

Developmental genetics supports creation theory

***Homology, Genes, and
Evolutionary Innovation***

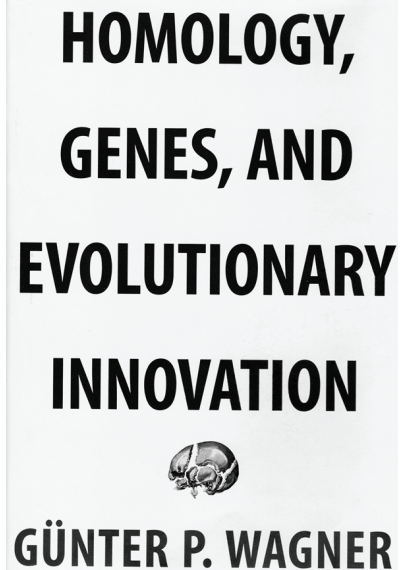
Günter P. Wagner

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Walter ReMine

This book focuses on the intersection of genetics and embryology—called developmental genetics—which seeks to understand how DNA strings are converted into functioning organs and body plans. Our understanding of this breathtakingly complex phenomenon is still exceedingly rudimentary, though modern techniques have finally opened up research. A typical technique maps out where and when, in the embryo, a particular gene is expressed. Another technique suppresses (or ‘knocks out’) a particular gene and then observes which embryonic characters do, and do not, develop. Most of Wagner’s book (~70%) is material of this type, and can be fully embraced by anyone (evolutionist or creationist). Offhand, I see no reason to doubt that material. However, it is quite technical—a slow, tedious read—and not recommended for the pedestrian. As a typical example:

“At stage 40, the pectoral fin buds show classical early colinear *HoxD* gene expression. *HoxD13* is expressed at the posterior margin of the fin bud nested within a slightly more extensive *HoxD12* expression domain, which itself is nested in a *HoxD11* expression domain that extends even further anteriorly” (p. 350).



There are creationist scholars for whom such material is fine dining.

This is an evolutionist book, but it never proclaims new evidence against creation or for macro-evolution. The book never engages the creation-evolution debate. There is an unspoken reason for that: evolutionists are bewildered by the new data and how to explain it. They are now vying to amend evolutionary theory to accommodate this new data. This book begins that process.

“Evo-devo”¹ is the nickname for this field that attempts to explain developmental genetics via evolutionary theory. Toward this explanatory goal, Wagner proposes new concepts and terminologies as a possible basis for further research. (That material comprises the other 30% of the book, which is a bit more accessible to non-specialist readers.) I will comment on that material.

