buttons passes the .5 mark, all of a sudden most of the clusters have become cross-connected into one giant structure.” Kauffman then draws an analogy between the kind of cross-connected structures that arise spontaneously in his computer simulation and the web of interconnected chemical reactions that characterize stable metabolism in the living cell. As he puts it, “when a large enough number of reactions are catalyzed in a chemical reaction system, a vast web of catalyzed reactions will suddenly crystallize.”<sup>117</sup>

Another model that Kauffman develops is a system of interconnected lights. Each light can flash in a variety of states—on, off, twinkling, and so forth. Since there is more than one possible state for each light and many lights, there are a vast number of possible states that the system as a whole can adopt. Further, in his system, rules determine how past states will influence future states. Kauffman asserts that, as a result of these rules, the system will soon, if properly tuned, produce a kind of order in which a few basic patterns of light activity recur with greater than random frequency. Further, insofar as these actual patterns of light activity represent a small portion of the total number of possible states in which the system can reside, Kauffman suggests that self-organizational laws might similarly find highly improbable biological outcomes—perhaps even sequences (of bases or amino acids) within a much larger sequence space of possibilities.

Do these simulations of self-organizational processes accurately model the origin of novel genetic information?



It's hard to think so.

First, in both examples, Kauffman presupposes but does not explain significant sources of preexisting information. In his buttons and strings system, the buttons represent proteins, themselves packets of information and the result of preexisting genetic information. Where does this information come from? Kauffman doesn't say, but the origin of such information is an essential part of what needs explanation in the history of life. Similarly, in his light system, the order that allegedly arises "for free"—that is, apart from an informational input by an agent—actually arises only if the programmer of the model system "tunes" it in such a way as to keep it from either generating an excessively rigid order or devolving into chaos.<sup>118</sup> Yet the tuning necessary to achieve this end involves an intelligent programmer selecting certain parameters and excluding others—that is, inputting information.

Second, Kauffman's model systems are not constrained by functional considerations and thus are not analogous to biological systems. A system of interconnected lights governed by preprogrammed rules may well settle into a small number of patterns within a much larger space of possibilities. But since these patterns have no function and need not meet any functional requirements, they have no specificity analogous to that present in actual organisms. Instead, examination of Kauffman's model systems shows that they do not produce sequences or systems characterized by specified complexity but instead by large amounts of symmetrical order or internal redundancy interspersed with aperiodicity or (mere) complexity.<sup>119</sup> Getting a law-governed system to generate repetitive patterns of flashing lights, even with a certain amount of variation, is clearly interesting but not biologically relevant. On the other hand, a system that generated the message "Eat at Joe's" would model a biologically relevant self-organizational process, at least, if the system produced such messages without agents having previously provided equivalent amounts of specified complexity. In any case, Kauffman's systems do not produce specified complexity and thus do not offer promising models for explaining an essential feature of the animals that arise in the Cambrian, namely, the specified information present in new genes and proteins.

#### 4. SELF-ORGANIZATIONAL MODELS AND NOVEL BODY PLANS

Even so, Kauffman suggests that his self-organizational models can specifically elucidate aspects of the Cambrian explosion. According to Kauffman,

new Cambrian animals emerged as the result of “long jump” mutations that established new body plans in a discrete rather than gradual fashion.<sup>120</sup> He also recognizes that mutations affecting early development are almost inevitably harmful. Thus, he concludes that body plans, once established, will not change and that any subsequent evolution must occur within an established *Baupläne*. And indeed, the fossil record does show a curious (from a Darwinian point of view) top-down pattern of appearance in which higher taxa (and the body plans they represent) appear first, only later to be followed by the appearance of lower taxa representing variations within those original body designs. Further, as Kauffman expects, body plans appear suddenly and persist without significant modification over time.

But here again Kauffman begs the most important question: What produced the new Cambrian body plans in the first place? Granted, he invokes “long jump” mutations to explain this, but he identifies no specific self-organizational process that can produce such mutations. Moreover, he concedes a principle that undermines the plausibility of his own proposal. Kauffman acknowledges that mutations that occur early in development are almost inevitably deleterious. Yet developmental biologists know that these are the only kind of mutations that have a realistic chance of producing large-scale evolutionary change—that is, the big jumps that Kauffman invokes. Though Kauffman repudiates the neo-Darwinian reliance upon random mutations in favor of self-organizing order, in the end he must invoke the most implausible kind of random mutation to provide a self-organizational account of the new Cambrian body plans. Clearly, his model is not sufficient.

## 5. INTELLIGENT DESIGN AND THE ORIGIN OF BIOLOGICAL INFORMATION

We have argued that the two most widely held materialistic mechanisms for generating biological form are not causally adequate to produce the discrete increases of specified complexity or information that would have been necessary to produce the new Cambrian animals. But do intelligent agents have causal powers sufficient to produce such increases in information, either in the form of sequence-specific lines of code or hierarchically arranged systems of parts? Clearly, they do.

In the first place, we know that intelligent human agents have the power to produce linear sequence-specific arrangements of characters. Indeed, experience affirms that specified complex information of this type

routinely arises from the activity of intelligent agents. Human agents can generate information-rich lines of software and text. Further, whenever we encounter linear sequence-specific arrays of information and trace them back to their source, invariably we come to a mind—to that of a programmer or writer. In his essay, “DNA and the Origin of Life: Information, Specification, and Explanation,” Meyer notes, “our experience-based knowledge of information-flow confirms that systems with large amounts of specified complexity (especially codes and languages) invariably originate from an intelligent source—that is, from a mind or personal agent.” Clearly, intelligent agents have the causal powers to generate novel linear information-rich sequences of characters. To quote Henry Quastler again, the “creation of new information is habitually associated with conscious activity.”<sup>121</sup> Experience teaches this obvious truth.

Further, intelligent agents have just those necessary powers that natural selection lacks as a condition of its causal adequacy. Recall that at several points in our previous analysis, natural selection lacked the ability to generate novel information precisely because it could only act after the fact of new functional information having arisen. Natural selection can favor new proteins and genes, but only after they provide some function. The job of generating new functional genes, proteins, and systems of proteins fell instead to entirely random mutations. Yet without functional criteria to guide a search through the space of possible sequences, random variation is probabilistically doomed. What is needed is not just a source of variation (that is, the freedom to search a space of possibilities) or a mode of selection that can operate after the fact of a successful search but instead a means of selection that (a) operates during a search—before success—and (b) is informed by knowledge of a functional target.

