

The Cambrian Explosion: Biology's Big Bang

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I. INTRODUCTION: DESIGN WITHOUT A DESIGNER?

Both 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, 1994 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.[Darwin's] mechanism, natural selection, excluded God as the explanation accounting for the obvious design of organisms.¹

According to Darwin, and his contemporary followers, the mechanism of natural selection acting on random variation suffices to explain the origin of those features of life that once seemed to require explanation by reference to an intelligent 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 structure.

Yet does Darwinism, in either its classical or contemporary versions, fully succeed in explaining the origin of biological form and function? 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 micro-evolutionary 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.² But what about the origin of the larger-scale innovations in the history of life? What about the origin of completely new organs, body plans and structures? What about the macro-evolutionary innovation to which the fossil record attests? Can Darwinism, or neo-Darwinism, or any other model of evolutionary change, explain the origin of the basic body plans or structural “designs” of animal life, without invoking actual design?

In this paper we test the claims of neo-Darwinism, and another fully naturalistic version of evolutionary theory known as “punctuated equilibrium.” We will do so by

comparing the empirical expectations of these two theories about the history of life against the data of “the Cambrian explosion”—a term that refers to the geologically sudden appearance of at least twenty-five animal body plans 530 million years ago. We shall show that the Cambrian fossil record contradicts the empirical expectations of both these theories in several significant respects. We will further show that neither neo-Darwinism’s selection/mutation mechanism nor punctuated equilibrium’s species selection mechanism can explain the pattern of fossil evidence surrounding the “Cambrian explosion.” Instead, we suggest that actual (that is, intelligent) design explains the origin of the animal body plans in the Cambrian period better than either of the fully naturalistic mechanisms of evolutionary change currently under consideration within the scientific community.

II. THE CAMBRIAN EXPLOSION

The term Cambrian Explosion describes the geologically sudden appearance of multi-cellular animals in the fossil record during the Cambrian period of geologic time. By the close of this event, as many as forty-one separate phyla first made their appearance on earth.³ Phyla constitute the highest biological categories or taxa 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.

First, as the name implies, the fossils of the Cambrian explosion appear suddenly or abruptly within a very brief period of geologic time. (See Figure 1). As recently as 1992, paleontologists thought the Cambrian period began 570 million years ago (mya) and ended 510 mya, 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 period at 543 mya⁴ and the beginning of the first appearance of the animal phyla² (i.e., the Cambrian explosion itself) at 530 mya. (See Figure 2) These studies also showed that Cambrian explosion occurred within an exceedingly narrow window of geologic time, lasting no more than 5 million years. Geologically speaking, 5 million years represents an extremely small fraction of the Earth’s history. As Chinese paleontologist Chen Junyuan 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.”⁵ Yet almost all the major innovations in the basic architecture of living 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*).⁶

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 Ediacaran biota hold some hope in this regard, but as we will show below those hopes now seem remote. Moreover, the origin of the Ediacaran fossils themselves constitute a mystery for precisely the same reason as do the Cambrian fossils, namely, that no clear intermediates exist between the relatively complex Ediacaran animals and the much simpler bacteria and algae that preceded them.

Second, the Cambrian explosion exhibits an extraordinary morphological breadth, and completeness at the phyletic level. Cambrian rocks display at least two-thirds of the basic body plans or architectural designs of the animal kingdom. Representatives of twenty-eight of the forty-two known animal phyla definitely appear by the close of the Cambrian.⁷ (Fourteen minor phyla appear later in the fossil record, but for reasons described below almost all of these (as many as thirteen) might also have been present by the close of the Cambrian.) As Valentine, Jablonski and Erwin note, “All living phyla may have originated by the end of the [Cambrian] explosion.”⁸ Especially dramatic is the appearance of all the invertebrate phyla with mineralized exoskeletons, including the advanced metazoa such as *Mollusca*, *Echinodermata* and *Arthropoda*. Trilobites, 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 an outer shield-like keratinized exoskeleton, the major piece of which, called a carapace, 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 *Anomolocaris* (up to six feet in length) (see Figure 3) which, together with spines on the lobopods (see Figure 4) indicate 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 and from the Lower Cambrian Maotianshan Shale member 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)⁹ including members of still extant phyla such as *Cnidaria*, *Ctenophora*, *Annelida*, *Onychophora*, *Phoronida* and *Priapulida*. The Burgess Shale of Canada from the middle Cambrian (515 mya) confirms that these phyla 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.¹⁰ Cambrian-level strata show the soft body parts of jelly-fish-like organisms (known as *Eldonia*), 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.¹¹ The Chengjiang fauna also confirm the presence of animals from the Phylum *Chordata*, including most prominently *Yunnanozoon lividum*, a fusiform eel-shaped animal with, among other features, a digestive tract, branchial arches and a large notocord. Paleontologists also have found many samples of the dorso-ventrally compressed cephalochordate *Pikaia* in the Burgess Shale.¹² Additionally, J.Y. Chen and colleagues 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 *et. al.*, *Haikouella* has many of the same features of the *Yunnanozoon lividum*, as well as several additional anatomic 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 lateral eyes, and a ventrally situated buccal cavity with short tentacles.”¹³ Lastly, Simon Conway Morris and several Chinese colleagues have made a dramatic find of two small fish fossils, *Myllokunmingia fengjiaoa* and *Haikouichthys ercaicunensis*, suggesting a much earlier appearance for vertebrates than previously thought.¹⁴ These specimens resemble hagfishes and Ostracoderms (extinct bony jawless fish) respectively. As noted, in addition to these chordate specimens, the Cambrian fossil record reveals the abrupt appearance of at least two thirds of all the basic body plans of the animal kingdom (three Precambrian phyla pre-existed the Cambrian) in an explosion of creativity some 530 million-years ago.

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,¹⁵ each of these body plans exhibit clear morphological differences (and, thus, disparity) from the others. The animal body plans (as represented in the fossil record) do not grade imperceptibly one into another, either at a given time or over the course of geological history. Instead, the body plans of the animals characterizing the separate phyla maintain their morphological isolation or disparity from all the other types of animals. They also exhibit a remarkable stability or “stasis” during their time on earth.¹⁶ After the major body plans arise in the Cambrian period they maintain their characteristics without any evidence of incremental alteration. This morphological stasis or “lack of directional change” has characterized each of the animal body plans corresponding to the separate phyla since the Cambrian period. In one sense, of course, the morphological stasis of the “phyla” 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. 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 genus *Phacops*. Eldredge sampled Middle Devonian strata across the United States, only to discover, that the trilobites did not varying smoothly and gradually between species as he had expected. They too exhibited stasis.

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 three 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.¹⁷ About one billion years ago, multi-cellular grade algae appeared, followed by the gradual increase of oxygen in the Earth’s atmosphere. Then beginning about 570 million years ago, the first primitive multi-cellular animals arrived on the scene, including sponges and the peculiar Ediacaran biota. (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 (3.5-3.85 billion years ago) and the first appearance of multi-cellular algae (1 billion years ago), the emergence of the Ediacaran biota (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)¹⁸ information content of the biological world.

One way to measure the increase in the 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.¹⁹ Functionally more complex animals require more cell types to perform their more diverse functions. Each new cell type requires many new and specialized proteins. 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. For example, molecular biologists have recently estimated that a minimally complex cell would require between 318 to 562 kilobase pairs of DNA to produce the proteins necessary to maintain life.²⁰ Yet to build the proteins necessary to sustain a complex arthropod such as a trilobite would require an amount of DNA greater by several orders of magnitude (e.g., the genome size of the worm *Caenorhabditis elegans* is approximately 97 million base pairs²¹ while that of the fly *Drosophila melanogaster* (an arthropod), is approximately 120 million base pairs.²² For this reason, transitions from a single cell to colonies of cells to complex animals represent significant (and in principle measurable) increases in complexity and information content. Even *C. elegans*, a tiny worm about one millimeter long, comprises several highly specialized cells organized into unique tissues and organs with functions as diverse as gathering, processing and digesting

food, eliminating waste, external protection, internal absorption and integration, circulation of fluids, perception, locomotion and reproduction. The functions corresponding to these specialized cells in turn require many specialized proteins, genes and cellular regulatory systems, representing an enormous increase in specified biological complexity. Figure 5 shows the complexity increase involved as one moves upward from cellular grade to tissue grade to organ grade life forms. Note the jump in complexity required to build complex Cambrian animals starting from, say, sponges in the late Precambrian. As Figure 5 shows Cambrian animals required 50 or more different cell types to function, whereas sponges required only 5 cell types.

III. TESTING THE NEO-DARWINIAN AND PUNCTUATIONALIST MECHANISMS

In the following we will evaluate the efficacy of both neo-Darwinism and punctuated equilibrium as explanations for the Cambrian explosion. We will particularly seek to evaluate the neo-Darwinian mechanism of natural selection acting on random genetic variations by assessing the extent to which this mechanism can explain the key features of the Cambrian fossil record that we have just discussed. We will also test the efficacy of punctuated equilibrium's "species selection" mechanism in the same way. Because (a) neo-Darwinism especially purports to offer a truly creative mechanism of biological change and because (b) 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 of the efficacy of neo-Darwinism's mutation/selection mechanism.

Despite the common perception that the fossil record provides confirmation for the neo-Darwinian account of the origin of new biological forms, the data of the Cambrian explosion actually contradict the empirical expectations of neo-Darwinism at nearly every point. According to neo-Darwinism, biological change occurs as natural selection acts on random genetic changes and mutations, selecting those changes that favor the survival of the organisms that possess them. Over time, small-scale advantageous genetic changes accumulate, eventually resulting in large-scale changes in the morphology of organisms. Thus, according to a neo-Darwinian account, biological complexity should accumulate in a gradual bit-by-bit fashion over vast periods of geologic time.

A neo-Darwinian understanding of the mechanism for generating 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 phyla-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, a steady increase in the number of phyla over time. As noted below, punctuated equilibrium has a very similar set of expectations about what the fossil evidence should show, though, in some cases, its expectations differ in degree from neo-Darwinism's. We explain and consider each of these predictions or expectations in turn.

III.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 fossil record 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.”²³ 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.²⁴

Darwin’s prediction is significant because of his appreciation of 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 19th 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. 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. As Susumo 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 year 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 of the Kingdom *Animalia* within the time span of 6-10 million years can’t possibly be explained by mutational divergence of individual gene functions.²⁵

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 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 intermediates forms that Darwinian gradualism entails. Indeed, since the variation/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 6 and 7). 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. In the words of Oxford Zoologist Richard Dawkins: “It is as though they [the invertebrate phyla] were just planted there, without any evolutionary history.”²⁶

Darwin was, of course, well aware even in the 19th 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.”²⁷ Contrary to Darwin’s hope, however, in the 140 years since the publication of the *Origin of Species*, 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 in 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.

The difficulty posed by the absence of transitional intermediates for both neo-Darwinism and, to a lesser but significant extent, punctuationalist evolutionary theories is illustrated below. The diagrams below graph morphological change versus time. The first diagram shows the Darwinian and neo-Darwinian expectation that changes in morphology should arise gradually as minute micro-evolutionary changes accumulate. This Darwinian commitment to gradual phyletic change via microevolution, produces the classic representation of the history of life as a branching tree. (Figure 8a)

The second diagram (Figure 8b) 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, in so far 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. The diagram below details how punctuationalists conceive of evolutionary change, and thus also, their expectations for what the fossil record ought to show. According to many

punctuationalists, 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 8b shows, punctuationalists still envision many transitional forms as a result of a series of rapid evolutionary changes (albeit representing larger jumps in morphology).

The Figure 8c 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 occurs *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 7) Fewer have recognized, however, that the absence of transitional forms also represents a severe (if relatively lesser) difficulty for punctuated equilibrium. Note that both standard neo-Darwinian and more recent punctuationalist 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 phyla, but virtually all the phyla represented in Cambrian explosion. (See section IV.B below).

In a seminal paper titled “Interpreting Great Developmental Experiments: The Fossil Record,” (from which diagrams A and B above are derived),²⁸ 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.”²⁹ Clearly, neo-Darwinism does not explain this pattern. But as Valentine and Erwin point out, neither does punctuated equilibrium. For one thing, 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. . .”³⁰

Recent work on statistical paleontology by Michael Foote of the University of Chicago, 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.”³¹ His method provides a way to evaluate as he puts it, “whether the small number of documented major

transitions provides strong evidence against evolution.”³² Because variables [a], [b] and [d] are reasonably well established, [c] the time required for plausible mechanisms to produce macro-evolutionary 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 [a], [b], and [d], 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, [c] must be very low. In other words, the explanatory success of punctuated equilibrium depends upon the existence of a mechanism that can produce rapid macro-evolutionary change. As Foote and Gould note elsewhere, the punctuationalist model of Cambrian evolution requires a mechanism of unusual “flexibility and speed.”³³ As yet, however, neither Foote, 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”³⁴ and thus, we now require “a [new] theory for the evolution of novelty, not diversity.”³⁵

III.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 addressed by this paper, “What are the mechanisms to account for disparity?” 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 themes, whereas diversity refers to the variations on those themes.³⁶

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 8 and 9). 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 molluscs, which we see as built upon utterly different ‘fundamental body plans’ were once just two species within a genus.³⁷

Indeed, because the selection/variation 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 9) 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:

the 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...³⁸

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.³⁹

Thus, Darwin described small-scale variations producing new species, genera, and orders. This process would doubtless, on a Darwinian view, continue 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 8b also shows). Thus, for both current evolutionary models, novel body plans (disparity) are built bottom-up as the result of many smaller-scale genetic changes (i.e., diversity).