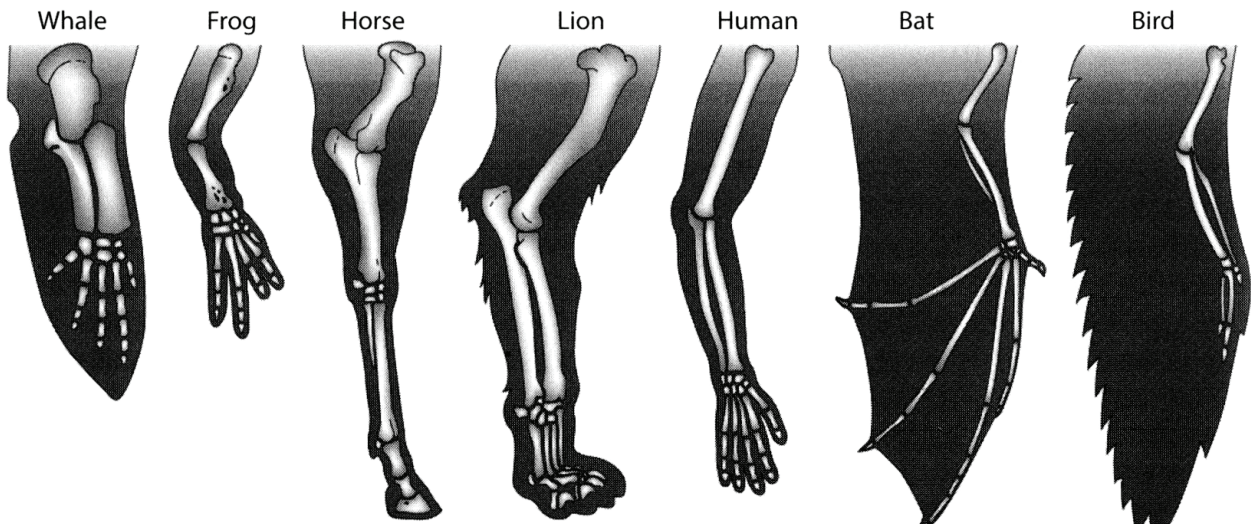


Figure 1. Wagner's 'textbook example of homology' (p. 24)

Homology and body plans

The book focuses on the evolutionary concept of homology. Unfortunately, homology is almost always defined by how it is *explained*, not by how it is observed. For example, Wikipedia defines homology as “the existence of shared ancestry between a pair of structures, or genes, in different species”. Traditional examples are the hands, paws, hooves, wings, and fins of mammals, which evolutionists say are ‘homologous’, or due to shared ancestry (see also figure 1).

The book ties three concepts together: (1) there exists a set of genes; (2) these are essential in the development of innovative body plans; and (3) evolutionists *believe* these are inherited from some common ancestor (i.e. these are a homology). In short, *Homology, genes, and evolutionary innovation* is an apt title for the book.

The evolutionary origin of novel body plans has always been controversial, especially these days due to Stephen Meyer’s excellent book, *Darwin’s Doubt* (2013),² about the sudden appearance of very disparate body plans during the Cambrian Explosion of fossil life-forms. Wagner acknowledges that the origin of novel characters and novel body plans “is one of the most important but least

researched questions in evolutionary biology” (p. 3). The fossil record and Cambrian Explosion show only the form and shape of organs and body plans (this is called morphology). Wagner acknowledges these are “one of the most difficult classes of homology relationships to explain” (p. 1).

Though homology is said to be a major evidence for evolution, the concept itself is problematic. Wagner notes: “There is no consensus, nor even a narrow consensus on the subject of homology and its mechanistic foundations. ... Every biologist will agree that homology is a confused and confusing subject” (p. xii). “No lasting progress can be made in explaining body plan evolution without a thorough housecleaning. The problem is that *many contradictory positions* on homology *made sense within* the research programs in which they were introduced [emphasis added]” (p. 5). So Wagner aims to update the homology concept, to make it suitable specifically for evo-devo research.

Major problems

The book indicates various problems facing evo-devo. For example: “It is now well established and common place that all animals

share a set of conserved genes that are causally important for the development of body plan characters. This was a *deeply surprising discovery* because, in the tradition of neo-Darwinian evolutionary biology, the possibility of homologous genes among distantly related species was explicitly dismissed [emphasis added]” (p. 26).

Wagner does a poor job revealing that fundamental problem. So, I clarify it here. Many of the important body plan genes are widely shared among disparate animal phyla. To evolutionists, that means these genes must have existed within some ancient common ancestor of all these groups. But these body plans are quite different from each other, as different as vertebrates, starfish, jellyfish, and insects. Therefore the common ancestor must have existed *much earlier* than the first appearance of these groups—much earlier than the Cambrian Explosion. In other words, these *widely important body plan genes* must have originated back at a time when there were microorganisms and *relatively little else with a body*. How could genes originating in microorganisms or proto-jellyfish, say, be essential in widely diverse body plans today? It is awkward to claim natural selection *originally* created these genes to control diverse

body plans: (1) because that common ancestor (whatever it was) didn't have much of a body; (2) because natural selection cannot create something for a *future* use; and (3) it is unlikely these genes, at their original inception, *just happened* to be well-suited to a future use for creating such diverse body plans.

This problem is causing a revolution in evolutionary thinking. Many evolutionary specialists now assert that natural selection is *not sufficient*, and some additional explanations are needed.^{3,4}

Wagner likewise thinks natural selection is not sufficient.⁵ He emphasizes an additional explanation, called structuralism.⁶ Structuralism focuses on form (or structure), and says this places *constraints* on the types of change that can occur. Thus, evolution is *constrained* by the structure of an organism, and this limits the direction evolution can go. Some characters are kept, not because of their function, but because they are built into the structure of the organism. In a sense, evolution is 'stuck' with them.

