EVOLUTION

A Scientifically-Guided Thought Experiment

BOOK ONE

Evolution by Other Means…?

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(PhD, but not in Evolution)

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‘The Butterfly Nebula’

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Evolution: A Scientifically-Guided Thought Experiment

This volume is dedicated to Jean-Baptiste Lamarck:
the Original Founder of Evolutionary Theory

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PREFACE

Why I'm not qualified to write this book, but reasons to read it anyway

Although, this is a presentation of a particular thought experiment, it is not actually my own and perhaps therefore, the main reason why you should read it is because it is a deeply researched and diligently guided thought-experiment, and gleaned from some of the best scientific minds on the subject spanning the past 200 years. All I have attempted to do is to collate and interpret, to the best of my ability, much of the scientifically-based evolutionary thinking and concepts, which have for the most part: become historically obscured, and presented these in the light of our most up-to-date understanding of biological complexity. When viewed collectively, these seemingly disparate evolutionary concepts begin to converge into a cohesive and rather surprising overarching evolutionary synthesis that is highly distinct from our current one.

Although, I have a PhD in archaeology, which certainly helped with the know-how of the level of research required and it has also given me the tools to decipher much of the technical language in science papers in general, it obviously doesn't qualify me to tackle such a broad .subject straddling many different fields of science and history and requiring expertise in micro and molecular biology, physics and complex theory and a little about quantum mechanics. But then again, no amount of PhD's would cover it and besides: I would only have been allowed to investigate a narrow field within each discipline and not be able to see the evolutionary woods from the rather large Darwinian tree in my path.

Furthermore, as far as I know, you can't do a PhD in evolution. Instead, this level of research was made possible by the vast historical resources and high quality peer-reviewed science information now available online along, with all the expert guidance pertinent to so many diverse disciplines. Therefore, thankfully, I didn't have to do it the old-fashioned way (as I once did) by physically going to libraries and reading real books. Although, I must say – I miss the real thing too, but by spending my time in cyberspace reading libraries, I was able to make this massive topic an accessible reality and it only took a few years, rather than decades.

The research itself was guided by delving deeply into the historical archives and assessing what I discovered (mostly from first-hand sources) with what was comparable in the more modern scientific literature and this: let's see where the evidence leads us sort of approach, led me to asking question that I would not have otherwise thought to ask: discover things that I could not have possibly considered from logic alone and, to conclusions that were contrary to my own expectations. So, even though I am not specifically qualified to write this book, I do hope that you will read it anyway, and get a great deal from it in the process, because, as far as I know, it is the first time that all these scientific voices have been heard collectively and presented in a more modern and unbiased scientific light with the result of paving the way for a completely distinct and much more dynamic understanding of evolution by other means. I do hope you find it at least thought-provoking, if not fully satisfying and refreshing as a fully comprehensive scientific alternative to our current theory of evolution.

INTRODUCTION

EVOLUTION BY OTHER MEANS...?

This is the first of two distinct, but interrelated books which seeks to offer an alternative evolutionary scenario to our current standard Neo-Darwinian model by way of a scientifically-guided thought experiment. Book One is based upon the accumulative research spanning the past 200 years of a diverse range of highly respected scientists who have offered distinctively different pieces of the evolutionary puzzle and these are assessed in the light of our most current understanding of biological complexity and Book Two applies these alternative and rather novel, but scientifically supported evolutionary scenarios to what we currently know regarding the ancient environmental and fossil record.

The need for a radical rethink of biological and evolutionary complexity and a solution to the many problems embedded in our current Neo-Darwinian model, became clearly apparent as a result of delving deeply (and unintentionally I might add) into the vast and often ideologically invested topic of biological evolution and discovering, according to the opinions of an increasingly alarming number of well-credentialed scientists, that an alternative model was seriously overdue (O'Hare 2015). (For instance, see Free Flip book version: *But Old Mr. Darwin wasn't to Blame: The Little Book of Evolutionary "Quotes"*) [1].

This issue is highlighted quite succinctly by Professor Denis Noble (Professor Emeritus and Co-Director of Computational Physiology) below:

PHYSIOLOGY IS ROCKING THE FOUNDATIONS OF BIOLOGY

> *In this article, I will show that all the central assumptions of the Modern Synthesis (often also called Neo-Darwinism) have been disproved. Moreover, they have been disproved in ways that raise the tantalizing prospect of a totally new synthesis;...*
>
> Noble (2013, Introduction)
>
> [2]

As I took a rather broad and interdisciplinary approach with an emphasis on the historical context, I came to the realisation that this 'tantalising new synthesis' is actually not that new. For instance, our more modern and recent insights into biological complexity are actually lending increasing support to some of the oldest and particularly to some of the most historically obscured alternative views of evolutionary complexity.

Moreover, there is a common and cohesive thread that weaves all of these seemingly unrelated and diverse theories, concepts and discoveries together and in the end, a fascinating, elegant and surprisingly uncomplicated tapestry of biological complexity emerged, but with a somewhat unexpected quantum twist.

In many ways, perhaps the best way to explain what essentially emerged as the overarching and cohesive principle, would be to use the concept of the Matryoshka Principle of nested scales of complexity (akin to the Russian folk art wooden nested dolls). This has been employed here to help visualise the increasingly likely fact which, is both measurable and demonstrable, that life and biological complexity is governed by universal laws of scale.

From these universal patterns of life, we can perhaps begin to apply this knowledge to aspects of evolutionary development that we cannot test or know directly and thereby, at the very least, begin to formulate a fairly plausible hypothesis based upon empirical data as to how life got so complex in the first place.

This overarching scaling phenomenon which is seemingly embedded within all of Nature and I believe, best encapsulated in the concept of the Matryoshka nested scales principle, is the foundational scientific guide that informs, not just the first chapter of this book; but it was the main principle that guided the research at its most fundamental level and it informed which theories would be included in this present book and their respective order of their presentation.