The actual pattern in the fossil record, however, contradicts this prediction. (See Figures 10). 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. (See Figures 8c and 10). 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.⁴⁰

Or as Erwin, Valentine, and Sepkowski note 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.⁴¹

In other words, instead of numerous species and other representatives of lower-level taxa appearing first, building to the disparity of higher taxa, the highest taxonomic differences (i.e., those between phyla) appear first (instantiated by very few species-level representatives) followed later by class level differences, order level differences and so on.

In another article in *Science* entitled “A Lopsided Look at Evolution,”⁴² Roger Lewin documents this unanticipated pattern in the fossil record. He also quotes David Jablonski of the University of Chicago and David Bottjer of the University of Southern California as saying “The most dramatic kinds of evolutionary novelty, major innovations, are among the least understood components of the evolutionary process.”⁴³ He thus concluded that “the most obvious message is that a simple extrapolation from one level to another is an unlikely explanation of evolutionary innovation at the different levels.”⁴⁴ In other words, the neo-Darwinian mechanisms responsible for micro-evolutionary change cannot be extrapolated to explain macro-evolutionary innovation, including the origin of major body plans in the Cambrian period.

III.C. Prediction Number 3: The morphological distance between organic forms and thus the number of phyla will increase gradually over time.

According to Darwinism, 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 11). As can be seen, 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 12a and 12b graph numerically the first appearance of all animal phyla over geological time. Figure 12a graphs the first appearance of animal phyla based solely on the present body of paleontological evidence. Figure 12b graphs the total number of phyla that are often assumed to have had their first appearance in the Cambrian based on either evolutionary or geological/environmental considerations or both. 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, many neo-Darwinists and punctuationalists have assumed that these simpler phyla must have been present in the Cambrian. Additionally, theoretically independent 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 which have no fossil record at all, have one or more features that render their preservation unlikely. Thus, these factors suggest, independent of evolutionary assumptions, reasons for suspecting a Cambrian appearance for many of the phyla that first appear in the fossil record later. Indeed, only one of the fourteen post-Cambrian phyla (phylum *Acanthocephala*—gut parasites of vertebrates) can be definitively excluded from a Cambrian first appearance given present knowledge.

Of course, how one weighs and assesses these various factors will result in differing estimates for the number of phyla that first appear during the Cambrian. Values ranging from 60% to 95% of all phyla are consistent with existing data. Though we are skeptical of strictly presuppositionally driven arguments, we do favor, on geological and environmental grounds, estimates that tend toward the mid to high end of this range.⁴⁵ Nevertheless, Figures 10a and 10b graph phyletic first appearance 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 phyletic first appearance. Indeed, rather than conforming to neo-Darwinian and punctuationalist expectations of a steadily increasing number of phyla over geologic time, the fossil record shows a very different pattern; namely, a sudden burst of phyletic first appearance in the Cambrian, followed either by (as in 10a) a few small subsequent bursts (involving simple, phyla), or (as in 10b) a nearly complete quiescence of phyletic first appearance after the Cambrian.⁴⁶ Indeed, for 525 million years after the Cambrian explosion, and for three billion years before it, the fossil record does not show anything like a steadily increasing number of new phyla. Nor can the sudden explosive appearance of between 25 and 38 new phyla within a five million year window during the Cambrian period fit the pattern of steady

increase that one would expect given either of the two current evolutionary models.

We have provided two other graphs that reinforce these points. Several animal phyla actually comprise several separate subphyla. These sub-phyla represent major morphological divisions within their respective phyla (distinctions even greater than those seen between classes). Since we can regard subphyla as nearly equivalent to phyla,⁴⁷ we have also graphed Figures 11a and 11b to show the stratigraphic first appearance, and presumed first appearance, not only for all the animal phyla, but also for the eighteen animal subphyla. Figure 13a graphs the first appearance of the phyla and subphyla on strictly empirical grounds. Figure 13b graphs the presumed first appearance of the phyla and subphyla conceding the most favorable estimates taking the other considerations discussed above into account. Again we see, to an even more pronounced degree, that the pattern first appearance (of the phyla and sub-phyla) contradicts that predicted by both the neo-Darwinian and punctuationalist mechanisms.

III.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 phyletic 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. Though, as we have seen, the newer punctuationalist 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 inverted cone of diversity and the pattern of phyletic first appearance. Furthermore, punctuated equilibrium lacks a sufficient mechanism to explain the origin of the major body plans in the Cambrian strata.

These problems underscore a more significant theoretical difficulty for evolutionary theory generally, namely, the insufficiency of attempts to extrapolate micro-evolutionary mechanisms to explain macro-evolutionary development. As developmental biologists Gilbert, Opitz, and Raff have noted:

The Modern Synthesis is a remarkable achievement. However, starting in the 1970's, 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.⁴⁸

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.⁴⁹

The origin of major innovations and complexity are increasingly recognized as unsolved problems for all fully naturalistic versions of evolutionary theory, and biologists, especially developmental biologists, are beginning an intensive search for solutions.⁵⁰ Before considering whether intelligent design should be considered in this search, we will consider some objections to arguments that we have marshaled against the adequacy of neo-Darwinism and punctuated equilibrium.

IV. OBJECTIONS

IV.A. The Artifact Theory: Is The Cambrian Explosion Real?

Many have argued that absence of Precambrian transitional intermediates does not disconfirm neo-Darwinian predictions, but instead testifies to the incompleteness of the fossil record. Indeed, 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, but the fossil record. Initially, however, Darwinists adopted a different approach. For many decades after the publication of the *Origin of Species*, 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 hypotheses were proposed to explain the missing ancestors, all falling under the heading of the “artifact theory.” The artifact theory holds that the fossil ancestors existed, but for various reasons were not preserved in an “imperfect and biased” fossil record. On this theory, the absence of the fossil ancestors represents “an artifact” of incomplete sampling, a not accurate representation of the history of life. Gaps in the fossil record are apparent, not real.

A popular version of the artifact theory was proposed by the prominent American geologist, Charles Walcott, in the early 1900s. Taking his lead from Darwin, Walcott proposed a so-called “Lipalian interval.” According to Walcott, the ancestors of 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 the (then) 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.⁵¹ Thus, he 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 Lipalian 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 off-shore drilling technology advanced to allow for the sampling of the buried offshore sedimentary rocks. Unfortunately for Walcott's hypothesis, such technology has now been developed and offshore drilling cores have repeatedly failed to verify the existence of the predicted Precambrian fossils.⁵²

Various other forms of "missing strata" hypotheses have been proposed over the years to explain the missing ancestors. Some have claimed that rocks containing the requisite Precambrian transitional fossils have been metamorphosed or melted beyond recognition. Others have 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.⁵³

Proponents of the artifact theory have advanced other explanations. One asserts that the Precambrian ancestors of the Cambrian animals lacked hard parts such as shells and exoskeletons. Thus, we should not expect to find remains of these ancestral forms in the fossil record. While clearly the fossil record does not preserve soft body parts of organisms as frequently as hard body parts, it has preserved enough soft body animals and organs to render this version of the artifact theory suspect. Indeed, several phyla are known to have entirely soft-bodied representatives in the Cambrian.⁵⁴ Even so, none of the Precambrian organisms present in Chengjiang 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 appears far too great.

Furthermore, the postulation of exclusively soft-bodied ancestors for hard-bodied Cambrian organisms seems implausible on anatomical grounds.⁵⁵ Many phyla such as brachiopods 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.⁵⁶ As Valentine notes for the brachiopod, "the brachiopod Bauplan cannot function without a durable skeleton."⁵⁷ 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.⁵⁸ As Chen and Zhou explain:

"animals 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.”⁵⁹

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.⁶⁰ 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.⁶¹ 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.⁶² If paleontologists can find minuscule single cells in formations which are far older (and therefore far rarer 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 biota clearly reveal the presence of tiny sponge embryos⁶³ at the very earliest stages of cell division. Again, if fossils have revealed such tiny features in Precambrian strata, why have they not turned up any of the allegedly miniature transitional or ancestral forms of Cambrian animals?

Of course, there are good reasons why many organisms do not appear in the fossil record, even though they may have existed long before present times. In our discussions above of the completeness of the Cambrian fossil record and the pattern of phyletic first appearance we noted as much. Nevertheless, the factors that render preservation unlikely in general do not help to account for the specific absence of Precambrian ancestral forms. We know that near-shore 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).⁶⁴ 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 near shore 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 animal remains in fine detail. Yet no forms plausibly ancestral 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. University of Chicago

paleontologist Michael Foote⁶⁵ 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 (i.e., those corresponding to the nodes). As more and more fossil finds fall within existing phyletic 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, Foote argues based on sampling theory that "we have a representative sample of morphological diversity and therefore we can rely on patterns documented in the fossil record."⁶⁶ 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."⁶⁷

IV.B. The Ediacaran/Vendian Radiation

As we have seen above, some have attempted to defend neo-Darwinism by questioning the completeness of the fossil record. Nevertheless, others have defended it by accepting the testimony of the fossil record, but by denying that the record fails to reveal ancestral forms. Recently, a few biologists have suggested that an enigmatic group of multi-cellular organisms known as the Ediacaran fauna might represent transitional intermediates to the Cambrian animals—a kind of "fuse" on the Cambrian explosion.

The Ediacaran fauna derive its name from its most notable locality, the Ediacaran hills in the outback of Southwestern Australia. Some paleontologists also refer to the Ediacaran fauna as the Vendian fauna (for the name of the late Precambrian period of geological time in which it first appeared) or Vendobionta. Paleontologists have made additional discoveries of the Ediacaran fauna in England, Newfoundland, the White Sea in northwestern Russia, and the Namibian desert in southern Africa, thus suggesting a near world wide distribution of these organisms during the Vendian (i.e., the late Precambrian). 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 Ediacaran at 565 mya, and the last appearance at the Cambrian boundary about 543 mya.⁶⁸

The Ediacaran fauna comprise three types of fossils all of which first appeared between 565 and 543 mya. The first includes a strange group of organisms such as 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 of fossils include trace fossils (the possible remains of animal activity) such as tracks, burrows and fecal pellets. These may represent the remains of primitive worm-like creatures or primitive mollusks. The third 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 Ediacaran. There, Russian scientists have discovered 35 distinctive specimens of *Kimberella*, a simple animal form. These new White Sea specimens, dated at 550 Mya, show that *Kimberella* “had a strong, limpet like shell, crept along the sea floor, and resembled a mollusk.”⁶⁹ Paleontologist Douglas Erwin of the Smithsonian Institution in Washington D. C. has commented that “its the first animal that you can convincingly demonstrate is more complicated than a flatworm.”⁷⁰ 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.⁷¹ The authors of the original descriptive paper in *Nature*, Mikhail Fedonkin from the Russian Academy of Sciences and Benjamin Waggoner from University of California at Berkeley, conclude on the basis of their finds that “metazoan triploblastic lineages, including ‘molluscan-grade bilaterians’, began to diversify before the beginning of the Cambrian.”⁷²

Though fascinating, the presence of the Ediacaran fauna in the 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 the visible fossilized organisms (as opposed to trace fossils) bear no clear relationship to any of the organisms in the Cambrian explosion (or thereafter).⁷³ Indeed, some scientists doubt that organisms such as *Dickinsonia* even belong in the animal Kingdom.⁷⁴ 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.*⁷⁵ [Emphasis Added]

Second, even granting the most optimistic estimates of the significance of trace fossils, the Ediacaran fauna represent very few types of animals, three (or at most four) phyla (mollusca, porifera and possibly cnidaria and a worm phylum⁷⁶). Though the *Dickinsonia* and other similar organisms may have too many morphological dissimilarities with known Cambrian animals to qualify as probable ancestral forms, some have argued that the organisms responsible for Ediacaran trace fossils may tell a different story. They note that Ediacaran trace fossils consist of surface tracks and burrows, along with fecal

pellets, which, though small, could only have been made by animal 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.⁷⁷ These inferred physical characteristics would indicate organisms of “organ grade” complexity, above that of flatworms. Some paleobiologists have speculated that the tracks, burrows and feeding trails indicate the existence of two (probably mollusca and a worm phyla) or so types of animals prior to the Cambrian.⁷⁸

Much of the discussion about trace fossils is, of course, necessarily speculative. Nevertheless, even on the most optimistic interpretation, these remains suggest the existence of no more than two or so animal body plans (of largely unknown characteristics). Thus, the Ediacaran data taken as a whole hardly establishes the existence of the wide variety of transitional intermediates that neo-Darwinism and punctuated equilibrium require in order explain the origin of the animal phyla in the Cambrian. First, even if one grants that representatives of three phyla did exist in the Ediacaran, it does not follow that these forms were transitional intermediates. Some were, or may have been, representatives of known Cambrian phyla, thus demonstrating not a gradual transformation, but instead only the earlier appearance of a few previously known phyla. Further, the Cambrian attests to organisms representing at least twenty-eight phyla. In the best case, the Ediacaran organisms represent ancestral forms for, at most, just a few (three or four) Cambrian animals. This leaves nearly ninety percent of the Cambrian phyla with no such ancestors in the Precambrian rocks.