Demonstration of this requirement has come from an unlikely quarter: genetic algorithms. Genetic algorithms are programs that allegedly simulate the creative power of mutation and selection. Richard Dawkins and Bernd-Olaf Koppers, for example, have developed computer programs that putatively simulate the production of genetic information by mutation and natural selection.<sup>122</sup> Nevertheless, as Meyer shows in his essay, “DNA and the Origin of Life: Information, Specification, and Explanation,” these programs only succeed by the illicit expedient of providing the computer with a “target sequence” and then treating relatively greater proximity to *future* function (that is, the target sequence), not actual present function, as a selection criterion.<sup>123</sup> As David Berlinski has argued, genetic algorithms need something akin to a “forward looking memory” in order to succeed.<sup>124</sup> Yet

such foresighted selection has no analogue in nature. In biology, where differential survival depends upon maintaining function, selection cannot occur before new functional sequencing arises. Natural selection lacks foresight.

What natural selection lacks, intelligent selection—that is, design—provides. Agents can arrange matter with distant goals in mind. In their use of language, intelligent human agents also routinely “find” highly isolated and improbable functional sequences within a vast space of combinatorial possibilities. Analysis of the problem of the origin of biological information exposes a deficiency in the causal powers of natural selection that corresponds precisely to powers that agents are uniquely known to possess. Agents do have foresight. Agents can also select functional goals *before* they exist. They can devise or select material means to meet those goals from among an array of other possible states and then actualize those goals in accord with a *preconceived* design and independent set of functional requirements. The causal powers that natural selection lacks—almost by definition—are associated with the attributes of consciousness, rationality, and purposive intelligence. Thus, by invoking intelligent design to explain the origin of new information, design theorists are not positing an arbitrary explanatory element unmotivated by a consideration of the evidence. Instead, they are positing an entity with precisely the attributes and causal powers that the phenomenon in question requires as a condition of its production and explanation.

Second, the highly specified hierarchical arrangements of parts in animal body plans also bespeak design. At every level of the biological hierarchy, organisms require specified and highly improbable arrangements of lower-level constituents in order to maintain their form and function. Genes require specified arrangements of nucleotide bases; proteins require specified arrangements of amino acids; new cell types require specified arrangements of proteins and systems of proteins; new body plans require specialized arrangements of cell types and organs. Organisms not only contain information-rich components (such as proteins and genes), but they comprise information-rich arrangements of those components and the sub-systems that comprise them.

Based on experience, we know that intelligent human agents have—by virtue of their rationality, consciousness, and foresight—the ability to produce information-rich arrangements of parts in which both individual modules and also the hierarchical arrangements of those modules exhibit complexity and functional specificity—information so defined. Individual

transistors, resistors, and capacitors exhibit considerable complexity and specificity of design; at a higher level of organization, their specific arrangement and connection within an integrated circuit reflects further design. Conscious and rational human agents have, as a consequence of their powers of agency, the capacity to arrange parts in functionally specified, hierarchical patterns. Further, we know of no undirected process that has this capacity. Certainly, we have good reasons to doubt that either the mutation/selection mechanism or self-organizational processes can produce such information-rich hierarchies and structures. Instead, explaining the origin of biological information (at whatever level) requires causal powers that we uniquely associate with conscious and rational activity—with intelligent causes, not purely natural processes or material mechanisms. Thus, based on our experience and analysis of the causal powers of various explanatory processes and entities, we can infer the activity of a purposeful designing agent (with rational powers not unlike those of intelligent human beings) as the best, most causally adequate, explanation for the origin of the specified information required to build the Cambrian animals. In other words, intelligent design best explains the Cambrian information explosion.

## **B. Morphological Disparity Preceding Diversity: The Top-Down Pattern of Appearance**

Design can also explain another feature of the Cambrian explosion: the so-called top-down pattern of appearance in which major morphological innovation and disparity precede minor variations of form (diversity) within those established body-plan designs. As noted above, the fossil record shows a hierarchical top-down pattern in which phyla-level morphological disparity appears first, followed only later by species-level diversity. This pattern suggests intelligent design for several reasons.

First, as noted earlier, standard materialistic models of evolutionary change are decidedly inconsistent with this pattern of fossil evidence since all such models employ what might be called bottom-up modes of causation. Neo-Darwinism, for example, seeks to explain the origin of novel body plans by starting with simpler animal forms and gradually assembling animals with more complex body plans via the gradual accumulation of small, successive material variations. Punctuated equilibrium employs a similar bottom-up strategy of explanation, albeit relying on larger jumps to move from simple to complex forms. Bottom-up models, generally, expect small-scale diversification to emerge first, followed later by enough large-scale morphological disparity to constitute a new body plan. (Self-organizational

models partially avoid making this commitment but only at the cost of invoking biologically implausible “large jump,” mutations as we have seen.) The bottom-up metaphor thus describes a kind of self-assembly in which the gradual production of the material parts eventually generates a new mode of organization for the whole. This approach suggests that the parts stand causally prior to the organization of the whole. As we have argued, however, this approach encounters both paleontological and biological difficulties: the fossil record leaves no evidence of the occurrence of such precursors, and the morphological transformations that the bottom-up approach requires are, in any case, biologically untenable. Further, the subsequent fossil record shows precisely a top-down pattern of appearance that is inconsistent with bottom-up models of evolutionary development. Bottom-up models do not produce top-down patterns. Thus, all such models lack causal adequacy as explanations for this feature of the Cambrian fossil record.