When we have assessed each theory and evolutionary concept in the light of our most up-to-date understanding of biological complexity, we should not only have an overarching model by which to test and assess the fossil record – the main topic of Book Two, but, also: a fully comprehensive and powerfully explanatory, and testable theory of the complexity of biological life itself.

CHAPTER ONE

D'Arcy Wentworth Thompson

(1860 – 1948)

EVOLUTIONARY SCALING LAWS OF LIFE

The Matryoshka Principle

D’Arcy Thompson was born the year after Darwin published his famous book *On the Origin of Species*. And in 1917 D’Arcy published his own quite famous book: *On the Growth and Form* and much extended and updated version in the 1940s Thompson (1917) [3] and Thompson (1945) [4]. In his major treatise, he uses the known processes and principles of the physical sciences of chemistry, physics etc in conjunction with biology and by applying the language and tools of mathematics, he essentially quantified and established inherent patterns of growth and form that Nature appeared to consistently use in the production of even the most complex organisms.

It is D’Arcy Thompson’s overarching concept that guided the nature of research questions and possibilities posed and hopefully, answered throughout this book. Therefore, I have summarised his ideas and principles in the section that follows, as they are fundamental to what was discovered about the deeper processes embedded in all of Nature and explored throughout the rest of this book through the lens of several other evolutionary theories and concepts in their updated form.

From the smallest and least complex to the largest and most complex and at quantifiable factors of magnitudes in-between, D’Arcy Thompson drew on his observations of predictable patterning at all scales in Nature to propose a fundamentally distinct form of descent to the simplistic continuous linear Darwinian model. He essentially, came to a distinctively different way of understanding evolutionary development and ultimate complexity by applying the main principles of the processes known to operate within non-biological complex systems, to biological systems and discovering that there was something universal unpinning them all as indicated in his 1945 edition *On Growth and Form*.

There is something, an essential and indispensable something, which is common to them all, something which is the subject of all our transformations, and remains invariant (as the mathematicians say) under them all.

D'Arcy Thompson (1945, 1085)

[5]

For instance, by looking to fundamental properties within naturally developing non-biological complex systems, where, under certain conditions, rapid and profound changes can be brought about via catalysing the whole system in a single leap, D'Arcy Thompson applied this principle to evolutionary development and suggested that whole functional cellular life and its highly organised organisms could have come into being likewise a number of times under broadly similar catalytic conditions. He also understood that a very small change (initial starting conditions) at the beginning; can make a huge difference further down the line, reflecting yet another fundamental characteristic of natural complex systems. This led him to suggest that primitive life could have been triggered into taking fundamentally divergent paths by simply having different starting conditions.

For instance, D'Arcy Thompson suggested that as several distinct groups were discernible, based upon his study and observations of quite distinct body-plans and internal systems of a broad range of species, that these may represent the resultant divergent forms alluded to above. He referred to these distinct groupings of organisms as "discontinuous types", meaning that Nature drew upon their underlying form and inherent systems to produce many scaled-up and increasingly complex versions of the same fundamental forms "Types" with degrees of modification according to the group's intrinsic evolutionary potential.

The most obvious of D'Arcy Thompson's discontinuous "Types" would be something along the lines of: fungi, plants, single-celled organisms, and several distinctive groups of animals such as invertebrates of insect and worm-type forms, with or without shells, or sponge animals, and star-fish and of course, complex vertebrates showing varying degrees of major divergences from the commonly shared body-plan, but he was not explicit about the detail of these groups, just that they were discernible.

From the initial starting conditions and of their primordial environment in which organisms developed, D'Arcy Thompson suggested that all were driven to their respective levels of complexity thereafter, according to the overarching principles and laws of universal scaling and natural ordering. In other words, D'Arcy Thompson came to understand from his in-depth studies that Nature and the development of all of its organisms, was anything but random and disordered. Instead, he saw that life operated on scales or magnitudes that were mathematically measurable and predictable and common to all (universals and invariants).

Analogous to this understanding, just as water finds the most direct route and its equilibrium: so too does other fluids and molecules in Nature. D'Arcy Thompson describes the self-similar (fractal-like as we would refer to these patterns embedded in Nature today) properties and patterns identifiable on seemingly every scale, as the result of Nature finding the most efficient means to produce order out of relative chaos.

D'Arcy Thompson proposed that natural solutions to making the best use of available resources; fulfilling energy requirements and building according to the most economic use of space, may have informed the mathematically quantifiable growth patterns, simple equations and orders of magnitude discernible within the patterning of spiral shells, or how the branching tree and its branching pattern reflected on a smaller scale within each leaf, or the symmetry (mirror-image) of the animal body-plan along its central axes.

Essentially, from these observations, D'Arcy Thompson proposed that Nature has been driven to natural order and by taking the path of least resistance has ultimately resulted in every level of life finding its own optimum level of function and its natural equilibrium within the whole spectrum and on every scale of existence.

All of the above, of course, contrasts significantly with the Darwinian *continuous* linear descent model from a single or perhaps a few cellular types with its gradual and incremental (direct ancestral inheritance of modification under the guiding principle of selection), where the species are formed according to how successful or not, they are by sheer random luck of survival to fit in, or not fit in with their environments (selection) and pass on those mutant genes. D'Arcy Thompson, model could not be more different.

It might be useful at this stage to introduce you to the concept that has greatly aided this present thought-experiment and I believe encapsulates the essence of what might be best described as: D'Arcy Thompson's universal nested scales model of evolutionary development which is the overarching principle employed throughout this book as noted in the introduction.

The Matryoshka (nested-dolls) Concept

If you think of the Matryoshka concept or principle; an analogy to the nested cups or dolls concept, where ever-decreasing brightly, and sometimes highly elaborate, painted, wooded dolls, are cupped/nested inside each other to make up a full set enclosed by a self-similar but proportionally scaled outer mother type doll – (the Matryoshka term comes from the original Russian meaning matriarch or mother, but in our case we might see it as referring to Mother Nature) then, D'Arcy Thompson's scaling concept becomes, I believe, a little more tangible and easier to conceptualise.