There is another reason that the Ediacaran fauna does not make it easier for neo-Darwinism to explain the pattern of appearance in the fossil record. The Ediacaran fauna 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 Ediacaran organisms such as *Kimbrella* and *Dickinsonia* (and sponges which appear only slightly earlier), the only living forms documented in the fossil record for over three billion years are one-celled organisms and colonial algae. The emergence of primitive molluscs, the two-dimensional animal-like *Dickinsonia*, 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 may attest to a separate sudden increase in biological complexity with the emergence of a few true animal forms (representing phylum *Mollusca* and possibly *Cnidaria* and a worm phylum) within a short window of geological time (less than 15 million years) following roughly three billion years in which only bacteria and algae inhabited the earth. The complexity jump required by the appearance of true animals in this short period of time again appears to exceed the explanatory resources of either the selection/mutation or the species selection mechanism (see discussion in Section V.A below). Thus, the appearance of the Ediacaran fauna does not solve the problem of

the sudden increase in biological complexity during the Cambrian, it constitutes another, though lesser, manifestation of the same problem in the earlier strata of the Vendian.

Finally, even if one regards the appearance of the Ediacaran animals as a kind of “fuse” on the Cambrian explosion,⁷⁹ the total time encompassed by the Vendian and Cambrian radiations still remains exceedingly brief relative to neo-Darwinian expectations and requirements. Only forty million years elapsed between the beginning of the Vendian radiation (565 Mya) and the end of the Cambrian explosion (525 Mya). This represents about 7% of the time that modern neo-Darwinists expect for the development of complex animals from their alleged common ancestor (see discussion of deep divergence below), and, by nearly all accounts, far less time than the selection/mutation mechanism would require to build such animals (see Section V.A below). 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 re-dating) status—hardly a positive state of affairs for advocates of neo-Darwinism.

IV.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 pre-Cambrian, beginning from a common ancestor, some 1.2 billion years ago. To support these 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 Gregory A. Wray, Jeffrey S. Levinton, and Leo H. Shapiro, entitled "Molecular Evidence for Deep Precambrian Divergences Among Metazoan Phyla"⁸⁰, 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). Wray *et. al.* 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 theory, namely, that Precambrian ancestors existed in an exclusively soft-bodied form until the Cambrian explosion occurred.

Wray *et. al.* 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 different animals began to diverge from each other, Wray *et al.* 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 the study of Wray, *et al.* was to disconfirm the traditional view "that the animal phyla diverged in an 'explosion' near the beginning of the Cambrian period."⁸¹ They argue rather 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."⁸² And, they conclude, "[o]ur 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."⁸³

From a neo-Darwinian point of view, the results of Wray's study seem almost axiomatic, since the neo-Darwinian mechanism would require extensive amounts of time to produce the specified complexity 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."⁸⁴ Nevertheless, the "deep divergence" hypothesis suffers from several severe difficulties. First, the postulation of an extensive 700 million year period of undetectable evolution (from a paleontological point of view) remains highly problematic. As noted above, the preservation of numerous soft-bodied Cambrian animals, as well as Precambrian embryos and microorganisms (the latter dating from 3.5 billion years), undermines the plausibility of those versions of the artifact theory that invoke an extensive period of soft-bodied evolution as the reason for an absence of Precambrian transitional intermediates. Moreover, the existence 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 (e.g., a crab or an insect) exist without its exoskeleton. Any plausible ancestor to such organisms should have had hard body parts to fossilize, yet none have been found in the Precambrian.

The analysis of Wray *et al.* has a second difficulty: its results vary dramatically from other similar sequence comparisons. In a more recent publication, Ayala *et al.* have recalculated the divergence times, using the same protein-coding genes as Wray *et al.* (but eliminating 18S rRNA, an RNA-coding gene, because of problems with obtaining a reliable alignment), and adding an additional 12 protein-coding genes. Correcting what they argue are "a host of statistical problems"⁸⁵ in the Wray *et al.* study, Ayala and colleagues 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 *et al.*, "are fraught with danger."⁸⁶

Nevertheless, to the extent that such estimates can be made, contend Ayala *et al.*, their results correspond with the standard paleontological estimates.

Third, all analyses of sequence data make assumptions that raise serious questions about their reliability as indicators of very ancient common ancestors. For example, all sequence analyses assume, rather than demonstrate, the doctrine of 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. In effect, 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. These analyses also presuppose that mutation rates of organisms remained relatively constant throughout geological time.

Both these assumptions are problematic.

First, whether the Cambrian animals had a common ancestor is part of the point at issue, or should be.⁸⁷ 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 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 employ a tacitly neo-Darwinian assumption to legitimate an explicitly neo-Darwinian claim does not provide evidential warrant for the claim. Certainly, it provides no reason for privileging molecular evidence over fossil evidence.

Second, the basic housekeeping proteins (and ribosomal RNAs) that Wray *et al.* analyzed would have had little role in the origin of novel body plans. Nearly all of the proteins analyzed by Wray *et al.* are found in any organism, from the simplest one-celled prokaryotes or protists (eukaryotes) to multi-cellular 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 *et al.* 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.”⁸⁸ The kinds of proteins that Wray *et al.* did analyze simply do not suffice to explain body plan formation. Yet Wray *et al.* use their analyses of the differences between these molecules to make a claim about the time at which body plans began to diverge.

Third, even if one assumes that the extrapolation of micro-evolutionary Darwinian processes over time can account for the emergence of novel proteins and body plans, one cannot assume that the protein molecular clock ticks at a constant rate. Unlike radiometric clocks, molecular clocks depend upon a whole host of contingent factors, both biological and environmental. 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.”⁸⁹ Moreover, many environmental factors influence mutation rates, including the many 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 550 Mya) with which to calibrate the molecular clock, its reliability in dating the origin of the Cambrian animal phyla (at between 1 and 1.2 bya) remains highly questionable.⁹⁰ 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.⁹¹

Thus, as paleontologist Simon Conway Morris concludes, “a deep history extending to an origination in excess of 1,000 Myr is very unlikely.”⁹²

V. EVIDENCE OF DESIGN?

Our discussion has suggested the inadequacy of the neo-Darwinian and punctuationalist mechanisms as explanations for the origin of the new organisms and body plans that arise in the Cambrian period. We have suggested that the punctuationalist model of evolutionary change also fails to explain key features of the fossil record. In this section, we now expand our critique of these models of undirected evolutionary change and propose an alternative. In particular, we want to suggest that the pattern of Cambrian fossil evidence suggests intelligent foresight, planning and design—not merely apparent design. We will argue, moreover, that the design hypothesis constitutes a better—more causally adequate—explanation than its naturalistic competitors for the salient features of the fossil record that we have analyzed above.

Opponents of the contemporary design hypothesis object to it claiming that it constitutes an argument from ignorance. Since, critics charge, we don't know yet know how certain features of organisms arose, design theorists invoke intelligent design to cover our ignorance. Yet design theorists do not infer design just because known natural processes cannot explain the origin of certain features of biological organisms. Rather they infer design because biological organisms manifest distinctive features, hallmarks or positive indicators of intelligently design systems—that is, organisms possess features that in any other realm of experience would trigger the recognition of prior intelligent activity. For example in his book *Darwin's Black Box*, Michael Behe⁹³ has inferred design not only because the gradualistic mechanism of natural selection acting on random variation does not seem sufficient to produce “irreducibly complex” systems, but also because in our experience “irreducible complexity” is invariably a feature of systems known to have been designed by intelligent agents or engineers. That is, whenever we see systems that have the feature of irreducible complexity and we know the causal story about how such systems originated, invariably intelligent design played a role in the origin

of such systems. Thus, Behe infers intelligent design as the best explanation for the origin of irreducibly complexity in cellular molecular motors, for example, based upon what we *know*, not what we do not know, about the causal powers of nature and intelligent agents, respectively.

Similarly, earlier in this volume Stephen Meyer (writing on his own) argued that the “specified complexity” or “information content” of DNA and proteins implicates a prior intelligent cause, again because “specified complexity” and “high information content” constitute a distinctive hallmark (or signature) of intelligence. Indeed, in all cases where we know the causal origin of “high information content” or “specified complexity,” experience has shown that intelligent design played a causal role. Thus, when we encounter such information in the bio-macromolecules necessary to life, we may infer—based upon our *knowledge* of established cause-effect relationships—that an intelligent cause operated in the past to produce the information necessary to the origin of life. Design theorists infer a past intelligent cause based upon knowledge of present cause and effect relationships. Inferences to design thus employ the standard uniformitarian method of reasoning used in all historical sciences. These inferences do not constitute arguments from ignorance any more than any other well-grounded inferences in geology, archeology or paleontology—where provisional knowledge of cause-effect relationships derived from present experience guides our inferences about the causal past.

Our inference to intelligent design based upon the data of the Cambrian explosion will employ a similar method of reasoning. We have already shown that present naturalistic models of explanation do not adequately explain the pattern of fossil evidence associated with the Cambrian explosion. We will now argue that, based upon our experience, intelligent design does provide a better explanation of the salient features of the Cambrian fossil data. We now consider these features (in the roughly the reverse order as they were discussed in Part II).

V.A. The “Quantum” Increase in Specified Biological Information

To build an animal—that is, a multi-cellular system with specialized tissues, organs, and architectural features—from a single-celled organism requires a vast amount of new functionally specified information. Suppose we begin with single-celled eukaryotes (say, ciliated protists such as *Tetrahymena* or *Paramecium*), and ask what separates such organisms from a trilobite or a mollusk. As noted above, one useful metric of complexity is number of cell types.⁹⁴ (See Figure 5) 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. To build an animal, therefore, requires at a minimum building novel cell types. But cell types themselves require specialized proteins. An epithelial cell lining a gut or intestine which secretes a digestive enzyme, for instance, requires (minimally) structural proteins to modify its shape, regulatory enzymes to control the secretion of the digestive enzyme, and, the digestive enzyme itself. All such novel proteins will derive from novel gene sequences—that is, from new specified information. Moreover, 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 can we best explain such a discontinuous or “quantum” increase in biological information? As Meyer argued in a previous essay about the origin of life, intelligent design does provide 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.”⁹⁵ Yet whether intelligent design constitutes a necessary or best causal explanation for the biological information that arises in the Cambrian depends upon whether or not other causally adequate explanations exist. In Meyer’s previous discussion of the origin of genetic information in a pre-biotic 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 pre-biotic natural selection acting on random variations, nor physical-chemical necessity (i.e, self-organization) sufficed to explain the origin of biological information starting from simple chemistry. Since only intelligent design suffices 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. And, as Meyer noted, aperiodic specified information of any type, cannot in principle arise from self-organizational principles or laws of necessity. Nevertheless, neo-Darwinists would argue that in a biological as opposed to a pre-biotic context, the neo-Darwinian mechanism of natural selection acting on random variation does play a significant role in generating novel information. Thus, for intelligent design to stand as *the best*, rather than just *a plausible*, explanation for the origin of biological information in the Cambrian, one must show the inadequacy of the Darwinian mechanism as an explanation for the origin of the information required to build a new body plan.

V.A.1. Natural Selection, Genes and Proteins

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. Neo-Darwinists assume that, given the complexity of proteins and DNA (to say nothing of whole organisms), chance variations and mutations alone will not suffice to explain the origin of new biological forms. Richard Dawkins, for example, likens an organism to a high mountain peak. He compares the task of climbing the sheer precipice up the front side of the mountain to that of building a new organism by chance. He acknowledges that this approach up “Mt. Improbable” will not succeed. Yet he suggests that there is a gradual slope up the back side of the mountain that could be climbed in

small incremental steps. In his analogy, the back side up “Mt. 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, natural selection (acting on random variations and mutations) can accomplish through the cumulative effect of many slight successive steps. Thus, according to neo-Darwinists, evolution does not leap from one cell type directly to five, or from 6,000 genes to 10,000, but occurs as natural selection preserves many small, advantageous mutations resulting initially in new individual proteins.

Even so, neo-Darwinism still envisions biological information arising initially from random mutations in the genetic text. According to the synthetic theory, novel biological information first arises as the result of mutations in DNA and then gradually accumulates as natural selection favors any resulting functionally advantageous changes. Natural selection can only select what random variations and mutations first generate. Thus, even in neo-Darwinism, random mutations remain the initial engine of information generation.

This ineliminable element of randomness poses several probabilistic problems for neo-Darwinism, even if one takes the action of natural selection into account. First, experimental work in molecular biology, particularly some using a technique known as cassette mutagenesis, has shown that proteins (and thus the genes that produce them) are highly specified relative to biological function.⁹⁶ Though many amino acid sites do tolerate considerable variation, many key active sites in proteins do not. At many active sites any amino acid substitution will result in a radical loss of biological function.⁹⁷ Moreover, even many sites that allow some variation still do not allow just any amino acid as a substitute.⁹⁸ Further, multiple as opposed to single amino acid substitutions very quickly result in functional loss, even at sites that allow considerable variation when all other sites are not changed (from their wild type).⁹⁹ The cumulative affect of these constraints suggests that the set of functional polypeptide sequences represents an exceedingly small proportion of the total number of combinatorial possibilities and that, as a consequence, individual proteins represent highly improbable arrangements of matter.¹⁰⁰

Second, developments in probability and complexity theory have made possible a rigorous calculation of the Universal Probability Bound—the point at which appeals to chance in explanations become unreasonable even on a cosmic scale. In particular, the probability theorist William Dembski¹⁰¹ has recently refined the work of the earlier probabilist Emile Borel. Dembski shows that chance can be eliminated as a plausible explanation for specified systems of small probability, whenever the complexity of the system exceeds the available probabilistic (or more, precisely, specificational)¹⁰² resources. He then (conservatively) calculates a universal probability bound of $1/10^{150}$ corresponding to the probabilistic/specificational resources of the known universe. This number provides a theoretical basis for excluding appeals to chance as the best explanation for specified events of probability less than $1/2 \times 1/10^{150}$. As Richard Dawkins has said, “we can accept a certain amount of luck in our explanations, but not too much.”¹⁰³ Dembski’s work establishes a theoretical upper limit on the amount of “luck” that any theory can plausibly invoke in explanation.