Second, the history of our own technological innovation manifests the same top-down pattern of appearance that we see in the Cambrian explosion (compare figures 15 and 22). As Stuart Kauffman has observed, “qualitative features of technological evolution appear rather strikingly like the Cambrian explosion . . . the ‘taxa’ fill in from the top-down.”<sup>125</sup> Kauffman notes that in the history of human technological innovation with objects such as guns, bicycles, cars, and airplanes, “early diversity of forms appears more radical and then settles down to minor tuning” of the basic design plan.<sup>126</sup> Since the invention of the automobile, for example, all such systems have included four wheels, two axles, a drive shaft, and a motor. Though many new variations on the original model have arisen *after* the invention of the basic automobile design, all exemplify this same basic design plan. Curiously, we observe this pattern in the fossil record. In the Cambrian fossil record, morphological disparity precedes diversity. The major animal body plans appear first instantiated by only a single (or very few) species. Then later many other varieties arise with many new features, yet with all still exhibiting the same basic body plan. Phylogeny resembles technology.

But this suggests intelligent design in the history of life. The top-down metaphor implies the persistence of an organizational plan through generations of complex systems (whether technological or biological). Yet in such top-down sequences complex systems need not have any material connection to one another. Both the Model-T and the Ford Mustang instantiate the same basic automobile design (a motor, two axles, a steering

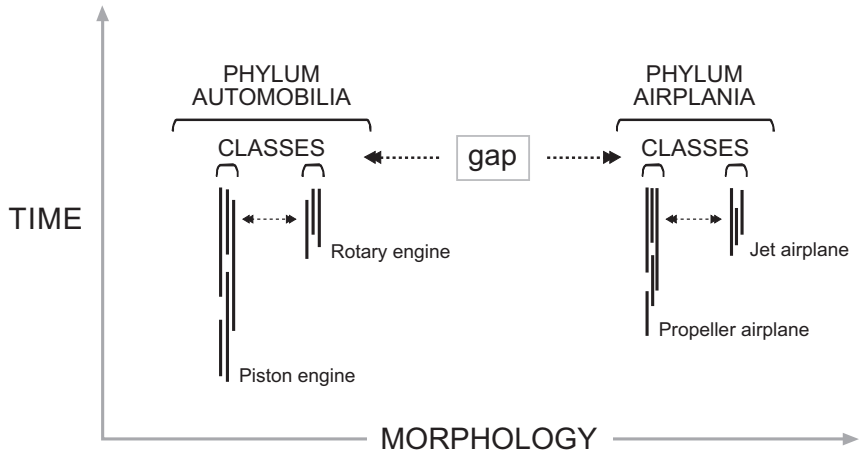


FIGURE 22. This hypothetical classification scheme suggests that the history of human technology manifests the same kind of top-down pattern of appearance and morphological isolation that is evident in the Cambrian fossil record.

column, a drive shaft, and so forth) though they share none of the same material parts. What, then, explains their continuity of organizational structure? Clearly, the answer is: an idea passed from one generation of engineers to another. In the case of different biological organisms that share a common body plan, evolutionary biologists would argue that the body plans remain constant even as the material systems instantiating them evolve gradually from one to another over many generations. Perhaps. But what explains the origin of the body plan itself that provides the pattern to which subsequent types animals will conform? We have seen that both neo-Darwinism and self-organizational mechanisms fail to explain the origin of the body plans that are necessary to establishing a top-down pattern of innovation. Further, the fossil record fails to attest to any material precursors (transitional intermediates) of these body plans. If this is so, if there are no material antecedents to the new body plans that arise in the Cambrian, could there have been a mental antecedent for them, as there most certainly has been in the case of the invention of the automobile and other technological systems that conform to the top-down pattern evident in the history of human technology?

In the top-down patterns that we know from human technology, an idea (often represented as a blueprint) stands causally prior to the assembly and arrangement of the parts of the system. A blueprint or plan for the

whole precedes and guides the assembly of parts in accord with that plan. But if novel body plans do not arise by the self-assembly of preexisting material constituents (as required by all bottom-up mechanisms of evolutionary development), where does the *plan* for the body plan come from? One possibility involves mental rather than material causation. We know from experience that intelligent agents often conceive of plans prior to the material instantiation of the systems that conform to the plans—that is, the intelligent design of a blueprint often precedes the assembly of parts in accord with a blueprint or preconceived design plan. In such systems, the parts do not generate the whole. Rather, an idea of the whole directs the assembly of the parts.

Could this form of causation explain the pattern in the fossil record? Critics of this idea could correctly point out that the fossil record can offer no direct evidence of the existence of mental cause—a preexisting design plan. Yet we lack similarly direct evidence of the ideas that shaped the assembly of parts in our own technology. An observer touring the assembly plant at General Motors plant will see no direct evidence of a prior plan (or even physical blueprint) for General Motors' new models but will perceive the basic design plan upon observing the finished product at the end of the assembly line. Such an observer will have no difficulty attributing this organizational plan to an intelligent source. Students of the history of technological systems may also perceive the activity of mind in the pattern of novel innovation followed by minor variations on an initial design concept. Indeed, we know that intelligent designers have produced precisely such top-down patterns of innovation in the history of designed systems. Thus, while the fossil record does not (and cannot) directly establish the prior existence of a mental rather than material cause, the preexistence of such a design plan could certainly explain the top-down pattern of morphological innovation evident in the fossil record. In other words, if the body plans of the Cambrian animals did arise as the result of an intelligent cause involving preconceived design plan, we would expect, from our experience of the histories of designed systems, to see precisely the kind of top-down pattern of innovation that we see in the fossil record.

Intelligent design, operating over time, often produces top-down patterns of innovation in technological systems. The Cambrian fossil record manifests such a top-down pattern. We know of no other type of cause that produces the kind of top-down patterns that are evident in both the fossil record and the history of human technology. Certainly, undirected bottom-up mechanisms of evolutionary development would not be



expected to produce such top-down patterns. Thus, intelligent design provides a better, more causally adequate explanation of the pattern of morphological innovation in the fossil record than any of its materialistic bottom-up competitors.

### C. Persistent Morphological Isolation or Disparity

The design hypothesis can also help explain why smaller-scale diversity arises *after*, and not before, morphological disparity in the fossil record and why this morphological disparity persists through geologic time.