For instance, a nested doll set, using the traditional Matryoshka theme of the great Russian family, may have the outer appearance of fairly complex design and decoration, but these are only distracting details in a sense, because as we look to the underlying form of the carved dolls what we discover is the fundamental rules that are followed to create the Matryoshka nested doll set in the first place. We simple follow the pattern that each doll is scaled according to the others and the individual is reflected in the whole and vice versa.

We can also begin to see how each doll is a complete and functional entity (a whole form) even at its most primitive scale; within the set or isolated from it. In other words, the more elaborate and larger dolls would not be made until the former is completed as, the later and larger doll takes its cue from the preceding pattern. Each doll takes its form from the previous doll at predictable scales and we know that the space in-between each nested doll will be just large enough to set each inside the other, but close enough to follow the contours of the others using the least amount of space. In its main principle, the beginning (the earlier dolls) will inform the overall shape and contours of the scaled up versions of later, larger and more complex dolls until it forms a complete nested set.

Perhaps we can investigate these sets and even look within, to try and trace the origin of their earlier and less elaborate forms. We may begin to understand the underlying theme in simpler terms and recognise the slight protrusions or curvature that becomes more exaggerated as the set becomes more elaborate. Think about the variations on the theme of the Matryoshka doll sets where, each set of dolls of increasing/decreasing complexity and scale may have a distinctive theme; obviously, the patterning would not be as elaborate on the earlier, tiny and primitive type dolls as they may be on the later, larger and more complex/refined and spacious outer doll.

One set may even be carved differently to another set, but all sets still follow the same rules and principles of form and shape and patterning. So it seems that Nature has retained the whole range of sets from the bottom up and we can begin to look within the distinctive sets and look collectively at all the different versions and scales of the sets themselves, to try and understand the evolution of their fundamental form and emergent complexity.

The nested dolls concept applied, also helps us to gain an insight into how profoundly efficient Nature has been. For instance, each level of life is self-sufficient and does not have to have more complex forms for it to operate. We could have little simple Matryoshka sets to begin with, and if the opportunity arose to access more materials and resources became increasingly abundant: you could always build on more (modules) of even larger and more elaborate proportions, but of course, you would be still keeping with the same fundamental theme and form.

For example, you wouldn't build half a Matryoshka set and then start radically remodelling it. You would start another set or use a, as yet unfinished, starter set to shape and form this and keep going until another opportunity arises to build up the set to include even more elaborate and increasingly larger dolls following the same fundamental theme.

Let's say that this more elaborate set *in-the-making* was going to have 3D limbs, and to make things simpler, we could imagine trying to make a set of dolls with a single protrusion such as Pinocchio's nose (the little puppet that wanted to be a real boy and his nose started growing longer each time he lied). The Pinocchio doll set would be carved (probably a vertically split nested set for ease of carving the nose) from the earliest stages to accommodate a fully extended nose (remember he is made out of wood and then becomes a real boy) in the end.

Every time we carved a new Pinocchio form from the tiny non-descript one with the smallest and slimmest protrusion (more like a miniature pointed bud) for a nose that will scale up to be much more extended in the end, it would be a proportionally scaled up nose in relation to everything else at each scale; growing telescopic extensions, fitting like a hand in a glove, until the final outer doll with a fully recognisable and elaborated painted Pinocchio wooden puppet emerged. If it were a telescopic nose, we could perhaps push it back into each of the hollowed-out heads and it would maybe look more like a normally proportioned nose.

Now, Pinocchio's nose in its most extended form, ultimately, would only become as long as the available wood would allow, or as long as the tools and skills required to carve it would allow, or as long as the proportion of the first and original solid miniature doll's head could accommodate (a pushed back) un-extended nose. Or the length of the nose might be determined by when Pinocchio stopped lying. But, even if you didn't make it a telescopic nose and you had enough wood, skill and tools, you might not carve the nose to ultimately end up any longer as it might look a bit ridiculous to have too long a nose and besides, Pinocchio would probably topple over from the over-extension.

Using this analogy, basically, it seems that Nature grows develops, proportions, and shapes everything in relation to everything else. It appears to form organisms according to spatial, material, resource availability and efficiency concerns and builds accordingly, just as D'Arcy Thompson proposed and it is these factors, ultimately driven by universal scaling laws (to do with efficiency), that makes it possible for us to investigate, measure and quantify so accurately, using the tools of mathematics which, then allows us to assess just as accurately how Nature may have formed and developed and diversified the species; recalling all the while, that all the varieties produced, may merely be variations of the same fundamental themes of life according to their developmental conditions, just as D'Arcy Thompson proposed as you will see below.

A Question of Universal Patterns of Life

The relatively simple underlying patterns of life…

"Thus, beyond all questions of quantity there lie questions of pattern, which are essential for the understanding of Nature." –

Alfred North Whitehead (1968, 143)

[6]

In the last chapter XVII of D'Arcy Thompson's book with the title of: *On the Theory of Transformations, or the Comparison of Related Forms*, he explains and illustrates the simple geometrical equations that underlay even the most complex patterns in Nature.

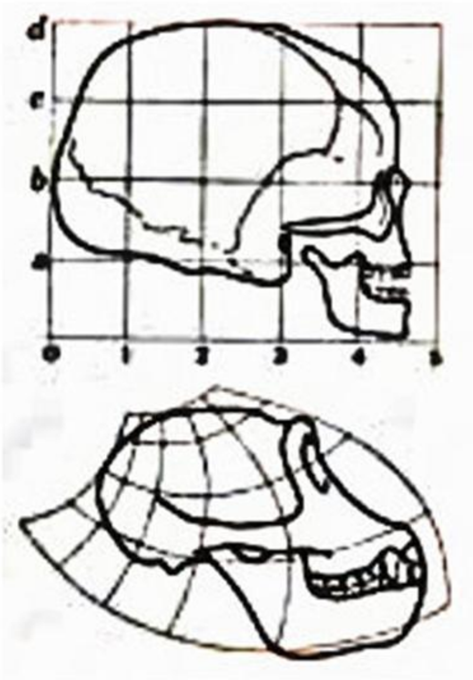

Fig. 1: Transformation of coordinates in ape compared to human skull.
Source: 'About D'Arcy' Web site

For instance, Figure 1 shows how D'Arcy Thompson viewed the formation of the skull of an ape compared to a human. The human skull illustrates that much of the flexible sheet area is filled by the much larger brain-case compared to the grid area for the entire jaw. It is just the opposite in the ape skull example, where the grid is almost entirely filled by the massive jaw area and conversely, the grid area occupied by the brain-case are minimal.