Conjoining the results of cassette mutagenesis experiments with Dembski's analysis, implies that random variations or mutations will not, in all probability, suffice to produce many of the essential genes and proteins necessary to the morphological innovations that appear with Cambrian animals. As Meyer discussed in an earlier essay, the improbability of randomly assembling even a modest protein (150 or so amino acids in length) in a pre-biotic domain vastly exceeds the so-called Universal Probability Bound, the point at which appeals to chance become unreasonable given the probabilistic resources of the entire universe.¹⁰⁴ Of course, the odds of generating a functional protein of the same length in a biotic, as opposed to a prebiotic, domain improve considerably (due to the homochirality of amino acids *in vivo* and the existence of an apparatus for polymerizing amino acids correctly [i.e., with peptide linkages]). Nevertheless, the complexity of the proteins required to achieve significant morphological innovations frequently far exceeds that of the simple 100-150 amino acid long molecules evaluated in the pre-biotic case. Recall that cassette mutagenesis work fixed the probability of attaining the correct sequencing at random for a single short protein 100 amino acids in length at less than 1 chance in 10^{65} . This number does not exceed the Universal Probability Bound (the point at which appeals to chance become unreasonable given the probabilistic resources of the entire universe), but it does arguably exceed the probabilistic resources corresponding to the time available for macroevolutionary transitions on the ancient earth.¹⁰⁵

In any case, the morphological changes required by macro-evolutionary transitions require many longer proteins with highly specialized functions. Susumu Ohno has noted that many Cambrian animals would have required complex proteins such as hemoglobin.¹⁰⁶ Hemoglobin molecules in extant organisms comprise more than 580 amino acids, many of which (especially in the protein's center) cannot be changed without dramatic losses of function.¹⁰⁷ These molecules represent vastly improbable (and information rich) arrangements of matter. Reasonable extrapolations of Sauer's work suggest that the probability of producing functionally sequenced proteins of this length at random far exceeds the Universal Probability Bound of 1 chance in 10^{150} . Clearly, random mutations alone will not explain the origin of the functionally specified genetic information necessary to produce many of the proteins necessary to major morphological innovations.

Of course, neo-Darwinists do not envision a completely random process of information generation or a random search through the space of combinatorially possible nucleotide sequences. They see natural selection acting to preserve small advantageous variations in genetic sequences and their corresponding protein products. Yet, the extreme specificity and complexity of proteins presents a difficulty, not only for the chance origin of specified biological information (i.e., for random mutations act alone), but also for the mechanism of natural selection acting on random mutations.

There are two reasons for this. First, many biologically necessary proteins pose a very high threshold of functionality for the operation of natural selection. Many neo-Darwinists envision novel proteins arising from genes produced by random variations in (what was originally) non-coding DNA. Yet by all accounts most functional genes and

proteins are far too complex to arise all at once by chance, even starting from some other existing gene or protein. Thus, any process of gradual assembly would necessarily generate many non-functional (or functionally unspecified) precursor sequences. Yet these sequences would confer no survival advantage on organisms that possess them. Natural selection only favors functional advantage. It cannot select or favor nucleotide sequences or polypeptide chains that do not yet perform biological functions. Yet evolving genes and proteins must in all probability range through a series of non-functional precursors or intermediate sequences that natural selection will not detect, “see,” or preserve.¹⁰⁸ As geneticist George Miklos explains the problem, “in most cases natural selection is an editor rather than a composer and an editor does not remove changes which it cannot perceive.”¹⁰⁹

Thus, on the one hand, many genes and their corresponding proteins are too highly complex and specified to arise by chance alone. On the other, natural selection cannot favor such information-rich sequences *until* they have arisen. Indeed, adaptive advantage accrues only *after* the generation of functional proteins and (the genes that produce them). Since natural selection cannot favor a polypeptide sequence until it confers functional advantage, essentially random processes must account for the assembly of novel genes and their protein products before natural selection can have any effect. And yet, again the complexity of many functionally essential proteins exceeds what one can reasonably expect to arise by an undirected mutations within a realistically limited amount of time.

This need for functional sequences to arise before natural selection can have any effect helps to explain why computer “simulations” of Darwinian information generation have no biological analogue. As Meyer noted in his essay on the origin of life, actual computer simulations of the mutation/selection mechanism only succeed in generating new specified information by the illicit expedient of providing the computer with a target sequence and treating relatively greater proximity to this sequence, not actual functional sequencing, as a selection criterion. In Richard Dawkins’ simulation, for example, he provides the computer with the specific information he wants it to generate (“Methinks it is like a weasel”).¹¹⁰ In biology, however, where differential survival depends upon maintaining function, selection can not occur before new functional sequencing arises. To employ Dawkins’ metaphor again, even the incremental steps up the back-side of Mt. Improbable (corresponding to the generation of new genes and proteins) actually involve steep vertical increases in complexity that exceed the reach of chance alone. In these cases, natural selection can do nothing to overcome the odds of scaling “Mt. Improbable,” since the new functional thresholds that natural selection needs to operate exceed what random variation alone could conceivably accomplish given available time. If Mt. Improbable represents the task of building highly complex novel proteins, then Mt. Improbable does not have a gradually sloping backside.

Neo-Darwinists also envision novel genes and proteins arising from existing genetic text by numerous successive mutations in genes that already code for functional proteins. To adapt Dawkins’ metaphor, they envision gradually climbing down one mountain peak and then scaling another. Nevertheless, cassette mutagenesis experiments

establishing the specificity of proteins show that most proteins will admit only a limited number of changes before losing function. Within “the adaptive landscape” corresponding to the space of combinatorially possible amino acid sequences, individual proteins represent highly isolated functional buttes or plateaus separated on all sides by vast stretches of flat desert. This “adaptive landscape” pictures a limit to the amount of change that proteins can allow in their amino acid sequences before losing the function that makes them advantageous to survival. Indeed, cassette mutagenesis experiments suggest that proteins will often tolerate some changes in amino acids at single sites without losing function, but will not tolerate multiple changes at separate sites—without dramatic functional loss. Yet to turn one protein into another with a completely novel function requires many coordinated changes at many separate amino acid sites. As Zuckerkandl has observed:

Although abstractly speaking, any polypeptide chain can be transformed into any other by successive amino acid substitutions and other mutational events, in concrete situations the pathways between a poorly and a highly adapted molecule will be mostly impracticable. Any such pathway, whether the theoretically shortest, or whether a longer one, will perforce include stages of favorable change as well as hurdles [to function]. Of the latter, some will be surmountable *and some will not.*¹¹¹ (Emphasis added).

More recent theorists concur. Stuart Kauffman who describes adaptive evolution as a “complex combinatorial optimization process,” has rejected the adequacy of the mutation and selection mechanism for a similar reason.¹¹² Kauffman notes that “peaks” of function are so highly isolated on “the adaptive landscape” that random methods of searching the space of combinatorial possibilities seems a highly implausible means of finding other functional peaks. He instead asserts the need for some kind of non-Darwinian “self-organizational” process or mechanism, though he has yet to provide any specific empirical support for the existence of one in nature.

Some would argue that the probabilistic difficulties described above apply only to random mutations that occur one nucleotide base pair at a time, either in the form of point mutations or deletions. They would argue that mutations involving larger sections of genetic text—such as those produced by gene duplications, insertions, inversions and recombinations—could conceivably overcome the probabilistic difficulties associated with generating new functional sequences in combinatorial sequence space. Nevertheless, if one must generate a specified text of small probability (i.e., functionally specified information), it matters very little whether one starts with an existing text and then rearranges blocks of letters at random, or whether one changes letters one at a time, or whether one begins with a pile of unsequenced letters. In each case, enormous probabilistic hurdles must be overcome. To see why imagine a computer “mutating” at random the text of the play *Hamlet* by duplicating, inverting, recombining and changing various sections. Rearranging larger sections of the text of *Hamlet* at random will yield

many meaningful sections of *Hamlet* interspersed with gibberish. Thus, to transmute *Hamlet* into some other meaningful text, say, Stephen Hawking's best seller *A Brief History of Time*, would still require altering longer strings of gibberish character by character (especially those produced by inversions of original text), breaking down the meaningful sections of the *Hamlet* text into smaller constitutive parts (such as single words or letters), and then rearranging the new shorter sections (words and letters) into a new meaningfully sequenced text. Consequently, an undirected shuffling of larger sections of the text of *Hamlet* would seem (appreciably) no more likely to result in another meaningful text such as Hawking's *A Brief History*, than would a random shuffling of single words or a random letter by letter alteration of the existing Shakespearean text. In either case, the path to a meaningful sequence requires sequencing or re-sequencing many, many short strings of characters. Similarly, to get functional sequencing from randomly assorted blocks of pre-existing genetic text would also seem to require re-sequencing short sections of larger blocks of text, (most probably still involving many individual base changes). In any case, random processes would not seem at all likely to produce either a complete copy of Hawking from *Hamlet*, or, for example, a gene for hemoglobin from a gene for an RNA-polymerase, even granting multiple millions of undirected iterations—a condition that living organisms cannot allow without risking death. As mathematician Marcel Schutzenberger explained as early as 1966 at the Wistar Institute “Mathematical Challenges to neo-Darwinism” conference:

if we try to simulate such a situation [the production of specified genetic information] by making changes randomly at the typographic level (letter by letter or *by blocks, the size of the unit doesn't really matter*) on computer programmes, we find that we have no chance (that is, less than one chance in 10(1000)) even to see what the modified program would compute; it just jams.¹¹³ (emphasis added)

Novel proteins represent the smallest unit of functional change in biology. New cell types, organs and structures all require many novel and specialized proteins and aggregates of proteins acting in close coordination. At the lowest level, morphological change is denominated in novel proteins. Yet if even some essential proteins represent functional plateaus too high or highly isolated on the adaptive landscape to be reached by chance variation alone, then these proteins will also exceed the creative power of the selection/mutation mechanism. Given the lack of other sufficient “self-organizational” or naturalistic mechanisms, intelligent design stands as the best, and only causally sufficient, explanation for the origin of the large amounts of specified information necessary to build novel proteins. Intelligent agents routinely create large amounts of specified information. They can select functional goals *before* they exist, and then actualize them in accord with a *preconceived* design. Natural selection cannot do this. It has no foresight.

Ironically, even attempts to avoid the difficulty posed by the Cambrian explosion often presuppose the need for such foresight. As noted, Susumo Uno, the originator of the hypothesis of macroevolution by gene duplication, has argued that mutation rates of

extant genes are not sufficiently rapid to account for the amount of genetic information that arose suddenly in the Cambrian.¹¹⁴ Hence he posits the existence of a prior “pananimalian genome” that would have contained all the genetic information necessary to build every protein needed to build the Cambrian animals. His hypothesis envisions this genome arising in a hypothetical common ancestor well before the Cambrian explosion began. On this hypothesis, the differing expression of separate genes on the same master genome would explain the great variety of new animal forms found in the Cambrian strata.

While Ohno’s hypothesis does preserve the core evolutionary commitment to common descent (or monophyly), it nevertheless has a curious feature from the standpoint of neo-Darwinism. In particular, it envisions the pananimalian genome arising well before its expression in individual animals.¹¹⁵ Specific genes would have arisen well before they were used, needed or functionally advantageous. Hence, the individual genes within the pananimalian genome would have arisen in a way that, again, would have made them imperceptible to natural selection. This not only creates a problem for the neo-Darwinian mechanism, but it also seems to suggest, as Simon Conway Morris has recently intimated,¹¹⁶ the need for foresight or teleology to explain the Cambrian explosion. Indeed, the origin of a massive, unexpressed pre-Cambrian genome containing all the information necessary to build the proteins required by not-yet-existent Cambrian animals, would strongly suggest intelligent foresight or design at work in whatever process gave rise to the pananimalian genome.

If there isn’t enough time to have a reasonable chance of “finding” (by chance) new functional gene sequences in combinatorial sequence space, then natural selection, operating as it does after the fact, will not have a new functionally advantageous sequence upon which to act. On the other hand, an intelligent designer, conceiving, as intelligent agents can do, of distant goals before they are actualized, can put in place complex structures or informational sequences in anticipation of their future use. For this reason, intelligent design constitutes a better explanation than the neo-Darwinian mechanism for the origin of the complex functionally specific information necessary to build the proteins required by the new cell types and animals that arise in the Cambrian.