Complex designed systems have a functional logic that makes their alteration difficult. Though the Model-A has been replaced by everything from the Yugo to the Honda Accord, the basic automobile "body plan" has remained unchanged from its first appearance in the late nineteenth century. Despite the appearance of many models, automobiles have also retained their "morphological distance" from other functionally distinct technological devices. Indeed, what we recognize as morphological disparity in biological systems has a direct analogue in our own technology. In biology, animals with different body plans differ fundamentally from each other in their overall organization. A starfish and a crab, for example, may exhibit some similarities in their low-level protein parts but they differ fundamentally in their digestive systems, their nervous systems, and in the overall organization of their organs and body parts. In the same way, automobiles and airplanes may have many similar parts, but they also differ in the composition of their distinguishing parts and in their overall organization. In both the biological and technological case, morphological discontinuities separate complex functionally integrated systems from one another.

Consider another example. The basic technology of the CD-ROM (as employed, for instance, in audio systems and computers) did not "evolve" incrementally from earlier technologies, such as magnetic media (for example, digital tape or disc storage) or analog systems such as the once-standard long-playing (LP) record. Indeed, it could not. In an analog recording, information is stored as three-dimensional microscopic grooves in a vinyl surface and is detected mechanically by a diamond stylus. This means of storing and detecting information differs fundamentally, *as a system*, from the digitally encoded pits storing data in the silvered surface of a CD-ROM, where information is detected optically, not mechanically, by a laser beam. Moreover, as a novel system, the CD-ROM had to be engineered from scratch, and, as a result, it displays a striking structural disparity or

isolation from all other types of technological devices, even those that perform roughly the same function. As Denton expresses the point, "What is true of sentences and watches is also true of computer programs, airplane engines, and in fact of all known complex systems. Almost invariably, function is restricted to unique and fantastically improbable combinations of subsystems, tiny islands of meaning lost in an infinite sea of incoherence."<sup>127</sup>

Such morphological isolation represents a distinctive feature of designed systems and is a consequence of a deeper design logic that makes the modification of basic architectures difficult or even impossible. Airplanes do not change gradually or incrementally into automobiles, nor do LP records gradually become CDs. Nevertheless, the logic of designed systems does allow minor variations within a basic body-plan design, provided the fundamental organizational plan of the original system is not altered in a way that destroys function. Experience shows a certain hierarchical relationship between functionally necessary and functionally optional features in designed systems. An automobile cannot function without two axles, but it can function with or without twin I-beam suspension, antilock brakes, or "stereo surround-sound." This distinction between functionally necessary and optional features suggests the possibility of future innovation and variation on basic design plans, even as it imposes limits on the extent to which the basic designs themselves can be altered.

The logic of designed systems, therefore, suggests why we see the limited variability within body plans that we see in the history of life and why we also see the persistent isolation (disparity) in the morphology of animals that exemplify those basic body plans. In our experience, morphologically isolated systems that perform specialized functions invariably result from intelligent design. Thus, morphological disparity or isolation constitutes a kind of diagnostic of designed systems. Intelligent agents produce systems that have this feature. Yet neither the neo-Darwinian mechanism nor self-organizational processes can account for the body plan innovation that is a necessary condition of morphological disparity at the body-plan level. Nor would we expect such mechanisms to produce the pattern of persistent isolation that we observe between the separate phyla throughout the history of life. Thus, intelligent design can offer a more causally adequate explanation of the existence and persistence of the morphological disparity in the animal forms that first appear in the Cambrian.

### D. Sudden Appearance and Absence of Ancestral Precursors

Finally, intelligent design can also explain the sudden appearance of the animal body plans that arise in the Cambrian and the absence of ancestral precursors in the Precambrian. The materialistic models of evolution that we have examined generally envision the existence of transitional intermediates leading to the emergence of distinct body plans. Though they disagree about the increments of morphological change, these theories envision bottom-up modes of causation in which material parts, or materially instantiated intermediate forms of organization, necessarily precede the emergence of fully developed new body plans. On the other hand, if body plans arose as the result of an intelligent agent acting to actualize an immaterial plan or mental concept, then material precursors to the animal body plans need not exist in the fossil record. Thus, intelligent design would expect, and thus can explain, the absence of material antecedents in the fossil record. Immaterial plans need not leave a material trace. Yet given the problems with the artifact hypothesis, none of the materialistic evolutionary models can explain the dearth of material precursors and transitional intermediates in the Precambrian rocks.

Similarly, each of the models of undirected evolutionary change that we have examined has a difficult time explaining the geologically sudden appearance of the Cambrian fauna—neo-Darwinism in part because its mechanism requires vast amounts of time; self-organization and punctuated equilibrium because they lack efficacious mechanisms of any kind. Neo-Darwinism in particular would not expect a geologically sudden appearance of animal form. As Darwin himself insisted, “*natura non facit saltum*” (nature takes no leaps). Yet intelligent agents can act suddenly or discretely in accord with their powers of purpose and volition. Thus, the geologically discrete appearance of the various animal phyla in the Cambrian fossil record does suggest the possibility of the purposeful and volitional action of a conscious agent—an intelligent designer. Darwin himself regarded evidence of saltation (sudden appearance) as evidence for an act of special creation (though he denied evidence of a real, as opposed to a merely apparent, saltation). A discrete volitional act (or acts) of creation by a purposeful designer would, therefore, explain the sudden appearance of the Cambrian animals in the fossil record. By contrast, sudden appearance stands as a formidable challenge to neo-Darwinism and to all other bottom-up models of evolutionary change. Thus, intelligent design provides a

better, more causally adequate, explanation of this feature of the Cambrian explosion as well.

## VI. Conclusion

Of course, scientists wedded to a purely materialistic explanation will instinctively deny the very possibility of top-down intelligent causation. Yet we regularly employ precisely this mode of explanation, especially when we encounter the kinds of patterns and features that we see in the fossil record. Indeed, we see in the fossil record several distinctive features or hallmarks of designed systems, including: (1) a quantum or discontinuous increase in specified complexity or information; (2) a top-down pattern of innovation in which large-scale morphological disparity arises *before* small-scale diversity; (3) the persistence of structural (or “morphological”) disparities between separate organizational systems; and (4) the discrete or simultaneous emergence of functionally integrated material parts within novel organizational body plans. When we encounter objects that manifest any of these several features and we know how they arose, we invariably find that a purposeful agent or intelligent designer played a causal role in their origin. Thus, when we encounter all these same features in the fossil record, we may infer—based upon established cause-and-effect relationships and uniformitarian principles—that the same kind of cause operated in the history of life. In other words, intelligent design constitutes the best, most causally adequate, explanation of the specific features of the Cambrian explosion, and the features of this explosion in turn attest to the activity and power of a purposeful intelligence.