D'Arcy Thompson used the grid concept to help visualise Nature's flexibility and pattern of growth. They help to draw attention to the fact that Nature makes transformation in a highly efficient manner by metaphorically stretching and skewing key origin/starting points (along the fundamental axis of growth on all planes) which changes the whole form in relation to everything else; obviously this is done when everything is much more flexible and plastic as even a small change at the beginning can lead to a much amplified exaggeration of a particular feature further down the line (just as the Matryoshka primitive dolls ultimately inform the outcome of the larger scaled up dolls). The details are the filling-in or, building up the contours patterns at different scales of the whole.

Take for example, the idea of rolling out dough. You will know that a small change at the beginning can lead to widely skewed shape by the time you are finished. Well, D'Arcy Thompson's concept is similar in that, if the skull was analogous to dough, by continually putting more pressure on rolling out the pastry to make a large area of cranium, we would end up with a much reduced jaw area at the expense of the larger area of dough representing the skull, and conversely, if we concentrated on expanding the dough representing the jaw area, this would be at the expense of the skull area as Nature is essentially working in principle with the same amount of dough, but distributing (deforming, moulding and shaping) it in different ways in proportion to itself

On Growth & Form

After easily transforming our coordinate diagram of the human skull into a corresponding diagram of ape or of baboon, we may effect a further transformation of man or monkey into dog no less easily; and we are thereby encouraged to believe that any two mammalian skulls may be compared with, or transformed into, one another by this method...In these transformations of ours every point may change its place, every line its curvature, every area its magnitude: but on the other hand every point and every line continues to exist, and keeps its relative order and position throughout all distortions and transformations.

D'Arcy Thompson (1945, 1085)

[7]

Continued...

From this comparison of the gorilla's or chimpanzee's with the human skull we realise that an inherent weakness underlies the anthropologist's method of comparing skulls by reference to a small number of axes...But it is, in the first place, evident that these axes are merely the principal axes of a system of coordinates, and that their restricted and isolated use neglects all that can be learned from the filling in of the rest of the coordinate network"

D'Arcy Thompson (1945, 1084)

[8]

Another way of perhaps visualising this concept is to imagine if D'Arcy Thompson had access to 3D computing software, he would have been able to input a few simple coordinates and equations/parameters and hit 'RUN'. He would have produced very different shapes from the same basic template form by simply shifting the orientation (skewing or deforming slightly) the grid prior to the main contour details being filled in. Below is a short excerpt relating to the above discussion on coordinates taken from the official site on D'Arcy Thompson's research *About D'Arcy* which explains, in perhaps rather oversimplified terms, that this is the basis underpinning his distinct view of speciation (how species change).

About D'Arcy

Perhaps the most famous images from 'On Growth and Form' are the transformations. D'Arcy showed that gross variation in form between related species could be modeled by the consistent deformation of a sheet. The consistency of the deformation is the crucial point here: it is obvious that any fish form could be made to look like any other fish form, if it were sketched on a perfectly deformable elastic sheet, and stretched in many directions at once. But D'Arcy Thompson showed that if the sheet were stretched in one particular pattern, then a new species form would be generated. This remarkable and curious observation has not been fully explained even today.

University of Dundee and the University of St Andrews (2010)

[9]

What is particularly interesting about the excerpt above is perhaps the fact that although we know that D'Arcy Thompson's observations are correct as this is how organisms actually do develop as any modern day embryologist would verify, is the fact that this phenomenon has no explanation, even today. Hopefully, by the time you have finished reading this entire book and as we proceed to present the evidence in support of D'Arcy's overall concept within this chapter, you will be considerably more enlightened and be able to take a stab at why this might be so.

Obviously, D'Arcy Thompson's principles of growth and formation of organisms/species, applies to all forms of life that were observable, from spiral shells to star-fish and from skinny fish to fat fish. Overall, the outward appearance of the great diversity of even a single species is rather superficial according to D'Arcy Thompson as seen in the example give below in Figure 2 of the fish; and the algorithmic formula can be described for all spiral patterning irrespective of how diverse that species may appear, the principle of concept is seemingly still applicable to them all; even if these (discrete groupings of organisms) discontinuous forms (Matryoshka sets?) have their own starter pattern to follow to their own ultimate evolutionary trajectory informed by their overall symmetry, shape, form and function resulting from that primordially established intrinsic form.