That conflicts with the selectionist explanation, which argues that a given character was kept, or lost, because of its effect on function. It also conflicts with the neutralist explanation, which argues that a given character was kept, or lost, precisely because it has *no effect* on function. All styles of explanation—structuralist, selectionist, neutralist, and much more—are part of the evolutionist's vast, structureless, theoretical smorgasbord—where each entrée is chosen, or omitted, based on the evolutionist's needs of the moment.

A second problem further surprised evolutionists: homologous characters are often not due to homologous genes.

"What is problematic, though, is the fact that clearly homologous characters can derive from different developmental mechanisms in different species" (p. 37).

"There is mounting evidence that homologous characters from distantly related organisms, like

grasshoppers and fruit flies, *often use quite different genes for the development of clearly homologous characters*, like insect body segments. Hence, *the identity of morphological characters cannot be explained by the identity of the set of genes that directs their development* [emphasis added]" (p. 2).

"... *the most challenging problem* when attempting to explain character identity; namely, *unquestionable homologies* (i.e. character identities across species) are often associated with *extensive variations in developmental pathways and mechanisms* that produce these characters [emphasis added]" (p. 6). "There is a growing body of evidence ... that shows that seemingly the same character can be realized by different genes in different species" (p. 74).

"Continuity of morphological characters is not subscribed by continuity of genetic information. This seems a *pretty depressing situation* ... and motivates the notion that homology may be an illusion ... [emphasis added]" (p. 90).

"... developmental pathways of homologous characters can vary considerably between species without affecting the identity of the characters concerned" (p. 412).

"... similarity of a gene regulatory network of some tissues, even one in which multiple genes are involved per se, is not strong evidence for homology" (p. 113).

In short, there is considerable independence, or disconnect, between morphology and its underlying genes—they are not homologous together. This throws a monkey wrench into the homology concept. Will the real homology please stand up: is it morphology, or is it genes, that determine homology?

It gets worse. As the embryo develops, fundamentally disparate cell types emerge, multiply, and eventually form distinctive body organs.

Traditionally, evolutionists viewed these distinctive cell types⁷ as an important clue about the homology of the organs they produce. Wagner indicates this view has been countered by modern evidence. Wagner writes there are,

"... a number of examples for which clearly homologous characters derived from *different* cell populations during embryogenesis or followed *different* developmental pathways to arrive at the same adult morphology. One possible reaction to this fact is to assert that homology is a meaningless concept [emphasis added]" (p. 90).

Nonetheless, he pursues a "second option—namely, to assume, for example, that embryological origins are *irrelevant* for the developmental basis of homology ... [emphasis added]" (p. 90).

So for Wagner, genes are not reliable, and embryological origins are not relevant, as indicators of homology. He therefore introduces a new concept involving 'networks' of genetic material. His concept, called a Character Identity Network or ChIN,⁸ serves as a possible source of homology, since none of the other things is a reliable source. The concept is as yet nebulous and unclear. Its purpose, it seems, is to encourage 'research', and to enable the spinning of new explanations.

Homology vs convergence

Homology has long been held as a major evidence in favour of evolution. Unfortunately, evolutionists typically define it in terms of *explanation*, not in terms of observation. That raises the question: how can we observe homology? Without a clear way to do that, evolutionists are precariously close to saying: "The shared similarities between mammalian hands, paws, hooves, wings, and fins are a homology, *because we evolutionists say it's a homology*—and homology, by definition, is due to shared ancestry.