## Notes

The authors wish to thank John Woester for inspiration and for sharing ideas that influenced the development of this article.

1. Francisco Ayala, “Darwin’s Revolution,” in *Creative Evolution?!*, ed. J. Campbell and J. Schopf (Boston: Jones and Bartlett, 1994), 4–5.
2. For a skeptical evaluation of the evolutionary significance of the classical Kettlewell experiments on industrial melanism: see Jonathan Wells, “Second Thoughts about Peppered Moths,” *Scientist* (24 May 1999): 13.
3. Data regarding the first appearance of the animal phyla and references used in this compilation are included in appendixes C and D.

4. S. A. Bowring, J. P. Grotzinger, C. E. Isachsen, A. H. Knoll, S. M. Pelechaty, and P. Kolosov, "Calibrating Rates of Early Cambrian Evolution," *Science* 261 (1993): 1293–98.
5. Cui Lili, "Traditional Theory of Evolution Challenged," *Beijing Review* (31 March–6 April 1997): 10.
6. Jeffrey Levinton, "The Big Bang of Animal Evolution," *Scientific America* (Nov. 1992): 84–91; Richard A. Kerr, "Evolution's Big Bang Gets Even More Explosive," *Science* 261 (1993): 1274–75; R. Monastersky, "Siberian Rocks Clock Biological Big Bang," *Science News* 144 (4 Sept. 1993): 148.
7. See appendixes C and D.
8. J. W. Valentine et al., "Fossils, Molecules, and Embryos: New Perspectives on the Cambrian Explosion," *Development* 126 (1999): 851–59.
9. J. Y. Chen, C. W. Li, Paul Chien, G. Q. Zhou, and Feng Gao, "Weng'an Biota—A Light Casting on the Precambrian World" paper presented to the Origin of Animal Body Plans and Their Fossil Records conference, Kunming, China, 20–26 June 1999, sponsored by the Early Life Research Center and the Chinese Academy of Sciences; Paul Chien, J. Y. Chen, C. W. Li, and Frederick Leung, "SEM Observation of Precambrian Sponge Embryos from Southern China, Revealing Ultrastructures Including Yolk Granules, Secretion Granules, Cytoskeleton, and Nuclei" (paper presented to North American Paleontological Convention, University of California, Berkeley, 26 June–1 July 2001).
10. Cui Lili, J. Y. Chen, G. Q. Zhou, M. Y. Zhu, and K. Y. Yeh, *The Chengjiang Biota: A Unique Window of the Cambrian Explosion*, vol. 10 (Taichung, Taiwan: National Museum of Natural Science, 1997), is currently available only in the Chinese language. The translated English version is being completed by Paul Chien, University of San Francisco.
11. J. Y. Chen, J. Dzik, G. D. Edgecombe, L. Ramsköld, and G. Q. Zhou, "A Possible Early Cambrian Chordate," *Nature* 377 (1995): 720–22; J. Y. Chen and C. W. Li, "Early Cambrian Chordate from Chengjiang, China," *Bulletin of the National Museum of Science*, (1997): 257–73; J. Dzik, "*Yunnanozoon* and the Ancestry of Chordates," *Acta Palaeontologica Polonica* 40, no. 4 (1995): 341–60. Note, however, that the assertion that *Yunnanozoon* is a chordate has been challenged. See D. Shu, X. Zhang, and L. Chen, "Reinterpretation of *Yunnanozoon* as the Earliest Known Hemichordate" *Nature* 380 (1996): 428–30; D. G. Shu, S.

- Conway Morris, and X. L. Zhang, "A Pikaia-like Chordate from the Lower Cambrian of China," *Nature* 384 (1996): 157–58.
12. Shu et al., "Pikaia-like Chordate," 157–58. Note, however, that the status of *Cathaymyrus* as a valid taxon has been challenged, with some paleontologists arguing that the single specimen of *Cathaymyrus* may actually be a dorso-ventrally compressed *Yunnanozoon*; see J. Y. Chen and C. W. Li "Early Cambrian Chordate," 257–72.
  13. See Shu et al., "Pikaia-like Chordate," 157–58; S. Conway Morris, *The Crucible of Creation: The Burgess Shale the Rise of Animals* (New York: Oxford University Press, 1998). Simon Conway Morris is currently preparing a monograph redescribing *Pikaia*.
  14. Jun-Yuan Chen, Di-Ying Huang, and Chia-Wei Li, "An Early Cambrian Craniate-like Chordate," *Nature* 402 (1999): 518–22.
  15. D. G. Shu, H. L. Lou, S. Conway Morris, X. L. Zhang, S. X. Hu, L. Chen, J. Han, M. Zhu, Y. Li, and L. Z. Chen, "Lower Cambrian Vertebrates from South China," *Nature* 402 (1999): 42–46.
  16. D. G. Shu, L. Chen, J. Han, and X. L. Zhang, "An Early Cambrian Tunicate from China" *Nature* 411 (2001): 472–73.
  17. Brian Hall, "Baupläne, Phylotypic Stages, and Constraint: Why There Are So Few Types of Animal," *Evolutionary Biology* 29 (1996): 215–61.
  18. James W. Valentine, "Why No New Phyla after the Cambrian? Genome and Ecospace Hypotheses Revisited," *Palaios* 10 (1995): 190–94. See also Jan Bergström, "Ideas on Early Animal Evolution," in *Early Life on Earth*, Nobel Symposium No. 84, ed. S. Bengtson (New York: Columbia University Press, 1994), 460–66. "There is absolutely no sign of convergence between phyla as we follow them backward to the Early Cambrian. They were as widely apart from the beginning as they are today. Hierarchical levels apparently include a biological reality, not only classificatory convention. In fact, the overwhelming taxonomic difficulty is to recognize relationships between phyla, not to distinguish between them" (Bergström, "Ideas," 464).
  19. D. Jablonski, "Micro- and Macroevolution: Scale and Hierarchy in Evolutionary Biology and Paleobiology," *Deep Time: Paleobiology's Perspective*, *Paleobiology* 26, supplement to no. 4 (2000): 15–52, esp. 24.
  20. In any case, stasis is also a pervasive characteristic of individual genera and species. The trilobite specialist Niles Eldredge of the American Museum in New York, for example, describes commencing his work in the 1960s on the trilobite species *Phacops Rana*. Eldredge sampled Middle Devonian strata across the United States only to discover that