V.A.2. Systems of Proteins, Novel Cell Types and Natural Selection

Some will, of course, categorically reject the conclusion that any individual protein could exceed the probabilistic resources available to the neo-Darwinian mechanism. Yet recent cassette mutagenesis experiments establishing the extreme specificity of proteins conjoined with the recent calculations of the Universal Probability Bound (based upon very conservative assumptions) entail precisely this conclusion. Nevertheless, perhaps individual proteins are not quite as functionally specified as recent experiments suggest. Perhaps recent calculations of the Universal Probability Bound need revising. Yet even if one concedes these assumptions and accepts that the neo-Darwinian mechanism might suffice to explain the origin of a novel protein (of average length and complexity), it does not follow this mechanism can account for the origin of the animals that arise in the Cambrian. As noted, the new animals of the Cambrian explosion would have required many new cell types and, with them, many new types of proteins acting in close

coordination. It follows, therefore, that if the neo-Darwinian mechanism cannot explain the origin of new cell types (and the systems of proteins they require), it cannot explain the origin of the Cambrian animals. Yet given the *number* of novel proteins required by even the most basic evolutionary transformations, this now seems to be precisely the case.

Consider, for example, the transition from a prokaryotic cell to a eukaryotic cell. This transition would have produced the first appearance of a novel cell type in the history of life. Compared to prokaryotes, eukaryotes have a more complex structure including a nucleus, a nuclear membrane, organelles (such as mitochondria, the endoplasmic reticulum, and the golgi apparatus), a complex cytoskeleton (with microtubules, actin microfilaments¹¹⁷ and intermediate filaments) and motor molecules.¹¹⁸ Each of these features requires new proteins to build or service, and thus, as a consequence, more genetic information. (For example, the spooled chromosome in a modern eukaryotic yeast [*Saccharomyces*] cell has about 12.5 million base pairs, compared to about 580,000 base pairs in the prokaryote *Mycoplasma*.)¹¹⁹ The need for more genetic information in eukaryotic cells in turn requires a more efficient means of storing genetic information. Thus, unlike prokaryotic cells which store their genetic information on relatively simple circular chromosomes, the much more complex eukaryotic cells store information via a sophisticated spooling mechanism.¹²⁰ Yet this single requirement—the need for a more efficient means of storing information—necessitates a host of other functional changes each of which requires new specialized proteins (and yet more genetic information) to maintain the integrity of the eukaryotic cellular system.

For example, nucleosome spooling requires a complex of specialized histone proteins (with multiple recognition and initiation factors) to form the spool around which the double stranded DNA can wind.¹²¹ Spooled eukaryotic DNA in turn uses “intron spacers,” (dedicated sections of non-coding DNA), in part to ensure a tight electrostatic fit between the nucleosome spool and the cords of DNA.¹²² This different means of storing DNA in turn requires a new type of DNA polymerase to help access, “read,” and copy genetic information during DNA replication. (Indeed, recent sequence comparisons show that prokaryotic and eukaryotic polymerases exhibit stark differences).¹²³ Further, eukaryotes also require a different type of RNA polymerase to facilitate transcription. They also require a massive complex of five jointly necessary enzymes to facilitate recognition of the promoter sequence on the spooled DNA molecule.¹²⁴ The presence of intron spacers in turn requires editing enzymes (including endonucleases, exonucleases and splicesomes) to remove the non-coding sections of the genetic text and to reconnect coding regions during gene expression.¹²⁵ Spooling also requires a special method of capping or extending the end of the DNA text in order to prevent degradation of the text on linear (non-circular) eukaryotic chromosomes.¹²⁶ The system used by eukaryotes to accomplish this end also requires a complex and uniquely specialized enzyme called a telomerase.¹²⁷

Thus, one of the “simplest” evolutionary transitions, that from one type of single-celled organism to another, requires the origin of many tens of specialized novel proteins, many of which (such as the polymerases) alone represent massively complex, and

improbably specified molecules.¹²⁸ Moreover, many, if not most, of these novel proteins play functionally necessary roles in the eukaryotic system as a whole. Without specialized polymerases cell division and protein synthesis will shut down. Yet polymerases have many protein subunits containing many thousands of precisely sequenced amino acids. Without editing enzymes, the cell would produce many non-functional polypeptides, wasting vital ATP energy and clogging the tight spaces within the cytoplasm with many large useless molecules. Without tubulin and actin the eukaryotic cytoskeleton would collapse (or would never have formed). Indeed, without the cytoskeleton the eukaryotic cell can not maintain its shape, divide, or transport vital materials (such as enzymes, nutrients, signal molecules, or structural proteins).¹²⁹ Without telomerases the genetic text on a linear spooled chromosome would degrade, again, preventing accurate DNA replication and eventually causing the parent cell to die.¹³⁰

Even a rudimentary analysis of eukaryotic cells suggests the need for, not just one, but many novel proteins acting in close coordination to maintain (or establish) the functional integrity of the eukaryotic system. Indeed, the most basic structural changes necessary to a eukaryotic cell produce a kind of cascade of functional necessity entailing many other innovations of design, each of which necessitates specialized proteins. Yet the functional integration of the proteins parts in the eukaryotic cell poses a severe set of probabilistic obstacles to the neo-Darwinian mechanism, since the suite of proteins necessary to eukaryotic function must, by definition, arise *before* natural selection can act to select them. This means that natural selection cannot contribute to the process of information generation until after the information necessary to build the requisite proteins has arisen. Thus, random variations alone must again do the creative work of information generation. Yet the odds against the random assembly of the genes required to produce the proteins for this most rudimentary evolutionary transition far exceed (by many hundreds of orders of magnitude) the odds against the chance origin of the information necessary to build a single protein of average length—itsself a most improbable proposition (see above).

Of course, neo-Darwinists imagine the origin of complex systems arising incrementally with each of the functionally necessary parts. As George Johnson recently argued, “each part of a complex molecular machine does not evolve by itself . . . The several parts evolve together, in concert, precisely because evolution acts on the system, not its parts. . . .”¹³¹ Yet this rhetorical gloss conceals formidable difficulties. To alter the proteins of one functionally integrated system to produce another, involves altering the genetic constituents of the system, which implies, most implausibly, that multiple coordinated mutations will occur virtually simultaneously and in succession. As T.H. Frazzetta has explained, “phenotypic alteration of integrated systems requires an improbable coincidence of genetic (and hence, heritable phenotypic) modifications of a tightly specified kind.”¹³² Yet the extreme specificity of the protein components, and the functional dependence of the whole system, implies probabilistic limits to allowable genetic change. Genetic change affecting any one of the necessary components, unless matched by many corresponding—and vastly improbable—genetic changes will result in

functional loss, and often, death. For this reason, as Frazzetta concludes, “We are still left with the unabating need to explain evolutionary changes in systems that have the operational integration characteristic of things we recognize as ‘machines.’”¹³³

In any case, evolutionary biologists have not offered any detailed neo-Darwinian account of the origin of the eukaryotic cellular system. True, Lynn Margulis’s endosymbiotic hypothesis seeks to explain how eukaryotes acquired their mitochondria, the organelle responsible for much of the eukaryotic cell’s energy production. Yet her hypothesis (which is fraught with difficulties on its own terms)¹³⁴ does not attempt to explain the origin of the eukaryotic cell as a whole. According to Margulis, prokaryotic bacteria somehow incorporated a primitive cellular system (without digesting it), and this system eventually became an independent subsystem within the emerging eukaryotes. Whatever its merits or difficulties, the endosymbiotic hypothesis gives no account for the origin of the other organelles specific to eukaryotes, or the cytoskeleton, or the eukaryotic information processing system (with its many complex and specialized proteins). Nor does the endosymbiotic hypothesis attempt to explain the origin of the system of proteins and nucleic acids operating within mitochondria itself. Instead, it merely posits the absorption of one tightly integrated system by another, without explaining how any mutually interdependent system of proteins could arise by neo-Darwinian means in the first place.

Yet if the neo-Darwinian mechanism cannot account for the origin of a single new cell type (and the system of functionally integrated proteins that it requires), it is difficult to see how it can account for whole new animal forms, since these forms require many new cell types and suites of proteins. If mutation/selection cannot account for the most rudimentary evolutionary transition—from one type of one-celled organism to another—it seems *a fortiori* highly doubtful that it could account for the origin of novel animal forms (each of which require many new types of cells and systems of proteins) whether starting from either a one-celled organism or some other simpler animal form. Indeed, given the number of new proteins represented by the origin of the Cambrian animals, it seems very doubtful that any plausible revision of the Universal Probability Bound or estimates of protein specificity will appreciably improve the plausibility of the neo-Darwinian mechanism as an explanation of the Cambrian explosion.

V.A.3. Morphological Development, Body Plans and Natural Selection

Yet the problem of explaining the Cambrian explosion by reference to the neo-Darwinian mechanism runs deeper still. To explain the origin of the Cambrian animals, one must not only explain the origin of new proteins and cell types, one must also account for the origin of new body plans. Yet if the selection/mutation mechanism cannot account for the origin of new cell types, it will again not account for the origin of new organs or body plans. To see why we must take a brief excursion into developmental biology.

More than any other subdiscipline of biology, the field of developmental biology has raised disquieting questions for neo-Darwinism. Developmental biology describes the process by which embryos develop into mature organisms. Within the past decade

developmental biologists have advanced tremendously in understanding how body plans are built during ontogeny. In model systems such as the fruit fly *Drosophila* and the nematode (worm) *Caenorhabditis elegans*, painstaking genetic research has uncovered many of the key embryonic regulators that switch cells into their differentiated adult types, and which set up the axes along which the body plan is organized. This research has also uncovered a profound difficulty cutting to the very core of the neo-Darwinian view of life.

To create significant changes in the form of organisms requires an attention to timing. Mutations in genetic material that are expressed late in the development of an organism will affect only few cells. Such mutations will not affect any significant changes in the form of the whole organism, and are unlikely to be inherited by the next generation. Mutations that are expressed early in development, however, may affect many cells and could conceivably produce gross changes in the morphology of an organism.¹³⁵ Thus, events that are expressed early in the development of organisms have the greatest, and probably the only realistic, chance of producing large scale macroevolutionary change.¹³⁶ As Miklos and John explain, "macroevolutionary change" requires changes in "very early embryogenesis."¹³⁷

Yet, as a number of recent studies in developmental biology make clear, mutations that are expressed early in development have inevitably deleterious (or at best neutral) effects,¹³⁸ 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.¹³⁹ 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, but does not modify the crankshaft accordingly, the engine won't start. Similarly, processes of development are so tightly integrated temporally and spatially that one change early in development will require a host of other coordinated changes in separate but functionally interrelated developmental processes downstream. As the noted theorist Leigh Van Valen has observed, "development is integrated," with early events affecting all later events. As he explains:

development ramifies out; later developmental decisions depend on earlier ones which are much fewer and have consequences which interact. Development is not a linear sequence. . .but an expanding network . . .¹⁴⁰

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 bi-thorax gene (expressed mid-way in the development of a fly) does produce an extra pair of wings on a normally two-winged creature. Nevertheless, this "innovation" produces a crippled fly that cannot fly because it lacks, among other things, a musculature to support the use of its new wings. Indeed, because the developmental mutation was not accompanied by the many other coordinated developmental changes that would have been

necessary to ensure the production of appropriate 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 University of Georgia geneticist John F. McDonald has called the "great Darwinian paradox."¹⁴¹ He notes that the genes that are obviously variable within natural populations seem to affect only minor aspects of form and function—while those genes which 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 within natural populations."¹⁴² In other words, the kind of mutations that macroevolution needs (namely, *beneficial* regulatory or *bauplane* mutations that are generally expressed during early development) don't occur, the kind it doesn't need (namely, viable genetic mutations in DNA generally expressed late in development) do occur (if still infrequently). Yet, as Darwin himself saw, and wrote, "nothing can be effected" by natural selection, "unless favorable variations occur."¹⁴³ As Soren Løvtrup put it:

...without variation, no selection: without selection, no evolution. This assertion is based on logic of the simplest kind, and it should be noted that the common implication of selection pressure as an evolutionary agent becomes void of sense unless the availability of the proper mutations is assumed.¹⁴⁴

Micro-evolution is insufficient; macroevolution—large scale change—is harmful. This paradox has beset neo-Darwinism from its inception. Discoveries about the genetic regulation of development in animals have made this paradox more acute and cast serious doubt on the efficacy of the neo-Darwinian mechanism as an explanation for the new body plans that arise in the Cambrian.

Developmental biology has also raised another, equally formidable, problem for the neo-Darwinian mutation/selection mechanism. Embryological evidence has long shown that DNA does not wholly determine morphological form.¹⁴⁵ Therefore, mutations in DNA cannot account for the structural or morphological innovation required to construct the body plans that arise in the Cambrian. DNA (in conjunction with many specific proteins) directs protein synthesis. It also helps to regulate the timing and expression of the synthesis of various proteins within cells. Nevertheless, it does not on its own determine how individual proteins assemble themselves into larger aggregates or structures. Novel cell types, tissues and organs comprise many proteins arranged in very different and specific ways. Novel body plans in turn comprise very specific arrangements of whole organs and systems of organs (themselves made of proteins). While DNA certainly plays an important role in the synthesis of individual proteins, it

does not determine the arrangement and configuration of proteins within these larger morphological structures.