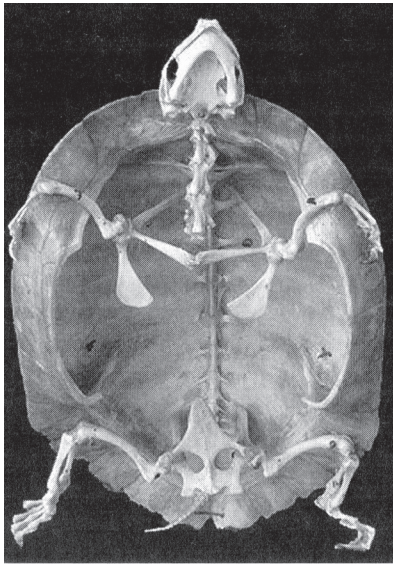


Figure 2. A turtle fossil from Wagner's book. Wagner writes: "This is the problem for the Darwinian way of thinking: what evolutionary sequence can explain the origin of the turtle body plan in a series of small steps when the scapula can be only either outside or inside of the rib cage? What would the intermediate steps be? Matters are not helped by the fact that the fossil record does not reveal any intermediate morphologies. Turtles seem to be the ultimate hopeful monsters—a sudden, radical deviation from the ancestral body plan without any plausible or documented intermediate forms. What further confounds the situation is that even their phylogenetic affiliation with fossil forms is difficult to assign" (p 180).

So, evolution is a fact!" We need a way to cut through any such argument by bald assertion or circular reasoning. In particular, how do we observe or identify a homology? Can that be done objectively, without relying on evolutionists' say so?

Here is the deeper problem. When two species share a similar character, then it might perhaps be explainable by common descent (i.e. a homology), but oftentimes it is *unexplainable by common descent*. Evolutionists call these latter characters 'convergences' or 'homoplasies', and these are abundant in nature—at the morphological, embryological, and molecular levels.⁹ An example is your eye and the octopus eye—which are remarkably similar,

each containing a lens, iris, retina, an optic nerve, and muscles for rotating the eye and controlling the iris—yet these similarities cannot be explained by common descent.

Evolutionists partition similar characters into two types: those that can be explained by common descent versus those that cannot. Typically, evolutionists silently set aside the latter group, omitting it from discussion as though it were irrelevant. Wagner does that. He attempts to clarify the concept of homology as a central focus of his book, yet remarkably he scarcely mentions convergence. That omission dooms any attempt at clarification.

Presentations aimed at convincing the general public that evolution is a 'fact' drastically downplay convergence, or omit it altogether. This approach—of brushing convergence aside—is used when evolutionists are *trying to convince you* that 'all is well in the house of evolution'. Wagner is in that mode when wading through the new data from developmental genetics—which is bewildering evolutionists. For Wagner's purposes, the topic of convergence would be an annoyance. Also, it would confound his attempt to clarify the homology concept. So he silently omitted it.

All evidence favours evolution?

Contrast that with the 2004 book, *Life's Solution: Inevitable Humans in a Lonely Universe*, where Simon Conway Morris *first* takes evolution as an undeniable fact, and *then* focuses exclusively on convergence, citing many striking examples of it. For example, according to evolutionists, the origin of sight occurred over 40 separate times (such as the compound eye of the fly), and the origin of a lens-bearing eye occurred at least seven separate times, as it occurs in vertebrates, cephalopods (e.g. octopus), jellyfish, a spider, annelid worms, and crustaceans. Morris then uses convergence (and its abundance) as *evidence*

for the power of natural selection. He therefore concludes: if life exists elsewhere in the universe, then (by convergence) it will almost surely be much like life on earth, and will likely include large-brained, bilateral, upright hominids much like ourselves. His book is packed with evidence against evolution, yet he takes evolution as an undeniable fact.¹⁰

Here is why. In the evolutionist's way of thinking, there can be no evidence against evolution. Instead, all evidence *against* evolution is reinterpreted as evidence *in favour* of some evolutionary explanation—no matter how far-fetched, no matter the paucity of experimental demonstration, and no matter how untestable—because evolution is a 'fact'! For example, there exist similar characters that cannot be explained by common descent,¹¹ and these are abundant in nature—which makes this remarkable evidence against evolution. Instead, evolutionists interpret all that as evidence *in favour* of the 'incredible power of natural selection'. This same faulty thinking occurs many more times: on the large morphological gaps in the fossil record (i.e. lack of gradualism over large scales); on the systematic absence of clear-cut ancestors and lineages; on the bacterial flagellum; on the biomolecular pattern they call 'concerted evolution'; and on the origin of life, to name a few. This type of thinking skews the evolutionist's wording everywhere. Raw, speculative evolutionary explanations are given as 'plausible', 'believable', 'satisfactory', or 'fact'. Virtually all evolutionist books, including Wagner's, fit this mould of thinking. This is reflected in the evolutionist's often repeated slogan: 'Evolution is a fact; we evolutionists are just uncertain *how* it occurred.'