- the trilobites did not vary smoothly and gradually between species as he had expected. They, too, exhibited stasis. Niles Eldredge and Stephen Jay Gould, "Punctuated Equilibria: An Alternative to Phyletic Gradualism," in *Models in Paleobiology*, ed. T. J. Schopf (San Francisco: Freeman, Cooper, and Company, 1972), 82–115, esp. page 107.
21. J. J. Brocks, G. A. Logan, R. Buick, and R. E. Summons, "Archean Molecular Fossils and the Early Rise of Eukaryotes," *Science* 285 (1999): 1033–36.
  22. Claude Shannon, "A Mathematical Theory of Communication." *Bell System Technical Journal* 27 (1948): 379–423, 623–56.
  23. Hubert P. Yockey, *Information Theory and Molecular Biology*. (Cambridge: Cambridge University Press, 1992), 110.
  24. Sahotra Sarkar, "Biological Information: A Skeptical Look at Some Central Dogmas of Molecular Biology," in *The Philosophy and History of Molecular Biology: New Perspectives*, ed. Sahotra Sarkar (Dordrecht: Kluwer Academic Publishers, 1996), 191.
  25. James W. Valentine, "Late Precambrian Bilaterians: Grades and Clades," in *Tempo and Mode in Evolution: Genetics and Paleontology 50 Years after Simpson*, ed. W. M. Fitch and F. J. Ayala (Washington, D.C.: National Academy Press, 1995), 87–107, esp. 91–93.
  26. Mitsuhiro Itaya, "An Estimation of the Minimal Genome Size Required for Life," *FEBS Letters* 362 (1995): 257–60; Claire Fraser et al., "The Minimal Gene Complement of *Mycoplasma genitalium*," *Science* 270 (1995): 397–403; Arcady R. Mushegian and Eugene V. Koonin, "A Minimal Gene Set for Cellular Life Derived by Comparison of Complete Bacterial Genomes," *Proceedings of the National Academy of Sciences USA* 93 (1996): 10268–73; Scott Peterson and Claire Fraser, "The Complexity of Simplicity," *Genome Biology* 2 (2001): 1–8.
  27. John Gerhart and Marc Kirschner, *Cells, Embryos, and Evolution* (London: Blackwell Science, 1997), 121.
  28. The *C. elegans* Sequencing Consortium, "Genome Sequence of the Nematode *C. elegans*: A Platform for Investigating Biology," *Science* 282 (1998): 2012–18.
  29. P. Ward, *On Methuselah's Trail, Living Fossils and the Great Extinctions* (New York: W. H. Freeman, 1992), 29–30.
  30. Charles Darwin, *The Origin of the Species* (Penguin Books, [1859] 1985), 313. See also Charles Darwin, *On the Origin of Species* (Cambridge: Harvard University Press, [1859] 1964), 307. Darwin's original quote used the "Silurian" rather than the "Cambrian" because in

Darwin's time, what we now label the Cambrian period was subsumed within the concept of the lower Silurian.

31. Susumo Ohno, "The Notion of the Cambrian Pananimalia Genome," *Proceedings of the National Academy of Sciences USA* 93 (Aug. 1996): 8475–78.
32. Richard Dawkins, *The Blind Watchmaker: Why the Evidence of Evolution Reveals a Universe without Design* (New York: W. W. Norton, 1986), 229.
33. Darwin, *Origin* (1985), 314; Darwin, *Origin* (1964), 308.
34. J. W. Valentine and D. H. Erwin, "Interpreting Great Developmental Experiments: The Fossil Record," in *Development as an Evolutionary Process*, ed. R. A. Raff and E. C. Raff (New York: Alan R. Liss, 1987), 74–77, 89, 96. See diagram on page 92.
35. Michael Foote, "On the Probability of Ancestors in the Fossil Record," *Paleobiology* 22 (1996): 141–51, 148.
36. Michael Foote and Stephen J. Gould, "Cambrian and Recent Morphological Disparity," *Science* 258 (1992): 1816.
37. Valentine and Erwin, "Interpreting," 74–77, 97. See diagram on page 92.
38. Stephen Jay Gould, *Wonderful Life: The Burgess Shale and the Nature of History* (New York: W. W. Norton, 1989), 49.
39. Richard Dawkins, *Unweaving the Rainbow: Science, Delusion, and the Appetite for Wonder* (Boston: Houghton Mifflin, 1998), 201.
40. Darwin, *Origin* (1985), 164, 168.
41. Roger Lewin, "A Lopsided Look at Evolution," *Science* 241 (1988): 292.
42. Douglas Erwin, James Valentine, and J. J. Sepkoski, "A Comparative Study of Diversification Events: The Early Paleozoic versus the Mesozoic," *Evolution* 41 (1987): 1177–86.
43. *Cycliophora* is thus far a monospecific phylum containing the species *Symbion pandora*. This organism is a small (about 350  $\mu\text{m}$  in length), baglike, ciliated metazoan that attaches itself to the mouthparts of the Norway lobster, *Nephrops*. For a description of this new phylum, see P. Funch, and R. M. Kristensen, "*Cycliophora* Is a New Phylum with Affinities to *Entoprocta* and *Ectoprocta*," *Nature* 378 (1995): 711–14.
44. Although the following considerations used for determining the possibility of a Cambrian origin for stratigraphically post-Cambrian phyla (or phyla having no fossil record) are fairly subjective, they are nonetheless a cautious inference based on important factors relevant to preservation in the geologic record. Factors taken into account in