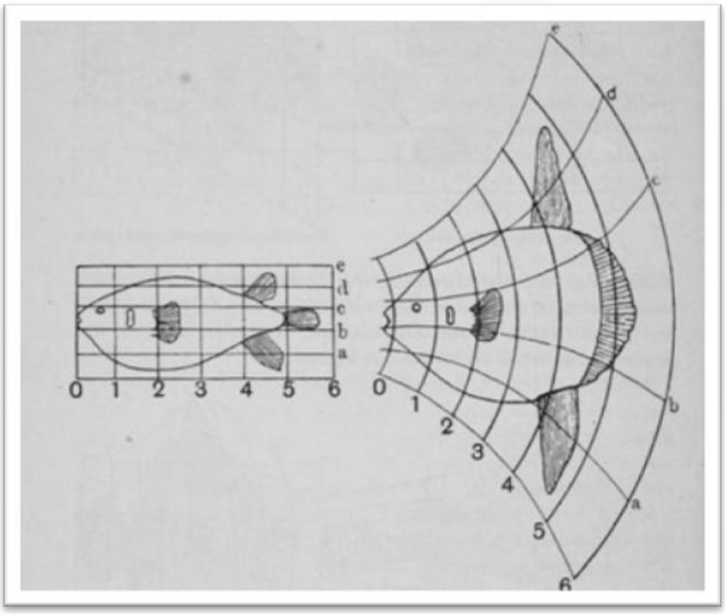

Fig. 2: Transformation of coordinates change the basic shape in every direction proportionally to itself (after D'Arcy Thompson 1917, figs 525-526)

For example, according to D'Arcy Thompson's way of seeing evolution and understanding of Nature, knowing the coordinates on his two idealised axes, he was able to work out the third axes as it was on a predictable pattern that could be tracked at each scale of magnitude according to its overall proportions. In many ways, he was working in 3D space in his mind, but he could only show these in a rather limited way in 2D. By metaphorically bending and stretching the flexible grids, he observed that these always grew (in magnitudes) scaled up or down in spatial arrangements in proportion to the whole.

Since Thompson's time, much research has taken place as noted above, particularly within embryological or embryogenesis/morphogenesis (the origination of embryo patterning and development) and developmental studies in general which dovetails very well with D'Arcy Thompson's growth and development grid/field concept. As you will see in the excerpt below, growth and development also includes limb/organ regeneration in species:

Morphogenetic fields in embryogenesis, regeneration, and cancer.....

A Question of Pattern

Embryonic development results when a single cell (the fertilized egg) reliably self-assembles a highly complex pattern appropriate to its species. This process is known as morphogenesis – the establishment and creation of 3-dimensional anatomy. During later life, multicellular creatures must maintain their pattern – an active process of morphostasis that works to maintain the whole while individual tissues age or are removed by traumatic injury. Some organisms replace large-scale structures during adulthood, illustrating the remarkable plasticity and dynamic control of shape by biological systems. For example, salamanders can regenerate eyes, limbs, lower jaws, hearts, and portions of the brain.

Levin (2012, 1)

[10]

Basically, what scientists are coming to understand (due to our more sophisticated tools of scientific investigation) about developmental process and regeneration, is that there is something akin to an invisible development field that is known by its predictable effects which appear to guide and precisely time the development of organisms and/or the regeneration of limbs at a cellular level.

This field, in many ways, is akin to the grid analogy in three dimensions described by D'Arcy Thompson and is perhaps best visualised by thinking about the effects of a bar magnet creating fields of attraction, or repulsion, or no effect at all. We can't see the field, but we know it is there from its effects on iron filings. Indeed, if we had enough iron filings and moved these bar magnets around at different 3D grid points, we could change, and sculpt these into many different forms.

The morphogenetic field, or the process of morphogenesis, is similarly known by its effects. What creates the ordering is another story which we will attempt address in due course. The important point is that studies of this nature are giving very strong support to D'Arcy Thompson's understanding of the highly orchestrated and predictable self-similar patterning formation on scales of magnitude as the organism develops or regenerates body parts. It is his extrapolation to the evolutionary scale of species formation that is my main focus here.

NASA Apply D'Arcy Thompson's Universal Principles and leaves the Neo-Darwinists behind

Thompson's observations have been picked up in more recent times by NASA scientists who are compiling a mathematically-based book of life (a computer program) to identify possible extraterrestrial life in whatever form of complexity based essentially upon D'Arcy Thompson's definitions of life and its unifying principles - its form and function which, has been updated and further applied as outlined in an article by the NASA website. Below is a short excerpt from this article as it relates to the main principles within D'Arcy Thompson's model of life:

Who Wrote The Book of Life? Picking Up Where D'Arcy Thompson Left Off

> *NASA scientists are using Thompson's biomathematical studies of life forms on Earth to postulate about life forms throughout the universe. There are certain universal conditions that will always affect the shape of a life form, wherever that life may be."Everywhere Nature works true to scale, and everything has a proper size accordingly," wrote Thompson. "Cell and tissue, shell and bone, leaf and flower are so many portions of matter, and it is in obedience to the laws of physics that their particles have been moved, moulded and conformed."*
>
> *.. Gravity, for instance, acts on all particles and affects matter cohesion, chemical affinity and body volume. Other influences that are consistent throughout the universe are temperature, pressure, electrical charge and chemistry.*

NASA (1999, May 28th)

[11]

In other words, none of this was just about pretty patterns and interesting mathematical abstractions, but D'Arcy Thompson's description and cataloguing of complex life, classified according to unifying and underlying simple equations, has very real applications. Finding universal patterns that apply to all life, even potentially from other planets, means that predictions about otherwise unknowable biological complexity can be discovered such as how the species may have arose and developed in complexity as D'Arcy did, which is an aspect of his research that many are not actually aware of, as it wasn't by Darwinian means and it certainly wasn't by Natural Selection according to D'Arcy Thompson as you will see further on.

Indeed, I noticed that NASA didn't use the Neo-Darwinian concept of species on their cosmic missions and I wonder if Richard Dawkins is aware that NASA is using D'Arcy Thompson's research to help them identify life on alien worlds. This is an interesting question in the light of what Dawkins states emphatically regarding how it can only have been by Darwinian means as seen below:

The Blind Watchmaker

I predict that, if a form of life is ever discovered in another part of the universe, however outlandish and weirdly alien that form of life may be in detail, it will be found to resemble life on earth in one key respect: it will have evolved by some kind of Darwinian natural selection.

Dawkins (1986, 290)

[12}

The Butterfly Effect

This brings us to another important, but interrelated aspect of Thompson's observations of growth and form and that is the concept that: a small change at the beginning can lead to a very big change further down the line, as indicated above in our pastry-rolling analogy. Or, recall the analogy of the 3D graphic software that of course D'Arcy Thompson did not have access to, but if he did, I would suggest that he would have made endless variations on the same fundamental shape/form by slightly adjusting the initial starting conditions.