Objective homology

Evolutionists need some objective method for *observing* and distinguishing homology from convergence.

One suggestion, often employed, is to use cladistics. Cladistics classifies species into a nested hierarchical pattern, called a cladogram. This is like the classification of library books, where some books are science books, *of which some* are physics books, *of which some* are nuclear physics books, and so forth, in a nested pattern of subsets, within subsets, within subsets—like nested Chinese boxes. In particular, cladistics *seeks to create* a classification that maximizes the number of nested characters, and minimizes the number of non-nested characters. This method (known as pattern cladistics or transformed cladistics) is scientifically neutral (and usable by anyone, creationist or evolutionist) and doesn't allow evolutionary storytelling to distort the results. Explaining the results comes later.

After the best cladogram is identified, evolutionists *explain* the non-nested characters as 'convergences' and the nested characters as 'homologies'. In short, cladistics robotically minimizes the number of 'convergences' and maximizes the number of 'homologies'.

However, pattern cladistics doesn't work well for evolutionists. So they created a version called evolutionary cladistics (or misleadingly, 'phylogenetic cladistics'¹²), which allows evolutionary storytelling to affect the results. Evolutionists can change the results by using a loss explanation, where they claim a given character was lost in some organisms and kept in others. Some evolutionists (including Wagner) also claim a character can be *re-evolved* after it was lost. These speculative scenarios can alter the topology of the cladogram, *thereby altering the identification of convergences and homologies*.¹³ In other words, by using evolutionary storytelling, evolutionists have some latitude to reclassify convergences and homologies in various ways—depending on their needs at the time. They have some flexibility.

Nonetheless, it's still not enough flexibility for Wagner's purposes, so he rejects any strict reliance on cladistics and regards it as incompatible with his research program.¹⁴ He is left with no independent means to identify homology. Instead, cladistic findings are viewed as merely suggestive: they are embraced or brushed aside, depending on the needs of evo-devo storytelling.

Wagner's solution is to define homology vaguely, in effect allowing evo-devo researchers to redefine it case-by-case. He says: "[W]e shall strive to fill in with biological detail what we mean when we say two characters are the same [emphasis in original]" (pp. 244–245). In other words, two characters may be 'the same' (and therefore homologous) based on morphology, or genes, or embryological cell-type, or ChINs, or whatever else the researcher chooses to grasp as a 'biological detail'. The concept is wide open. Wagner insists: "*it may not do any harm to abandon the quest for definitions of homology [emphasis in original]*" (p. 244).

Wagner wants to press onward with evo-devo research. He therefore thinks it better to have vaguely defined terms than no terms at all.

The separate-vs-shared problem

Other problems are encountered when attempting evolutionary explanations of specific body plans. Here are some commonplace issues: (1) Natural selection cannot improve a character unless its genetics are *exposed* to selection—or 'individualized'¹⁵—and that requires the genetics for that character to be *separate* and distinct from other things. On the other hand, (2) evolutionists often want improvements to be *shared* by many places in the body—so improvements in a design (say to fin, feather, limb, muscle, tendon, or eye) would occur to *all* instances of these in the body—and this would require some means of

sharing the same genetic instructions among all (and only) instances of that design. But those are two contradictory requirements—*separate* genetic instructions versus *shared* genetic instructions. *You cannot have them both at the same time*. Therefore, evolutionists need some means of switching back-and-forth, as needed in their storytelling. Also, the *genetic reorganizations* (both in the sharing and the separating directions) need to be *accurately targeted* to avoid disrupting the rest of the genome.

For example, suppose you want to explain the evolutionary origin of fish fins. You might suggest, say, that natural selection first created genetic instructions for a crude fin, eventually followed by a genetic instruction to "do it four times" (with bilateral symmetry), to make two crude front fins and two crude hind fins. At that point, it is not possible to specialize some fins separately from others, because "do it four times" does not expose the fins separately to selection. To allow specialization of front fins differently from hind fins, the fin genetics must first be *reorganized* to allow them to have separate genetics—so they can be separately selected. Such genetic reorganization is not, in itself, adaptive because it has no immediate benefit. And since natural selection cannot select for some future use, the genetic reorganization must occur without significant guidance from natural selection. Moreover, once that is done, one cannot explain *shared* changes to all four fins because they now have separate genetics.