- the determinations utilized for figures 17B, 18B, and 19B are: organism size, presence/absence of mineralized hard parts, mode of life, habitat/depositional environment, and trace fossil associations. Assumptions based on levels of complexity (that is, number of differentiated cell types) and evolutionary relatedness were not considered in the formulation of figures 17B, 18B, and 19B.
45. Of course, the pattern of body plan first appearance graphed in figures 17B, 18B, and 19B contradicts neo-Darwinism (and punctuated equilibrium) even more dramatically than the pattern graphed in figures 10A and 11A. As noted, evolutionary assumptions (about complex phyla necessarily evolving after simpler ones) provide one way of arriving at the higher estimates for the number of phyla present in the Cambrian as depicted in figures 17A, 18A, and 19A. Ironically, therefore, evolutionary assumptions lead to estimates for the number of phyla in the Cambrian that exacerbate the contradiction between current evolutionary models and the pattern of body plan first appearance. See appendixes C, D, and E.
  46. Subphyla are included here for the following reasons: (1) subphyla represent major divisions within phyla that are nearly equivalent to phyla in terms of their morphological isolation relative to each other and to other phyla; (2) phyla containing subphyla are rare (only six animal phyla have subphyla: Arthropoda, Brachiopoda, Chordata, Echinodermata, Mollusca, and Porifera) and therefore worthy of special consideration.
  47. S. Gilbert, J. Optiz, and R. Raff, "Review—Resynthesizing Evolutionary and Developmental Biology," *Developmental Biology* 173 (1996): 361.
  48. Roger Lewin, "Evolutionary Theory under Fire," *Science* 210 (1980): 883.
  49. Gilbert, Optiz, and Raff, "Resynthesizing," 357–72. See also Rudolf A. Raff, *The Shape of Life: Genes, Development, and the Evolution of Animal Form* (Chicago: University of Chicago Press, 1966); Wallace Arthur, *The Origin of Animal Body Plans: A Study in Evolutionary Developmental Biology* (Cambridge: Cambridge University Press, 1997).
  50. Gould, *Wonderful Life*, 274–75.
  51. *Ibid.*, 272, 275–76.
  52. *Ibid.*, 272–76.
  53. James W. Valentine, "The Macroevolution of Phyla," in *Origin and Early Evolution of the Metazoa*, ed. Jere H. Lipps and Phillip W. Signor

- (New York: Plenum Press, 1992), 525–53, see section 3.2, “Soft-bodied Body Fossils,” 529–31.
54. Bergström, “Ideas.” “Animals such as arthropods and brachiopods cannot exist without hard parts. The absence of remains of skeletons and shells in the Precambrian therefore proves that the phyla came into being with the Cambrian, not before, even if the lineages leading to the phyla were separate before the Cambrian” (Bergström, “Ideas,” 464).
  55. Valentine and Erwin, “Interpreting,” 74–77.
  56. James W. Valentine, “Fossil Record of the Origin of *Baupläne* and Its Implications,” in *Patterns and Processes in the History of Life*, ed. D. M. Raup and D. Jablonski (Berlin: Springer-Verlag, 1986), 209–22, esp. 215.
  57. Moreover, even if advocates of this version of the artifact hypothesis are correct about the existence of soft-bodied Precambrian ancestral forms, they still must explain the origin of the distinctive and functionally necessary hard-bodied parts (such as the arthropod exoskeleton) that actually do appear in the Cambrian. At the very least, they must explain “an explosion” of hard-bodied parts in the Cambrian.
  58. Lili et al., *Chengjiang Biota*.
  59. Eric H. Davidson, Kevin J. Peterson, and R. Andrew Cameron, “Origin of Bilaterian Body Plans: Evolution of Developmental Regulatory Mechanisms,” *Science* 270 (1995): 1319–24.
  60. William J. Schopf and Bonnie M. Packer, “Early Archean (3.3-Billion to 3.5-Billion-Year-Old) Microfossils from Warrawoona Group, Australia,” *Science* 237 (1987): 70.
  61. Jochen J. Brocks, Graham A. Logan, Roger Buick, and Roger E. Summons, “Archean Molecular Fossils and the Early Rise of Eukaryotes,” *Science* 285 (1999): 1033–36.
  62. Chien et al., “SEM Observation.” Sponges are assumed by most evolutionary biologists to represent a side branch, not a node on evolutionary tree of life leading to the Cambrian phyla. Thus, sponges are not regarded as plausible transitional intermediates between Precambrian and Cambrian forms (nor are they regarded as ancestral to the Cambrian phyla).
  63. As noted, the geological record does preserve soft tissues but only infrequently. When it does, researchers fortunate enough to make such finds will rarely want to destroy important specimens (of soft-tissue organs) in order to examine them for traces of parasitic infection or

habitation. Not surprisingly, therefore, paleontologists have not found the remains of many parasitic organisms in the fossil record.

64. Michael Foote, "Sampling, Taxonomic Description, and Our Evolving Knowledge of Morphological Diversity," *Paleobiology* 23 (1997): 181.

In the same vein, paleontologist Michael J. Benton of the University of Bristol writes, "[I]t could be argued that there are fossils out there waiting to be found. It is easy to dismiss the fossil record as seriously, and unpredictably, incomplete. For example, certain groups of organisms are almost unknown as fossils. . . . This kind of argument cannot be answered conclusively. However, an argument based on effort can be made. Paleontologists have been searching for fossils for years and, remarkably, very little has changed since 1859, when Darwin proposed that the fossil record would show us the pattern of the history of life" ("Early Origins of Modern Birds and Mammals: Molecules vs. Morphology," *BioEssays* 21 [1999]: 1043–51, esp. 1046).

65. John P. Grotzinger, Samuel A. Bowring, Beverly Z. Saylor, and Alan J. Kaufman, "Biostratigraphic and Geochronologic Constraints on Early Animal Evolution," *Science* 270 (1995): 598–604. A few Ediacarans may have survived until the middle Cambrian. See Simon Conway Morris, "Ediacaran-like Fossils in Cambrian Burgess Shale-type Faunas of North America," *Paleontology* 36 (1993), part 3: 593–635.
66. R. Monasterski, "Ancient Animal Sheds False Identity," *Science News* 152 (30 Aug. 1997): 32.
67. Mikhail A. Fedonkin and Benjamin M. Waggoner, "The Late Precambrian Fossil *Kimberella* Is a Mollusc-like Bilaterian Organism," *Nature* 388 (1997): 868.
68. Another reason the Ediacaran body fossils cannot be assigned to the animal phyla in a decisive manner is because of the coarse grain size of the beds in which they occur. Details of body form are too vague to allow a clear decision, and until better means of analysis or new beds with finer grain texture are found, these fossils will remain as intriguing "problematica," problematic forms about which it is not possible to come to a decision. See G. L. Miklos, "Emergence of Organizational Complexities during Metazoan Evolution: Perspectives from Molecular Biology, Paleontology and Neo-Darwinism," *Mem. Ass. Australas. Palaeontols* 15 (1993): 7–41. See also J. Bergström, "Metazoan Evolution around the Precambrian-Cambrian Transition," in *The Early Evolution of Metazoa and the Significance of Problematic Taxa*, ed. A. M.