This is a well-known concept established by observation within developmental evolutionary biological studies, but interestingly, it is also a well established and observable fact of physics and can be mathematically described. It is a principle within the specific field of Chaos theory, a branch of physics that tries to understand the tendency of systems to become disordered or chaotic and conversely, systems that seem disordered initially, tend to organise themselves. You may have heard of it – it is called the butterfly effect. It is explained in the MIT Technology Review *When the Butterfly Effect Took Flight* by Peter Dizikes (February 22, 2011) [13]

This concept came about as a result of trying to study the very unpredictable and highly complex system (seemingly chaotic and without pattern and certainly with limited predictability - the weather. The problem was that when numbers were rounded off and put into a computation machine to project the outcome of the weather, the actual rounding up of numbers rather than using all the smaller numbers after the decimal place was believed to have no effect or a very minimal one to the end result. However, this very minuscule change at the beginning led to wildly different results depending upon the starting conditions.

Therefore, it was given the analogy of a butterfly flapping its wings on one continent could have the potential to create a hurricane in another continent further down the line and coined the butterfly effect. However, as unpredictable as the weather is, it turns out that biological systems are slightly easier to predict, as D'Arcy Thompson clearly showed and the fact that it may be to do with Nature's space-saving and efficiency behaviour at a cellular level that begins to explain such predictable patterning. This is indicated below, again, from the official *About D'Arcy* website:

About D'Arcy

... the dynamic influence of starting conditions lies in the morphology of shells and horns. These are the permanent, non-living, three-dimensional record of a temporary, two-dimensional living state – the base of the horn, or the mantle of the shellfish. D'Arcy Thompson showed that all horn and shell morphologies could be described in simple mathematical terms readily derived from the incremental nature of growth...

For instance, geometrical rules of packing determine cell arrangements. These need not be specified, but can arise spontaneously. Yet the packing arrangement may be "useful" in minimising the space occupied by the cells, by maximizing cell-cell contacts, by establishing different categories of cells ("inside" versus "outside"), and so on.

University of Dundee and the University of St Andrews (2010)

[**14**]

This concept applied, means that context and conditions of development are crucial and suggests that even a minor change in the conditions of a developing species may and indeed, seems to have had a profound effect upon how it evolves and what it evolves into in the end and as Nature appears to do things incrementally and like water finding its level and most efficient route to its equilibrium, or arranging cells according to space saving packaging concerns, will be addressed in more detail as we go along.

However, returning to the initial starting conditions potentially having a rather divergent outcome to another bunch of cells starting out under slightly different conditions, informs another important aspect of D'Arcy Thompson's species development hypothesis.

For instance, D'Arcy Thompson was impressed by the fact that although biological forms differ widely, that the mathematics to describe them remains the same and he considered that initial starting conditions may have explain such widely divergent forms from commonly shared templates of life.

Indeed, he even had a mathematical description for certain spirals (self-similar patterns) as seen in the form of many shells and applied what he called a logarithmic (I'll explain more about this term as it applies to growth and development further on) spiral to these predicable forms, but realised that the variations on this theme, just like the deformation patterns of the fish or the ape/human skull, could become highly distinct further down the line when a species had fully matured.

He also understood that plasticity (that developing organisms such as those that live in shells start out as soft forms and the mature shell form becomes more rigid and fixed as it reaches full development of its entire form and grows bigger without changing anything fundamental; although structures may become more fixed and rigid as they stabilise and mature.

D'Arcy Thompson also considered that the principal pattern was formed early on, only to be filled in with detail of self-similar patterns at all scales. Essentially, he applied this to the formation of the species and suggested that when an organism was first developing, its fundamental patterning would be guided by universal laws of growth and form (space-saving and efficiency concerns), but its variations within these fundamental forms of life could vary greatly according to initial starting conditions and it is this that perhaps helps to shape and form and diversify simpler organisms into diversified and more complex species.

This brings us to the issues that D'Arcy Thompson had with the Darwinian model and why he felt another explanation was required which he believed from his own findings, was a very valid possibility that could be further explored and examined in the light of trying to understand evolutionary complexity

D'Arcy's Difficulties with Darwinism

Essentially, D'Arcy Thompson could not see how inheritance and Darwin's slow transformation via selection would create such diversity of traits and characters as highlighted from an article written in 1894 "*Some Difficulties of Darwinism*" in a paper entitled: *Transformations: The Visual Influence of D'Arcy Thompson* by Jarron (2013, 86) [15]. Instead, from the reading of D'Arcy's main publication, especially the more extended book *On Growth and Form* of the 1940s, his detailed understanding of cellular formation: from one cell (an egg cell); to two, then four, and doubling in perfectly predictable replication right up to 64 by factors of scale was more his focus.

D'Arcy Thompson had his own ideas regarding genetics, which he would have viewed as being intrinsically part of the whole cellular system (which is correct as it turns out as discussed in the next chapter) seemed to be taken more seriously by physicists than by biologists, although a few exceptions in developmental biology are noted by Jarron below

:

> *Transformations: The Visual Influence of D' Arcy Thompson*
>
> *For much of the twentieth century, D'Arcy's ideas seemed to run counter to biology's increasing focus on genetics…On Growth and Form shows how complex biological systems can be understood by fundamental mathematical principles, and as such D'Arcy's ideas provided the basis for the development of modern systems theory.*
>
> Jarron (2013, 88)
>
> [16]

D'Arcy Thompson does not appear to make a big fuss about his objections to the Darwinian view of evolution, but rather, he simply stated the scientific difficulties in applying the slow gradualism to evolutionary change or the selection model accounting for the changes within the species. Of course D'Arcy recognised the importance of creating similar off-spring via inheritance and was obviously well aware of genetic inheritance, but as noted above, instead, he offered the alternative view based upon his own understanding of the natural processes that were fundamental properties, guided more by chemical bonding and interactions and self-organising characteristics, heat and turbulence and molecule interactions.