Instead, other non-genetic factors—such as the structure and organization of the cell membrane and cytoskeleton—play important roles in determining cellular organization developmental pathways. For example, the shape and location of microtubules in the cytoskeleton influence the so-called “patterning” of embryos. Arrays of microtubules help distribute essential proteins used during development to their correct location in the cell.¹⁴⁶ Of course, microtubules themselves are made of many protein subunits—that is, of gene products. 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 development pathways. As Jonathan Wells put it, “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.”¹⁴⁷ Two analogies may help. At a building site, builders will make use of many materials: lumber, wires, nails, dry wall, piping and window panes. Yet these building materials do not determine the floor plan of the house, or the arrangement of houses in a neighborhood or subdivision. Similarly, electronic circuits are composed of many components such as resistors, capacitors, and transistors, for example. Yet these lower level components do not determine their arrangement on an integrated circuit. Biological systems also depend upon hierarchical arrangements of parts. Genes and proteins are made from simple building blocks, nucleotide bases and amino acids, for example. Yet, proteins themselves (such as those that form microtubules) function as building blocks within larger morphological structures (such as microtubule arrays) and organismal body plans. Like the building materials at a construction site, or the electronic components in personal computer, individual proteins do not determine the organization of these higher level structures and organizational patterns.¹⁴⁸ It follows, therefore, that the information on the DNA that codes for proteins does not determine them either.

These considerations present the most formidable, and indeed, in principle, 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 the selection of randomly arising variation, at a very low level within the biological hierarchy, namely, within the genetic text. Yet major morphological innovations depend upon a specificity of arrangement, at a much higher level of the organizational hierarchy, that DNA alone does not determine or produce. Therefore, mechanism of natural selection acting on random genetic mutation can not *in principle* account for the origin novel body plans.

Instead, the hierarchical and information-rich arrangements of parts in animal body plans bespeak design. At every level of the biological hierarchy organisms require a specified and highly improbable arrangements of lower lever 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 and organs require specified arrangements or systems of proteins, and 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 these components and the subsystems made from them.

Based on our experience, we know that intelligent agents have the capacity to generate complex but functionally specified arrangements of matter—that is, to generate specified complexity or (specified) information. Moreover, human agents often design information-rich hierarchies, in which both individual modules, and the arrangement of those modules, exhibit complexity and specificity. Individual transistors, resistors and capacitors in an integrated circuit exhibit considerable complexity and specificity of design. Yet at a higher level of organization, the specific arrangement and connection of these components within an integrated circuit reflects further design. This power to arrange parts in accord with a functionally specified (but initially unrealized) plan characterizes intelligent human agents. Intelligent agents certainly can, and do, produce hierarchically organized and functionally specified arrangements of matter. Further, we know of no other causal entity that has this capacity. Certainly, we have good reasons to doubt that the neo-Darwinian mechanism does. Thus, based upon our present experience of the causal powers of various entities, and our theoretical analysis of the alleged efficacy of the neo-Darwinian mechanism, we can infer intelligent design as the best explanation for the origin of the hierarchical organization and specified complexity (or information) required to build the animal body plans that arise in the Cambrian. In other words, we infer that an intelligent agent (not unlike humans in its intelligence and power of agency) acted to generate the information-rich arrangement of parts that characterize the Cambrian animals.

V.B. The Persistence of Morphological Isolation or Disparity (Stasis)

Design also explains the existence of the morphological continuity of individual body plans and the persistence of the morphological disparity between separate animal body plans after the Cambrian explosion. As noted in Part I, the animal body plans that define the phyla remain remarkably stable in their basic architectural designs showing “no directional change”¹⁴⁹ over geological history after their first appearance in the Cambrian. As a result of this observed “stasis” and the absence of “directional change,” the morphological disparity or isolation between distinct animal body plans has remained unbridged. Moreover, as noted in Parts V.A., developmental mechanisms constrain the degree to which organisms may vary without deleterious consequences.

Intelligent design also helps to explain these phenomena. Human experience suggests that designed objects have a functional integrity that makes the modification of some parts of their basic architecture difficult or even impossible. Though the Model-A has been replaced by everything from the *Yugo* to the *Honda Accord*, the basic automobile “body plan”—which includes four wheels, two axles, a drive shaft, and a motor, for example—has remained unchanged from its first appearance in the late 19th century. (These are minimal requirements, of course; a “stretch” limousine may have another axle or additional wheels.) Further, despite the creation of many innovative variations, automobiles have also retained their “morphological distance” or structural disparity 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, what we recognize as a different organismal body plans are systems differing fundamentally from each other in their overall organization. A crinoid 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 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, fundamental structural discontinuities often reflect different functional requirements.

Moreover, the presence of such structural disparities or discontinuities between complex functionally integrated systems represents another distinctive feature of designed systems. Consider a non-biological 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 (e.g., 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 of all other types of technological devices, indeed, even those that perform roughly the same function. While minor new features may “accrete” to its basic design architecture, a deep and impassable functional gulf separates the CD ROM as a system, from other technological systems. As Michael 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.”¹⁵⁰ In our experience, such complex and structurally isolated systems, i.e., those that perform specialized functions, invariably result from intelligent design. One might say, therefore, that functional and structural disparity or isolation constitutes a diagnostic of designed systems. Indeed, intelligent design explains the existence and persistence of structural or morphological disparity, or the morphological isolation and “stasis” of animal body plans in the fossil record.

V.C. An Inverted Cone of Diversity: Disparity Preceding Diversity

Design also explains another feature of the Cambrian explosion, the so-called “inverted cone of diversity.” As stated 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. Major innovations in body plans precede minor variations on basic designs. This pattern also suggests actual design for several reasons.

Neo-Darwinism seeks to explain the origin of novel body plans by starting with simpler body plans and gradually assembling animals with more complex body plans via the gradual accumulation of small successive material variations. Thus, neo-Darwinism employs what might be called a “bottom-up” mode of causation. On such a “bottom-up” approach, small-scale diversification eventually produces large-scale morphological disparity—which we recognize as a difference in body plan. The “bottom-up” metaphor thus describes a kind of self-assembly in which the gradual production of the material parts eventually generates the organization of the whole. Indeed, 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 a process and the morphological transformations that it requires are, in any case, biologically untenable.

But if a bottom-up approach to the generation of morphological disparity fails, perhaps a “top-down” approach will succeed. The “top-down” metaphor describes a form of causation that begins with a basic architecture, blueprint or plan for the whole and then proceeds to assemble parts in accord with it. On this scheme, the blueprint stands causally prior to the assembly and arrangement of the parts. But where could such a blueprint come from if not from the self-assembly of material constituents? One possibility involves a mental rather than material mode of causation. We know from experience that intelligent agents often conceive of plans prior to their material instantiation—that is, the intelligent design of a blue print often precedes the assembly of parts in a accord with a *pre*-conceived blue print. An observer touring the parts section of a General Motors plant will see no direct evidence of a prior blueprint for GM's new models, but will perceive the basic design plan immediately upon observing the finished product at the end of the assembly line. Designed systems, whether automobiles, airplanes or computers, invariably manifest a distinctive *bauplan* from their very first material instantiation. But the parts do not generate the whole. Rather, an idea of the whole directed the assembly of the parts.

This form of causation can certainly explain the pattern in the fossil record. As we have noted, the first material instantiation of new species in the Cambrian invariably manifest completely novel, morphologically disparate and functionally integrated body plans. Of course, the material parts and the body plans arise simultaneously, but so do they in other designed systems as we have seen. Thus, while the fossil record does not directly establish the existence of a prior mental plan or blue print, the existence of such a plan could certainly explain the top-down pattern of fossil evidence associated with the Cambrian explosion. In other words, if the body plans of the Cambrian animals did arise as the result of a “top down” mode of causation involving *pre*-conceived design plan, we would expect, from our experience of designed objects, to see precisely the pattern of evidence (with body plans arising simultaneously with their first material instantiation) that we do see in the fossil record. Further, as we have seen, materialistic “bottom-up” models of causation fail to explain this same pattern of fossil evidence because such models predict that the material parts of organisms should begin to arise within

intermediate forms *before* the appearance of novel and morphologically disparate body plans.

Design also explains why smaller-scale diversity arises *after*, and not before, morphological disparity in the fossil record, or, to put it more poetically, why the basic themes of life precede the variation on those themes. If, as we have argued, complex designed systems have a fundamental functional integrity that makes their alteration difficult, then we should not expect gradual mechanisms of change either to produce new body plans in the first place, or to alter them fundamentally after they have arisen. We might however expect to find *variations* on these basic themes within the functional limits established by a fundamental architecture or body plan. Fundamentally new forms of organization require design from scratch as in our CD ROM example above. (For example, airplanes did not arise gradually or incrementally from automobiles). Nevertheless, new innovations often accrete to novel designs provided the fundamental organizational plan is not altered. Since the invention of the automobile, 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. Interestingly, we also observe this pattern in the fossil record with morphological disparity preceding diversity. The major animal body plans appear first instantiated by a single (or very few) species. Then later many other varieties arise with many new features, yet all still exhibit the same basic body plan.

Experience shows a certain hierarchical relationship between functionally necessary and functionally optional features in designed systems. An automobile cannot function without two axles; it can function with or without twin I-beam suspension, anti-lock 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 precisely the kind of pattern that we see in the history of our own technological innovation and in the history of life following the Cambrian explosion (Compare Figures 9 and 14). For this reason, design can explain the pattern of morphological disparity *preceding* diversity in the Cambrian period (as well the persistence of body plan stasis after the emergence of disparity at the phyletic level).

V.D. Sudden Appearance and Absence of Ancestral Precursors

Finally the theory of intelligent design also explains both the sudden appearance of the animal body plans in the Cambrian and the absence of ancestral precursors in the pre-Cambrian. Given either a neo-Darwinian or punctuationalist theory of evolution, one would expect to find numerous transitional intermediate forms leading to the emergence of distinct body plans. Both these theories envision a “bottom-up” mode of causation in which material parts, or materially-instantiated intermediate forms of organization, necessarily precede the emergence of fully developed 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 can explain the absence of material antecedents in the fossil record. Immaterial plans need not leave a material trace. Conversely, given the problems with the artifact theory, neither evolutionary model can presently explain the dearth of material precursors and transitional intermediates in the pre-Cambrian rocks.

Similarly, both evolutionary models have a difficult time explaining the geologically sudden appearance of the Cambrian fauna—neo-Darwinism because its mechanism requires vast amounts of time; punctuated equilibrium because it lacks an efficacious mechanism 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 volition. And the relatively sudden appearance of the animal phyla does suggest the possibility of a volitional act of a Creator. Darwin himself regarded evidence of real saltation (sudden appearance) as evidence for Divine Creation, (though, of course, he denied the existence of any such evidence). A discrete volitional act (or acts) of creation by an intelligent designer could, therefore, explain the sudden appearance of the Cambrian animals. Whereas, the sudden appearance of the Cambrian animals presents a severe difficulty for the neo-Darwinian model. Thus, intelligent design provides a better, more causally adequate, explanation of this feature of the Cambrian explosion.

Of course, scientists wedded to a purely naturalistic approach to 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 that we see in the fossil record. Indeed, we see in the fossil record several features that indicate, based upon our experience, a prior intelligent design, including: (1) a quantum increase in specified biological information, (2) the presence of structural (or “morphological”) disparities between separate organizational systems and (3) the emergence of large scale morphological disparity *before* the emergence of small scale diversity, i.e., the emergence of basic themes before the variations on those themes and (4) the sudden and 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 intelligent agency or design 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-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 explanation for the origin of animal body plans in the Cambrian fossil record.

¹ Francisco Ayala, “Darwin’s Revolution,” in *Creative Evolution?!*, eds. J. Campbell and J. Schopf (Boston, Mass.: Jones and Bartlett Publishers, 1994), pp. 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,” *The Scientist* (May 24, 1999): 13.

³ Our numerical estimates for the number of phyla that first appear in the Cambrian are derived from an analysis of the discussions in the following scientific papers and paleontology texts: R.S. Boardman, A.H. Cheetman, and A.J. Rowell, eds., *Fossil Invertebrates* (Blackwell Scientific Publications, 1987), p. 18; Pat Wilmer, *Invertebrate Relationships: Patterns in Animal Evolution* (Cambridge: Cambridge University Press, 1990), pp. 62-70; J.Y. Chen and Guiqing Zhou, "Biology of the Chengjiang Fauna," in *The Cambrian Explosion and the Fossil Record*, eds. J.Y. Chen, Y.N. Chang, H.V. Iten (Bulletin of The National Museum of Science: 1997), pp. 11-106; J.W. Valentine, D. Jablonski, and D.H. Erwin, "Fossils, molecules, and embryos: new perspectives on the Cambrian explosion," *Development* 126 (March 1999): 851-59. Simon Conway Morris, *The Crucible of Creation: The Burgess Shale the Rise of Animals* (New York: Oxford University Press, 1998).

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* (March 31-April 6, 1997): 10.

⁶ Jeffrey Levinton, "The Big Bang of Animal Evolution," *Scientific America* (November 1992): 84-91; Richard A. Kerr, "Evolution's Big Bang Gets Even More Explosive," *Science* 261 (September 3, 1993): 1274-75; R. Monastersky, "Siberian Rocks Clock Biological Big Bang," *Science News* 144 (September 4, 1993): 148.