- Simonetta and S. Conway Morris (Cambridge: Cambridge University Press, 1991), 25–34.
69. Some paleontologists have suggested that *Dickinsonia* and other similar Ediacarans are actually colonial prokaryotes. See Michael Steiner and Joachim Reitner, "What Are the Ediacara-type Fossils?" (paper presented to the Origin of Animal Body Plans and Their Fossil Records conference, Kunming, China, 20–26 June 1999), sponsored by the Early Life Research Center and the Chinese Academy of Sciences.
  70. Valentine and Erwin, "Interpreting," 132.
  71. Sponges (phylum Porifera) actually predate the first appearance of the other phyla present in the Ediacaran.
  72. James W. Valentine, Douglas H. Erwin, and David Jablonski, "Developmental Evolution of Metazoan Body Plans: The Fossil Evidence," *Developmental Biology* 173 (1996): 373–81, article no. 0033, 375; B. Runnegar, "Evolution of the Earliest Animals," in *Major Events in the History of Life*, ed. J. W. Schopf (Boston: Jones and Bartlett, 1992).
  73. B. Runnegar, "Proterozoic Eukaryotes: Evidence from Biology and Geology," in Bengtson, *Early Life on Earth*; J. G. Gehling, "The Case for Ediacaran Fossil Roots to the Metazoan Tree," in *The World of Martin F. Glaessner: Memoir No. 20*, ed. B. P. Radhakrishna (Bangalore: Geological Society of India, 1991), 181–223.
  74. The beginning of the Cambrian period (and the Paleozoic era) 543 million years ago is marked by the appearance of small shelly fossils consisting of tubes, cones, and possibly spines and scales of larger animals. These fossils, together with trace fossils, gradually become more abundant and diverse as one moves upward in the earliest Cambrian strata (the Manykaian Stage, 543–530 million years ago). The small shelly fossils, together with the tracks and burrows of the Vendian and earliest Cambrian, may be also be regarded, metaphorically, as part of the "burning fuse" of the forthcoming Cambrian explosion. Whether these or any of the fossils in the Ediacaran constitute true transitionals remains highly debatable.
  75. Gregory A. Wray, Jeffrey S. Levinton, and Leo H. Shapiro, "Molecular Evidence for Deep Precambrian Divergences among Metazoan Phyla," *Science* 274 (1996): 568; for a similar study of molecular sequence data that comes to the same conclusion, see Daniel Y. C. Wang, Sudhir Kumar, S. Blair Hedges, "Divergence Time Estimates for the Early History of Animal Phyla and the Origin of Plants, Animals and Fungi,"

- Proceedings of the Royal Society of London*, Series B 266 (no. 1415): 163; see also Geerat J. Vermeij, "Animal Origins," *Proceedings of the Royal Society of London*, Series B 266 (no. 1415): 525–26; see also Richard A. Fortey, Erik E. G. Briggs, and Matthew A. Wills, "The Cambrian Evolutionary Explosion Recalibrated," *BioEssays* 19 (1997): 429–34.
76. Wray, Levinton, and Shapiro, "Molecular Evidence," 568.
77. R. L. Hotz, "Finding Turns Back Clock for Earth's First Animals," *Los Angeles Times*, 25 Oct. 1996.
78. Francisco José Ayala, Audrey Rzhetsky, and Francisco J. Ayala, "Origin of the Metazoan Phyla: Molecular Clocks Confirm Paleontological Estimates," *Proceedings of the National Academy of Sciences* 95 (1998): 606–611.
79. Valentine et al., "Fossils," 851–59, esp. 856.
80. Simon Conway Morris, "Evolution: Bringing Molecules into the Fold," *Cell* 100 (7 Jan. 2000): 5–6.
81. Simon Conway Morris, "Early Metazoan Evolution: Reconciling Paleontology and Molecular Biology," *American Zoologist* 38 (1998): 870.
82. Bernard Johns and George Miklos, *The Eukaryote Genome in Development and Evolution* (London: Allen and Unwin, 1988), 293.
83. For scientific challenges to the universal common ancestry thesis (that is, the monophyletic interpretation of the history of life), see Gerry Webster and Brian Goodwin, "The Origin of Species: A Structuralist Approach," *Journal of Social and Biological Structures* 5 (1982): 15–47; Christian Schwabe, "Theoretical Limitations of Molecular Phylogenetics and the Evolution of Relaxins," *Comparative Biochemistry and Physiology* 107B (1994): 167–77; Malcolm S. Gordon, "The Concept of Monophyly: A Speculative Essay," *Biology and Philosophy* 14 (1999): 331–48; Carl Woese, "The Universal Ancestor," *Proceedings of the National Academy of Sciences USA* 95 (1998): 6854–59.
84. Elliott Sober, *The Philosophy of Biology* (San Francisco: Westview Press, 1993), 44; Peter Lipton, *Inference to the Best Explanation* (New York: Routledge, 1991), 32–88; Stephen C. Meyer, "The Scientific Status of Intelligent Design: The Methodological Equivalence of Naturalistic and Non-Naturalistic Origins Theories," in *Science and Evidence for Design in the Universe: The Proceedings of the Wethersfield Institute* (San Francisco: Ignatius Press, 2000), 151–212; Stephen C. Meyer, "The Demarcation of Science and Religion," in *The History of Science and Religion in the Western Tradition: An Encyclopedia*, ed. G. B. Ferngren (New York: Garland, 2000), 17–23.

85. Francis Darwin, ed., *Life and Letters of Charles Darwin*, vol. 1 (London: D. Appleton, 1896), 437.
86. Lipton, *Inference*, 32–88.
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