A similar problem occurs for feathers, where a *shared* feather design is used all over the body, yet each feather is *specialized* for a purpose (e.g. flight feathers for flight versus downy feathers for warmth) and for length and colour.

In this way, one evolutionary explanation can make further evolutionary explanations awkward or implausible. When placed end-to-end, over the long haul, evolutionary explanations get

tripped up by their own feet, as they get entangled in their contradictory requirements. This type of problem occurs frequently in evo-devo.

Evo-devo explanations need accurately targeted genetic reorganization, back and forth between *separate* genetics versus *shared* genetics. The origin of finely designed fish fins—plus their further transformation into mammalian hands, paws, hooves, wings, and fins—would require it. Your hands are highly specialized *separately* from your feet, yet your hands and feet *share* the fact that each has five digits—quite unlike fish fins. Likewise for the wings and feet of bats. Likewise for the fins of whales. And so forth. Targeted genetic reorganization, of the proper sort, would be required many, many times,¹⁶ periodically interleaved with natural selection, of the proper sort.¹⁷ Are we to believe nature dances to the fancy tune plucked by evo-devo storytellers?

One-to-one correspondence

To explain the fate of a character, evolutionists typically assume it is controlled *cleanly by one gene*—that is, the gene has *only one effect* and no side effects. Therefore, any selective effect on the character (be it advantageous or disadvantageous) will directly apply likewise to the gene. Under that assumption, the fate of the character, and the fate of the gene, are substantially tied together, one-to-one.¹⁸ This made evolutionary storytelling seem vastly more plausible, and so it was used for decades in technical evolutionary genetics textbooks, in computer simulations, and especially in presentations aimed at an unwary general public.

That assumption is not plausible. It is now known that most genes affect *more than one* character—this is called *pleiotropy*. Think of it as side effects. Studies now show that, on average, each gene affects 7+ different characters, with some genes affecting

as many as 35 different characters. How can macro-evolution occur, when gene side effects are *interlocking* in so many different ways? This makes macro-evolution vastly more awkward to justify, which is why evolutionary apologists still avoid the issue and tend to omit it.¹⁹

A similar conceptual avoidance occurs in Wagner's book, where he assumes away these types of problems. He uses a variety of terms for special groupings of genes,²⁰ so I here simply call them 'gene networks'. At key points in his explanations, he needs his gene networks to have only *one* effect on development²¹—so they do not have multiple diverse (undesirable) effects on development—and therefore his gene networks are *cleanly exposed* to natural selection (at least, when he wants them to be). He assumes away the possibility that his gene networks have multiple undesirable side effects that are out of control of the evolutionary storyteller. His assumption is silent and implicit, accomplished by omitting any serious discussion of the problem.

Now combine these issues together: (1) development is controlled by networks of genes; (2) where each gene (and additionally, the 'emergent properties' of the evolving gene network) typically has *many side effects*; and (3) evolutionary storytelling *requires* frequent genetic reorganizations—which suddenly exposes these many various side effects *to a different genetic context*. Notice those three are *random* with respect to each other.²² Other than wishful thinking, are there any testable scientific grounds to believe this process isn't overwhelmingly harmful?

Concerning creation

Though Wagner did not intend it, his material is exceedingly encouraging to creationists, and to Message Theory in particular. I discuss this next.

Message Theory claims life-forms were reasonably designed to accomplish three goals simultaneously. The biological designs are: (1) for survival; (2) to look like the product of *one* designer (rather than the product of multiple designers acting independently); and also (3) to resist macro-evolutionary explanations (all of them, not just Darwin's). Wagner's material confirms 2 and 3 (and does not dispute 1).

For example, the existence of *shared genes*—essential to the body plans of diverse animals—helps unify life-forms as the product of one designer, while those same genes are a radical problem for macro-evolution. All three design goals (1, 2, and 3) are accomplished simultaneously. That fits Message Theory well.