These factors were inherent in many complex systems and this aspect of D'Arcy Thompson's understanding and thinking will become much clearer and actually deals with the role of genetics within the context of the cell and finds very strong support for his main proposals as discussed in the next two chapters of this book in particular. Essentially, D'Arcy Thompson viewed all the aspects of cellular organisms/species formation in terms of whole systems within the context of their evolutionary developmental environment.

This type of complex systems thinking developed from his research, led to him proposing a distinctly non-Darwinian form of evolutionary development, particularly in the light of the fundamental shortcomings that he highlighted within the Darwinian model. There is for instance, a fairly extensive discussion in his 1942 American Edition of *On Growth and Form*: Vol. 1, *The Rate of Growth* regarding this. See Thompson (1942) [17]. But, perhaps D'Arcy Thompson's general alternative views on evolutionary processes are best summarised in the excerpts given below taken from his epilogue of the 1945 edition *On Growth and Form.*

Note that protozoa refer to the entire kingdom of animals, and are four-limbed animals and that this is a later edition of D'Arcy's book (1945).

On Growth & Form

> *...for eighty years' study of Darwinian evolution has not taught us how birds descend from reptiles, mammals from earlier quadrupeds, quadrupeds from fishes, nor vertebrates from the invertebrate stock...*
>
> *... Our geometrical analogies weigh heavily against Darwin's conception of endless small continuous variations: they help to show that discontinuous variations are a natural thing, that "mutations" -or sudden changes, greater or less-are bound to have taken place, and new "types" to have arisen, now and then. Our argument indicates, if it does not prove, that such mutations, occurring on a comparatively few definite lines, or plain alternatives, of physico-mathematical possibility, are likely to repeat themselves: that the "higher" protozoa, for instance, may have sprung not from or through one another, but severally from the simpler forms; or that the worm-type, to take another example, may have come into being again and again.*

Thompson (1945, 1093-95, Epilogue)

[18]

In summary, D'Arcy Thompson seems to propose throughout all his chapters in relation to the main topics addressed, that biological life has followed the same fundamental processes inherent in other complex and naturally organising phenomenon and he believed that by tracing the intrinsic patterning and scale employed by Nature, we can begin to see the methods of producing continuous novel and increasingly diverse formations of shape and form that could be implicated in the great variety of species; and yet may be commonly connected by sharing underlying patterns of fundamentally similar properties and employing the same means of development to reach their own particular level of intrinsic complexity.

Instead, of linear common descent, he understood how Nature, by forming and shaping organisms as discontinuous (or fundamentally structured from the beginning and only producing different scales of complexity and size thereafter) whole organisms under slightly different circumstances and their ability to replicate/multiple all variations on these themes of fundamentally similarly patterned whole types, could ultimately give rise, rapidly and profoundly, to increasingly divergent organisms to create the vast varieties of species known today.

There is actually quite good support for this whole-system and fundamental or, archetypical forms developing independently or with diverging trajectories at all scales of expression and diversity within fundamentally discrete groups which should become apparent as we proceed through this book, particularly in view of what we are beginning to understand regarding the role of genetics and the understanding that we are not quite related genetically in the way that we are often told.

Essentially, what D'Arcy seems to be proposing, is that the vast variation may have come down to Nature's ability to keep producing simple forms or, it had a means of doing so when everything was still highly dynamic and pliable (which is seemingly the case as you will see as we proceed) and divergence may be guided via conditions such as how different the starting/developmental/chemical environment was between developing organisms; how primitive and plastic the organism was and how evolutionary scales of complexity could be directed according to space-saving and efficiency factors.

All these factors will come into a much clearer light as it will become apparent that these proposals given by D'Arcy Thompson are very likely the actual drivers of evolutionary complexity as borne out by a number of studies in the next chapter and beyond. As we delve deeper into life's complexities, only to find unifying and relatively simple principles of growth and form, increasingly, D'Arcy would appear to have grasped the very essence of Nature's means to develop (evolve) its biological systems.

But Everyone Stopped Talking to Each Other

I thought it would be important at this stage to draw attention to one of the reasons why I believe D'Arcy Thompson's concept of the formation of the species was not taken any further and explored deeper until NASA had the wit to employ his observations of the universal principle of all life.

It would take another book to explain, why anything non-Darwinian or alternative never made it into our modern institutions and classrooms, but I will look at one aspect that did have some influence in impeding D'Arcy Thompson's research from being widely read and understood within the context of biological processes with all its implications until more recent times.

For instance, in D'Arcy Thompson's era of teaching at a university (Scotland in his case) it was much more common for scientists within different fields of research to take the traditional multidisciplinary approach. D'Arcy Thompson did just that in order to investigate the broader issues of life itself. However, as indicated by D'Arcy Thompson himself, as seen in the excerpt below, this approach was becoming increasingly difficult and students and their professors were being forced to become more and more specialised and narrow within their scientific field of research.

> *D'Arcy passionately believed in giving students as great a breadth of knowledge as possible, telling them if you dream, as some of you, I doubt not, have a right to dream, of future discoveries and inventions, let me tell you that the fertile field of discovery lies for the most part on those borderlands where one science meets another. There is a cry in the land for specialization. . . but depend upon it, that the specialist who is not reinforced by a breadth of knowledge beyond his own specialty is apt very soon to find himself only the highly trained assistant to some other man. . .*
>
> *Try also to understand that though the sciences are defined from one another in books, there runs through them all what philosophers used to call the commune vinculum, a golden interweaving link, to their mutual support and interpretation.*
>
> Jarron (2013, 83-4).
>
> [19]

In other words, as D'Arcy tried to relate to his students, there is a bigger picture to be discovered on the borderlands of science and getting distracted in classification and details only clouds the issue as noted a number of times by D'Arcy and as he noted above and in his other writings reveals that this extreme specialisation makes one blind to the greater discoveries.