⁷ This estimate is based on our own analysis and harmonization of four authoritative paleontological texts which describe the first appearance of the animal phylum. See footnote 3 above.

⁸ J.W. Valentine, *et. al.*, "Fossils, molecules, and embryos: new perspectives on the Cambrian explosion," pp. 851-59.

⁹ All Chengjiang and Burgess animals are considered to be soft-bodied, because they all lack mineralized skeleton. Some of these soft-bodied animals have a keratinized exoskeleton and some do not. Those that do not have even an exoskeleton offered only soft tissue for preservation.

¹⁰ J.Y. Chen, C.W. Li, Paul Chien, G.Q. Zhou and Feng Gao, "Weng'an Biota—A Light Casting on the Precambrian World," presented to: *The Origin of Animal Body Plans and Their Fossil Records* conference (Kunming, China, June 20-26, 1999). Sponsored by the Early Life Research Center and The Chinese Academy of Sciences.

¹¹ 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* (1997), is currently available only in the Chinese language. The translated English version is being completed by Paul K. Chien, University of San Francisco.

¹² D.G. Shu, S. Morris, and X.L. Zhang, "A Pikaia-like chordate from the Lower Cambrian of China," *Nature* 384 (1996): 157-58.

¹³ Jun-Yuan Chen, Di-Ying Huang, and Chia-Wei Li, "An early Cambrian craniate-like chordate," *Nature* 402 (1999): 518-22.

¹⁴ 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 (November 4, 1999): 42-46.

¹⁵ Brian Hall, "Bauplane, Phylotypic Stages, and Constraint: Why There Are So Few Types of Animal," *Evolutionary Biology* 29 (1996): 215-61.

¹⁶ 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), pp. 460-66; p. 464: "There is absolutely no sign of convergence between phyla as we follow them backwards 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."

¹⁷ J.J. Brocks, G.A. Logan, R. Buick, and R.E. Summons, "Archean Molecular Fossils and the Early Rise of Eukaryotes," *Science* 28 (August 1999): 1033-36.

¹⁸ The term information content is used variously to denote both specified complexity and unspecified complexity. One can foreclose this ambiguity, however, by defining information content as equivalent to the joint properties of complexity and specification. Though the term is not used this way in classical information theory, it has been used this way by biologists from the beginning of the molecular biological revolution. As Sarkar points out, since the mid-1950s Francis Crick and others have equated *information* not only with complexity, but also with what they called "specificity" where they understood specificity to mean "necessary to function." This article will also use the term "information content" to mean functionally specified information, or specified complexity, not just complexity. See 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 (Kluwer Academic Publishers: Dordrecht, 1996), p. 191.

¹⁹ James W. Valentine, “Late Precambrian Bilaterians: Grades and Clades,” in *Tempo and Mode in Evolution: Genetics and Paleontology 50 Years After Simpson*, eds. W.M. Fitch and F.J. Ayala (Washington, DC: National Academy Press, 1995), pp. 87-107, especially 91-93.

²⁰ Mitsuhiro Itaya, “An estimation of the minimal genome size required for life,” *FEBS Letters* 362 (1995): 257-60. Claire Fraser, Jeannine D. Gocayne, Owen White, *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.

²¹ The *C. elegans* Sequencing Consortium, “Genome Sequence of the Nematode *C. elegans*: A Platform for Investigating Biology,” *Science* 282 (1998): 2012-18.

²² John Gerhart and Marc Kirschner, *Cells, Embryos, and Evolution* (London: Blackwell Science, 1997), p. 121.

²³ P. Ward, *On Methuselah’s Trail, Living Fossils and the Great Extinctions* (New York: W.H. Freeman & Co., 1992), pp. 29-30.

²⁴ Charles Darwin, *The Origin of the Species*, 1859, reprint (Penguin Books, 1985), p. 313. Also see first edition Harvard University Press, facsimile reprint (1964), p. 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 lower Silurian.

²⁵ Susumo Ohno, “The notion of the Cambrian pananimalia genome,” *Proceedings of the National Academy of Sciences USA* 93 (August 1996): 8475-78.

²⁶ Richard Dawkins, *The Blind Watchmaker* (New York: W.W. Norton & Company, 1987), p. 229.

²⁷ Darwin, *Origin*, p. 314; and Harvard edition, p. 308.

²⁸ J.W. Valentine and D.H. Erwin, “Interpreting Great Developmental Experiments: The Fossil Record,” in *Development as an Evolutionary Process*, eds. R.A. Raff and E.C. Raff (New York: Alan R. Liss, Inc., 1987), pp. 74-77. See diagram on p. 92.

²⁹ *Ibid.*, p. 89.

³⁰ *Ibid.*, p. 96.

³¹ Michael Foote, “On the probability of ancestors in the fossil record,” *Paleobiology* 22 (1996): 141-51.

³² *Ibid.*, p. 148.

³³ Michael Foote and Stephen J. Gould, “Cambrian and Recent Morphological Disparity,” *Science* 258 (1992): 1816.

³⁴ J.W. Valentine and D.H. Erwin, “Interpreting Great Developmental Experiments: The Fossil Record,” pp. 74-77. See diagram on p. 92.

³⁵ *Ibid.*, p. 97.

³⁶ Stephen Jay Gould, *Wonderful Life: The Burgess Shale and the Nature of History* (New York: W.W. Norton, 1989), p. 49.

³⁷ Richard Dawkins, *Unweaving the Rainbow: Science, Delusion, and the Appetite for Wonder* (Boston: Houghton Mifflin, 1998), p. 201.

³⁸ Darwin, *Origin*, p. 164.

³⁹ *Ibid.*, p. 168.

⁴⁰ Roger Lewin, “A Lopsided Look at Evolution,” *Science* 241 (July 15, 1988): 292.

⁴¹ 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.

⁴² Lewin, “Lopsided Look,” pp. 291-93.

⁴³ *Ibid.*, p. 291.

⁴⁴ *Ibid.*, p. 293.

⁴⁵ Although the following considerations used for determining the possibility of a Cambrian origin for stratigraphically post-Cambrian phyla are ultimately 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 9b and 10b 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 (i.e. number of differentiated cell types) and evolutionary relatedness were not considered in the formulation of Figures 9b or 10b.

⁴⁶ Of course, the pattern of phyletic first appearance graphed in 10b and 11b contradicts neo-Darwinism (and punctuated equilibrium) even more dramatically than the pattern graphed in 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 10b and 11b. 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 phyletic first appearance.

Recall also that our numerical estimates for the number of phyla and subphyla that first appear in the Cambrian are derived from an analysis of the references in the following scientific papers and paleontology texts: R.S. Boardman, *et. al.*, *Fossil Invertebrates*, p. 18; Wilmer, *Invertebrate Relationships: Patterns in Animal Evolution*, pp. 62-70; J.Y. Chen, *et. al.*, "Biology of the Chengjiang Fauna," pp. 11-106; J.W. Valentine, *et. al.*, "Fossils, molecules, and embryos: new perspectives on the Cambrian explosion," pp. 851-59.

⁴⁷ Subphyla are included here for the following reasons: 1) subphyla represent major variations on the phyletic *bauplan*; 2) phyla containing subphyla are rare (only five animal phyla have subphyla: Arthropoda, Chordata, Echinodermata, Mollusca, and Porifera), and therefore worthy of special consideration.

⁴⁸ S. Gilbert, J. Optiz, and R. Raff, "Review--Resynthesizing Evolutionary and Developmental Biology," *Developmental Biology* 173 (1996): 361.

⁴⁹ Roger Lewin, "Evolutionary Theory Under Fire," *Science* 210 (November 1980): 883.

⁵⁰ Gilbert, *et. al.*, "Review--Resynthesizing Evolutionary and Developmental Biology," pp. 357-72. Also see Rudolf A. Raff, *The Shape of Life: Genes, Development, and the Evolution of Animal Form* (Chicago: University of Chicago Press, 1966); also, Wallace Arthur, *The Origin of Animal Body Plans: A Study in Evolutionary Developmental Biology* (Cambridge: Cambridge University Press, 1997).

⁵¹ Gould, *Wonderful Life: The Burgess Shale and the Nature of History*, pp. 274-75.

⁵² *Ibid.*, pp. 272, 275-76.

⁵³ *Ibid.*, pp. 272-76.

⁵⁴ James W. Valentine, "The Macroevolution of Phyla," in *Origin and Early Evolution of the Metazoa*, eds. Jere H. Lipps and Phillip W. Signor (New York: Plenum Press, 1992), pp. 525-53; see section 3.2, "Soft-bodied Body Fossils," pp. 529-31.

⁵⁵ Jan Bergström, "Ideas on early animal evolution," p. 464: "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."

⁵⁶ Valentine, *et. al.*, "Interpreting Great Developmental Experiments: The Fossil Record," pp. 74-77.

⁵⁷ James W. Valentine, "Fossil Record of the Origin of Bauplane and Its Implications," in *Patterns and Processes in the History of Life*, eds. D.M. Raup and D. Jablonski (Berlin: Springer-Verlag, 1986), pp. 209-22, especially 215.

⁵⁸ 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.

⁵⁹ Chen *et. al.*, *The Chengjiang Biota*.

⁶⁰ Eric H. Davidson, Kevin J. Peterson, and R. Andrew Cameron, "Origin of Bilaterian Body Plans: Evolution of Developmental Regulatory Mechanisms," *Science* 270 (November 24, 1995): 1319-24.

⁶¹ 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 (July 3, 1987): 70.

⁶² 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.

⁶³ 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).

⁶⁴ 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.

⁶⁵ Michael Foote, "Sampling, taxonomic description, and our evolving knowledge of morphological diversity," *Paleobiology* 23 (1997): 181-206.

⁶⁶ *Ibid.*, p. 181

⁶⁷ *Ibid.* 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" (Michael J. Benton, "Early origins of modern birds and mammals: molecules vs. morphology," *BioEssays* 21 (1999): 1043-51; p. 1046.

⁶⁸ John P. Grotzinger, Samuel A. Bowring, Beverly Z. Saylor, and Alan J. Kaufman, "Biostratigraphic and Geochronologic Constraints on Early Animal Evolution," *Science* 270 (October 27, 1995): 598-604.

⁶⁹ R. Monasterski, "Ancient Animal Sheds False Identity," *Science News* 152 (August 30, 1997): 32.

⁷⁰ *Ibid.*

⁷¹ *Ibid.*

⁷² Mikhail A. Fedonkin and Benjamin M. Waggoner, "The Late Precambrian fossil *Kimberella* is a mollusc-like bilaterian organism," *Nature* 388 (August 28, 1997): 868.

⁷³ 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*, eds. A.M. Simonetta and S. Conway Morris (Cambridge: Cambridge University Press, 1991), pp. 25-34.

⁷⁴ 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?" presented to: *The Origin of Animal Body Plans and Their Fossil Records* conference (Kunming, China, June 20-26, 1999). Sponsored by the Early Life Research Center and The Chinese Academy of Sciences.

⁷⁵ Valentine, *et al.*, "Interpreting Great Developmental Experiments: The Fossil Record," p. 132.

⁷⁶ Sponges (phylum porifera) actually pre-date the first appearance of the other phyla present in the Ediacaran.

⁷⁷ 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, p. 375; B. Runnegar, "Evolution of the Earliest Animals," in *Major Events in The History of Life*, ed. J.W. Schopf (Boston: Jones & Bartlett, 1992).

⁷⁸ B. Runnegar, "Proterozoic eukaryotes: Evidence from biology and geology," in *Early Life on Earth*, Nobel Symposium No. 84, ed. S. Bengtson (New York: Columbia University Press, 1994); 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, India: Geological Society of India, 1991), pp. 181-223.

⁷⁹ The beginning of the Cambrian period (and the Paleozoic era) 543 mya 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 to 530 mya). 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.

⁸⁰ Gregory A. Wray, Jeffrey S. Levinton, and Leo H. Shapiro, "Molecular Evidence for Deep Precambrian Divergences Among Metazoan Phyla," *Science* 274 (October 25, 1996): 568; for another 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," *Royal Society of London, Series B* 266 (no. 1415): 163; see also Geerat J. Vermeij, "Animal Origins," pp. 525-26 of same issue; see also Richard A. Fortey, Erek E.G. Briggs, and Matthew A. Wills, "The Cambrian evolutionary explosion recalibrated," *BioEssays* 19, no. 5: 429-34.

⁸¹ *Ibid.*

⁸² *Ibid.*

⁸³ *Ibid.*

⁸⁴ R.L. Hotz, "Finding Turns Back Clock for Earth's First Animals," *Los Angeles Times*, October 25, 1996, PA1 and A14.

⁸⁵ Wray, *et al.*, "Molecular Evidence for Deep Precambrian Divergences Among Metazoan Phyla," p. 609.

⁸⁶ *Ibid.*, p. 611.

⁸⁷ 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):167-177. Malcolm S. Gordon, "The Concept of Monophyly: A Speculative Essay," *Biology and Philosophy* 14 (1999):331-348. Carl Woese, "The universal ancestor," *Proceedings of the National Academy of Sciences USA* 95 (1998):6854-6859.

⁸⁸ Bernard John and George Miklos, *The Eukaryote Genome in Development and Evolution* (London: Allen and Unwin, 1988), p. 293.