Or, take the other data: homologous structures are often not caused by homologous genes nor by homologous embryology. The similar structures shared between species indicates they had the *same* designer. But they are often caused by *different* genes and *different* embryological pathways, which *resists* macro-evolutionary explanations. All three design goals (1, 2, and 3) are accomplished simultaneously. That fits Message Theory well.

This pattern of data turns evo-devo explanations into mincemeat gobbledygook. Evo-devo explanations of homology are revealed as incoherent, structureless storytelling—where the basis for identifying and explaining 'homology' is contradicted from one case to the next. This is in accordance with design goal 3: life was designed (in part) to resist macro-evolutionary explanations.

Lastly, take Wagner's re-emphasis on structuralist explanations—the idea that form and structure of an organism *constrains* (or limits) its evolution. Though Wagner did not intend to, he has stepped closer to the creationist position. As a consequence of design goal 3, Message Theory predicts²³ life-forms were designed with *limits* to biological change.²⁴ In other words,

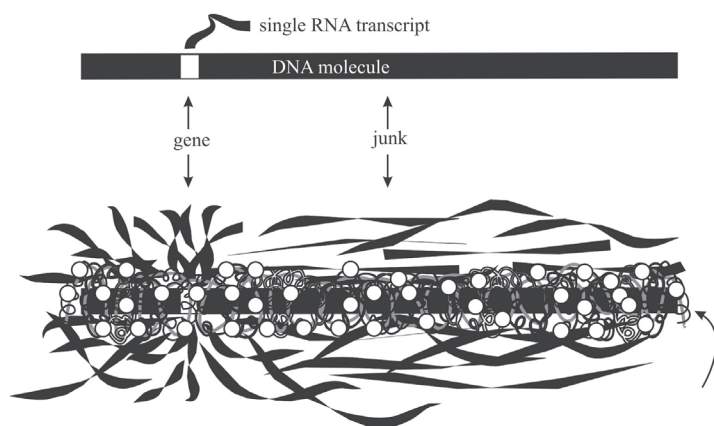


Figure 3. A general way to limit biological change is to use the same DNA sequence—the same gene—in various different ways (from Williams²⁷).

Message Theory predicts structuralism and *lots* of it!²⁵

A general way to limit biological change is to use the *same* DNA sequence—the same gene—in various *different* ways. This complex ‘matrix’ or *mosaic of interlocking* genes means large changes would be eliminated due to their adverse effects on survival. One example is genes that have multiple side effects (i.e. pleiotropy, discussed above). Another example is to have multiple genes *overlap each other* (in various possible ways) on the *same strand* or on *opposite strands* of the DNA double helix—these phenomena are already known to be common (figure 3). Another example is that, “there is increasing evidence that the gene regulatory network state of a cell is governed not by one core network, but by a *mosaic of densely interconnected* network modules [emphasis added]” (p. 423). A further example, predicted by Message Theory, is to have many key genes *used for both* body and sperm, and likewise many key genes *used for both* body and egg.²⁶ Again, the *same* DNA, used in *different* ways. Structures such as these help limit changes to those genes. More structuralism is expected to be discovered.

Creationists should not be scared by the material in Wagner’s book. On the contrary, they should be encouraged by it.