⁸⁹ James W. Valentine, *et al.*, "Fossils, molecules and embryos: new perspectives on the Cambrian explosion," pp. 851-59, especially 856.

⁹⁰ Simon Conway Morris, "Evolution: Bringing Molecules into the Fold," *Cell* 100 (Jan. 7, 2000): 5-6.

⁹¹ *Ibid.*

⁹² Simon Conway Morris, "Early Metazoan Evolution: Reconciling Paleontology and Molecular Biology," *American Zoologist* 38 (1998): 870.

⁹³ Michael Behe, *Darwin's Black Box*, (New York: The Free Press, 1996).

⁹⁴ James W. Valentine, "Late Precambrian Bilaterians: Grades and Clades," in *Tempo and Mode in Evolution: Genetics and Paleontology 50 Years After Simpson*, eds. W.M. Fitch and F.J. Ayala (Washington, DC: National Academy Press), pp. 87-107.

⁹⁵ (1964, p.16).

⁹⁶ J. Bowie and R. Sauer, "Identifying Determinants of Folding and Activity for a Protein of Unknown Sequences: Tolerance to Amino Acid Substitution," *Proceedings of the National Academy of Sciences USA* 86 (1989): 2152-56; J. Bowie, J. Reidhaar-Olson, W. Lim, and R. Sauer, "Deciphering the Message in Protein Sequences: Tolerance to Amino Acid Substitution," *Science* 247 (1990): 1306-10; J. Reidhaar-Olson and R. Sauer, "Functionally Acceptable Solutions in Two Alpha-Helical Regions of Lambda Repressor," *Proteins, Structure, Function, and Genetics* 7 (1990): 306-16.

⁹⁷ See also: M.F. Perutz and H. Lehmann, "Molecular Pathology of Human Hemoglobin," *Nature* 219 (1968): 902-09.

⁹⁸ J. Bowie and R. Sauer, "Identifying Determinants of Folding and Activity for a Protein of Unknown Sequences: Tolerance to Amino Acid Substitution," pp., 2152-56; J. Bowie, J. Reidhaar-Olson, W. Lim, and R. Sauer, "Deciphering the Message in Protein Sequences: Tolerance to Amino Acid Substitution," pp. 1306-10; J. Reidhaar-Olson and R. Sauer, "Functionally Acceptable Solutions in Two Alpha-Helical Regions of Lambda Repressor," pp. 306-16.

⁹⁹ Douglas D. Axe, "Biological function places unexpectedly tight constraints on protein sequences," *Journal of Molecular Biology* 301(3): 585-596.

¹⁰⁰ Michael Denton, *Evolution: A Theory in Crisis*, (London: Adler and Adler, 1986), p. 317-22.

¹⁰¹ Dembski, *The Design Inference* (Cambridge: Cambridge University Press, 1998).

¹⁰² Dembski's universal probability bound actually reflects the "specificational" resources not the probabilistic resources in the universe. Dembski's calculation determines the number of specifications possible in finite time. It nevertheless has the effect of limiting the "probabilistic resources" available to explain the origin of any *specified* event of small probability. Since living systems are precisely specified systems of small probability the universal probability bound effectively limits the probabilistic resources available to explain the origin of specified biological information. William A. Dembski, *The Design Inference* (Cambridge: Cambridge University Press, 1998), pp. 175-223. Emile Borel, *Probabilities and Life*, trans. M. Baudin (New York: Dover, 1962), p. 28.

¹⁰³ Richard Dawkins, *The Blind Watchmaker*, pp. 54, 139.

¹⁰⁴ Stephen C. Meyer, "DNA by Design: An Inference to the Best Explanation for the Origin of Biological Information," *Rhetoric and Public Affairs* 1, no. 4, (1998) 519-556, esp. 528-530.

¹⁰⁵ Ohno, "The notion of the Cambrian pananimalia genome," p. 8475-8.

¹⁰⁶ *Ibid.*, pp. 8475-6.

¹⁰⁷ M.F. Perutz and H. Lehmann, "Molecular Pathology of Human Hemoglobin," pp. 902-09.

- ¹⁰⁸ P.W.J. Rigby, B.D. Burleigh, and B.S. Hartley, "Gene Duplication in Experimental Enzyme Evolution," p.200. E. Zuckerkandl, "The Appearance of New Structures in Proteins During Evolution," p.21.
- ¹⁰⁹ George L.G. Miklos, "Emergence of organizational complexities during metazoan evolution: perspectives from molecular biology, paleontology and neo-Darwinism," *Memoirs of the Association of Australasian Paleontologists* 15 (1993): 7-41; p. 26.
- ¹¹⁰ Dawkins, *The Blind Watchmaker*, pp.47-49.
- ¹¹¹ E. Zuckerkandl, "The Appearance of New Structures in Proteins During Evolution," p.21.
- ¹¹² Stuart Kauffman and Simon Levin, "Towards a General Theory of Adaptive Walks on Rugged Landscapes," *Journal of Theoretical Biology* 128 (1987): 11-45. See also Stuart Kauffman, *Origins of Order: Self-Organization and Selection in Evolution* (Oxford: Oxford University Press, 1993), pp. 34-36; p. 35: "Thus adaptation, which must search such rugged landscapes, tends to become trapped in very small regions of the space. Worse, due to the increasing number of conflicting constraints, the peaks become ever poorer compromises among those constraints, withering to mere bumps hardly better than chance agglomerations of the parts."
- ¹¹³ Marcel Shutzenberger, "Algorithms and the Neo-Darwinian Theory of Evolution," in P.S. Morehead and M.M. Kaplan, eds., *Mathematical Challenges to the Darwinian Interpretation of Evolution*, (Wistar Institute Symposium Monograph, 1967).
- ¹¹⁴ Ohno, "The notion of the Cambrian pananimalia genome," pp. 8475-78.
- ¹¹⁵ *Ibid.*
- ¹¹⁶ Simon Conway Morris, "Evolution: Bringing Molecules into the Fold," pp. 1-11.
- ¹¹⁷ Russell F. Doolittle, "The Origins and Evolution of Eukaryotic Proteins," *Philosophical Transactions of the Royal Society of London B* 349 (1995): 235-40.
- ¹¹⁸ Stephen L. Wolfe, *Molecular and Cellular Biology* (Belmont, CA: Wadsworth, 1993), pp. 3, 6-19.
- ¹¹⁹ Rebecca A. Clayton, Owen White, Karen A. Ketchum, and J. Craig Ventner, "The First Genome from the Third Domain of Life," *Nature* 387 (1997): 4459-62.
- ¹²⁰ Stephen L. Wolfe, *Molecular and Cellular Biology*, pp. 546-50.
- ¹²¹ *Ibid.*
- ¹²² H. Lodish, D. Baltimore, et. al., *Molecular Cell Biology* (New York: W.H. Freeman, 1994), pp. 347-48. Stephen L. Wolfe, *Molecular and Cellular Biology*, pp. 546-47.
- ¹²³ Edgell and Russell Doolittle, "Archaeobacterial genomics: the complete genome sequence of *Methanococcus jannaschii*," *BioEssays* 19 (no. 1, 1997): 1-4. Michael Y. Galperin, D. Roland Walker, and Eugene V. Coonin, "Analogous Enzymes: Independent Inventions in Enzyme Evolution," *Genome Research* 8 (1998): 779-90.
- ¹²⁴ Stephen L. Wolfe, *Molecular and Cellular Biology*, pp. 580-81, 597.
- ¹²⁵ *Ibid.*, pp. 581-82, 598-600, 894-96.
- ¹²⁶ *Ibid.*, p. 975.
- ¹²⁷ *Ibid.*, pp. 955-975.
- ¹²⁸ *Ibid.*, p. 580.
- ¹²⁹ *Ibid.*, pp. 17-19.
- ¹³⁰ *Ibid.*, pp. 955-975.
- ¹³¹ George Johnson, "Molecular Biology Doesn't Disprove Evolution, Despite Arguments Put Forth By Creationists," *St. Louis Post-Dispatch*, November 12, 1999, A15.
- ¹³² T.H. Frazzetta, "Modeling Complex Morphological Change in Evolution, and A Possible Ecological Analogy," *Evolutionary Theory* 6 (1982): 127-41; p. 129.
- ¹³³ *Ibid.*, p. 130.
- ¹³⁴ According to the serial endosymbiotic theory (SET), a proto-eukaryote engulfed, via the complex process of phagocytosis, an alpha-proteobacterium (which then evolved into mitochondria) and cyanobacterium (which then evolved into plastids [chloroplasts]). Obviously an essential step in this hypothesis would be the ability to engulf another organism – yet SET provides no candidates for the proto-eukaryote equipped with this function. "The proto-eukaryote," J.R. Brown and W.F. Doolittle note, "was proposed to have a rudimentary cytoskeleton, since such innovation would be necessary for phagocytosis...Although bacteria living intracellularly in a different bacterial species have been reported, phagocytosis by a bacterium has never been observed. Nor is there any evidence for the existence of the sophisticated RNA-based organisms with cytoskeletons" ("*Archaea* and the Prokaryote-to-Eukaryote Transition," *Microbiology and Molecular Biology Reviews* 61 (1997): 456-502; p. 463).

¹³⁵ Leigh Van Valen, "How do major evolutionary changes occur?" *Evolutionary Theory* 8 (1988): 173-76; p. 173.

¹³⁶ Keith Stewart Thomson, "Macroevolution: The Morphological Problem," *American Zoologist* 32 (1992): 106-12; p. 111.

¹³⁷ Bernard John and George L.G. Miklos, *The Eukaryote Genome in Development and Evolution* (London: Allen & Unwin, 1988), p. 309.

¹³⁸ See, e.g., the special issue of *Development* dedicated to the large-scale mutagenesis of the model vertebrate, *Danio rerio* (the zebrafish), P. Haffter *et al.*, "The identification of genes with unique and essential functions in the development of the zebrafish, *Danio rerio*," *Development* 123 (1996):1-36; or the many fruitfly mutagenesis experiments summarized in Michael Bate and Alfonso Martinez Arias, eds., *The Development of Drosophila melanogaster* (Plainview, N.Y.: Cold Spring Harbor Laboratory Press, 1993), 2 vols. Summarizing the evidence from a wide range of animal systems, Wallace Arthur writes, "Those genes that control key early developmental processes are involved in the establishment of the basic body plan. Mutations in these genes will usually be extremely disadvantageous, and it is conceivable that they are *always so* (*The Origin of Animal Body Plans* [Cambridge: Cambridge University Press, 1997], p. 14; emphasis in original). Arthur goes on to speculate that because developmental regulatory genes often differ between phyla, perhaps "mutations of these genes are sometimes advantageous" (p. 15). He offers no evidence for such mutations, however, other than as a deduction from his prior assumption of common descent.

¹³⁹ C. Nusslein-Volhard and E. Wieschaus, "Mutations affecting segment number and polarity in *Drosophila*." *Nature* 287 (1980): 795-801. P.A. Lawrence and G. Struhl. "Morphogens, Compartments and Pattern: Lessons from *Drosophila*?" *Cell* 85 (1996): 951-61.

¹⁴⁰ Leigh Van Valen, "How do major evolutionary changes occur?" *Evolutionary Theory* 8 (1988): 173-76; p. 173.

¹⁴¹ John F. McDonald, "The Molecular Basis of Adaptation: A Critical Review of Relevant Ideas and Observations," *Annual Review of Ecology and Systematics* 14 (1983): 77-102; p. 93.

¹⁴² *Ibid.*

¹⁴³ Charles Darwin, *The Origin of Species*, p. 108 (first edition).

¹⁴⁴ Soren Lovtrup, "Semantics, Logic and Vulgate Neo-Darwinism," *Evolutionary Theory* 4 (1979): 157-72; p. 162.

¹⁴⁵ Brian C. Goodwin, "What Are The Causes of Morphogenesis?" *BioEssays* 3 (1985): 32-36, and *How The Leopard Changed Its Spots* (New York: Scribner's, 1994). H.F. Nijhout, "Metaphors and the role of genes in development," *BioEssays* 12 (1990): 441-46. Jonathan Wells, "Unseating Naturalism: Recent Insights from Developmental Biology," in *Mere Creation*, ed. by William A. Dembski (Downer's Grove, IL: Intervarsity Press, 1998). Jan Sapp, *Beyond The Gene* (New York: Oxford University Press, 1987).

¹⁴⁶ Wolfe, *Molecular and Cell Biology*, p.17-19.

¹⁴⁷ Jonathan Wells, "Making Sense of Biology: The Evidence for Development by Design," *Touchstone*, July/August (1999): pp. 51-55, esp. p.52.

¹⁴⁸ Of course, many proteins do have binding affinities with other proteins and these "self-organizational" properties do account for the structure and function of many protein complexes and structures within cells. Nevertheless, these affinities do not fully account for (a) the structure of cells, (b) the structures formed by cells within organisms, or (c) the architecture of novel animal body plans.

¹⁴⁹ James W. Valentine, "Why No New Phyla after the Cambrian? Genome and Ecospace Hypotheses Revisited," *Palaaios* 10 (1995): 190-94; see also Jan Bergström, "Ideas on early animal evolution," pp. 460-66; p. 464: "There is absolutely no sign of convergence between phyla as we follow them backwards 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."

¹⁵⁰ Michael Denton, *Evolution: A Theory in Crisis*, (London: Adler and Adler, 1986), p. 313.