References

1. The alternative word order, ‘devo-evo’, is also used.
2. See review: Woodmorappe, J., Darwin’s dirty fossil secret, *J. Creation* 28(1):45–49, 2014; creation.com/images/pdfs/tj/j28_1/j28_1_45-49.pdf.
3. See Mazur, S., *The Altenberg 16: An Exposé of the Evolution Industry*, North Atlantic Books, Berkeley, CA, 2010.
4. ReMine, W.R., Desperate attempts to discover ‘the elusive process of evolution’ (review of *The Altenberg 16*), *J. Creation* 26(1):24–30, 2012.
5. Wagner is quite vague (almost non-existent) about his description of the problem, and his rejection of the purely selectionist solutions to it. He scarcely discusses these things. That is mysterious because that is a central driver of his book, so why would he be vague about it? Perhaps it is due to the evolutionist’s habit of *avoiding* statements that would aid and abet the creationists.
6. Wagner also revives the concept of typology, which was soundly rejected throughout most of the 20th century, most notably by Ernst Mayr.
7. Even at the level of cells, cell homology is ‘decoupled’ (or disconnected) from cell function and cell phenotype (p. 270).
8. Wagner allows ChINs to become masked, and later unmasked, to produce genetic throwbacks or ‘atavisms’ (p. 418).
9. The abundance of the pattern called ‘convergence’ is a prediction of Message Theory, because it precisely meets the three design goals given by Message Theory.
10. See review: ReMine, W.R., Evidence for Message Theory, *J. Creation* 20(2):29–35, 2006.
11. More precisely, there exist shared similarities that cannot be explained by common descent, nor by atavism, nor by lateral DNA transfer—so evolutionists call these ‘convergences’.
12. Cladistics never identifies real ancestors. (Where ‘real’ means you can hold their fossils in your hands.)
13. Such storytelling is used so often it threatens to undermine the objectivity of evolutionary cladistics. That is why a group of evolutionists, including Colin Patterson, broke away to found the more objective transformed cladistics.
14. Wagner writes: “certain conceptualizations of homology, as for example those made in the cladistics tradition of taxonomy, are incompatible with this program” (p. 4).
15. Wagner fails to seriously discuss the separate-versus-shared problem. It is effectively omitted. Instead, he often speaks of “individualization”, which does not reveal the problem and which obscures the complex mechanisms (e.g. targeted genetic reorganization) necessary to achieve it. He considers individualization so unimportant, it is omitted from his extensive index.
16. Also, Wagner writes: “Novelties likely require large-scale reorganizations of the gene regulatory network” (p. 125).
17. Wagner writes: “To this point, [evolutionary] research on the origin of paired appendages in vertebrates has not provided a coherent explanation” (p. 333); and “we still struggle with some of the most fundamental questions regarding the fin-limb transition” (p. 334).
18. This evolutionist desire—to neatly disallow or minimize genetic side effects—caused evolutionists to commonly assume ‘hierarchical homology’, where the gene networks have *hierarchically circumscribed* side effects. Wagner says evolutionists have to “emancipate” their thinking from that idea, because the evidence shows, “Homology is not hierarchical” but instead it is “cross-cutting” (p. 420–422). This ‘cross-cutting’ genetic pattern—or many-to-many relationship between characters and genes—is expected by Message Theory (see below).
19. On the other hand, evolutionists actively embrace pleiotropy on those rare occasions *when it helps* their storytelling.
20. Wagner uses various names for collections of genetic material that are larger than a gene, and that control development of organs and body plans, and that may incorporate positive and/or negative feedback. He uses terms such as: gene regulatory networks, Core Regulatory Complex, and Character Identity Network.
21. Or perhaps a well-circumscribed group of effects, that just happen to correlate with the traits Wagner wants exposed to selection.
22. Also, recall that the process of separating the genetics—even if precisely targeted—would have no immediate selective benefit.
23. Creation theory, as traditionally practised, does not actually *predict* the limits to biological change. Instead, the limits to biological change were *observed* and used as evidence *against* evolution, and *for* creation.
24. More precisely, design goal 3 predicts the organismal changes that can be experimentally demonstrated (say, in the breeding pens) will always be much smaller than the large gaps in the record of life. Though design goal 1—that life-forms be reasonably designed for survival—allows some ability of life-forms to adapt for survival in changing environments. Message Theory claims tradeoffs had to be made to achieve all three design goals simultaneously—and this was reasonably accomplished.
25. Message Theory expects structural changes to basic body plans (i.e. phylum characteristics) should tend to be the *most limited* (and hardest to achieve experimentally), with somewhat looser limits on less generalized designs (e.g. class characteristics) and so forth (e.g. to orders, to families, etc). This helps life resist macro-evolutionary explanations. The easiest changes to experimentally demonstrate will be those characteristics at the species and genera levels, such as colouration or length of a leg bone.
26. I am not aware of this yet being discovered.
27. Williams, A., Astonishing DNA complexity demolishes neo-Darwinism, *J. Creation* 21(3): 111–117, 2007; creation.com/images/pdfs/tj/j21_3/j21_3_111-117.pdf.