In many ways, you could say that this approach promoted by D'Arcy as hugely important if we want to make real discoveries and gain important insights from science, is an inspiration to the way I have conducted my own scientifically-guided thought experiment, in taking a really broad approach and letting the evidence take me where it was leading. Obviously, I am in the fortunate position to draw on the expert advice required from time to time in such a broad endeavour, from the fantastic resources available online. Long may it last!

Thankfully, in our more modern era, even within mainstream universities this narrow approach is slowly beginning to reverse itself. This can be seen in the collaborations of scientists such as: Geoffrey, B. West and James H. Brown and their expertise in biology and physics have joined forces to try and resolve issues, which there are many, concerning biological complexity. Their research is discussed in an interview where I have highlighted a pertinent excerpt below.

Of Mice and Elephants: A Matter of Scale

''Physicists tend to look for universals and invariants whereas biologists often get preoccupied with all the variations in nature,'' Dr. Brown said... Dr. West liked to joke that if Galileo had been a biologist, he would have written volumes cataloging how objects of different shapes fall from the Leaning Tower of Pisa at slightly different velocities. He would not have seen through the distracting details to the underlying truth: if you ignore air resistance, all objects fall at the same rate regardless of their weight.

Johnston (1999, 'The New York Times' 12th January)

[20]

This type of blinkered mindset is certainly one important reason, amongst many, why D'Arcy Thompson's observations of universals and simple underlying principles of growth and form that are calculable, have not being recognised until more recent times. This blinkered approach on the part of many biologists is again highlighted below by Geoffrey West in another interview article entitled: *Yeah, but what about the crayfish?* (...Where, the title refers to the not uncommon response– concern for the crayfish rather than seeing the bigger and more profound universal patterns embedded in Nature).

A different mind set

"In general," ... "although this was not true of my collaborators, biology tends to be dominated by a certain type of person in the opposite way to physics. They are always looking at the particular, and everything is an exception." ... [West] does not understand how such people can work in science if they do not believe there are such things as universal laws. "If you had biologists working, for example, in nuclear physics you would have someone working on deuterium and then someone else working on helium and they would not realize they were working in the same field."

Cartlidge (2001)

[21]

Physics begins to reunite with biology

In many ways these types of collaborations between physicists and some biologists, epitomised by the research of Geoffrey and Brown in particular, indicates a long awaited return to the more traditional approach to novel problem solving in science; just how D'Arcy Thompson suggested it could be resolved some hundred years earlier, as you will see shortly, this type of broader interdisciplinary research is really beginning to make some in-roads into resolving several fairly fundamental issues. For instance, as a result of his research, Geoffrey West has been led to discover and express similar sentiments to that of D'Arcy Thompson as seen in some excerpts from his interview in the *New York Times* below:

> ''*Everything around us is scale dependent...*
>
> *It's woven into the fabric of the universe...*
>
> *It is truly amazing because life is easily the most complex of complex systems,...*
>
> *'But in spite of this, it has this absurdly simple scaling law. Something universal is going on ...''*
>
> Johnson (1999, 'New York Times' 12th January)
>
> [22]

Perhaps, I should point out at this stage, that the more recent collaborations between physics and biology have at least recognised and acknowledged D'Arcy Thompson's contributions to revealing the deeper complexity of biology, but they take the cautionary approach to stating these laws and invariants of scale and form in more general and less emphatic terms than D'Arcy Thompson did as indicated below:

Life's Universal Scaling Laws

> *Although few today would articulate Thompson's position so provocatively, the spirit of his characterization remains to a large extent valid, despite the extraordinary progress during the intervening century. The basic question implicit in his discussion remains unanswered: Do biological phenomena obey underlying universal laws of life that can be mathematized so that biology can be formulated as a predictive, quantitative science?*
>
> *Most would regard it as unlikely that scientists will ever discover "Newton's laws of biology" that could lead to precise calculations of detailed biological phenomena. Indeed, one could convincingly argue that the extraordinary complexity of most biological systems precludes such a possibility. Nevertheless, it is reasonable to conjecture that the coarse-grained behavior of living systems might obey quantifiable universal laws that capture the systems' essential features. This more modest view presumes that, at every organizational level, one can construct idealized biological systems whose average properties are calculable.*
>
> West and Brown (2004, 36)
>
> [23]

Therefore, we could go one of two ways here and either acknowledge that even in the light of our more modern approach to trying to understand biological complexity, D'Arcy Thompson's model is still highly relevant; albeit as an idealised concept and useful for grasping the essence of biological systems and how they appear to work. On the other hand, we could take the position that D'Arcy Thompson took, based upon a much broader approach to the most up-to-date evidence from many fields of study and apply them to biological systems and restate his universal patterning of life in terms of biological laws that hold at every level in Nature.

I have taken the latter approach and as you will see: his dream of placing biology *en par* with the mathematical descriptions afforded physics and chemistry really do appear to hold across the entire spectrum and at every scale of life. They are quantifiable and predictable, not just descriptions of life, but a key to unlocking many of its mysteries embedded in the evolutionary process itself. In my mind, this is good science, as these laws and equations of scale can be tested and applied to find out things we could not otherwise directly measure.

As I indicated above, things are at last beginning to change, particularly as more physicists and biologists collaborate on problem solving projects, or more biologists begin to apply the known processes and methods of studying non-biological systems to biological systems, are discovering essentially what D'Arcy Thompson already outlined in terms of the equilibrium exchange between organisms and its environment and the cellular, molecular dynamics being driven by the same underlying processes as seen in complex chemistry and other non-biological complex physical systems. This type of approach in our more modern era to resolving long- embedded paradoxes and quandaries concerning biology and genetics are given below as a starting example:

Scale-free flow of life: on the biology, economics, and physics of the cell

The present work is intended to demonstrate that most of the paradoxes, controversies, and contradictions accumulated in molecular and cell biology over many years of research can be readily resolved if the cell and living systems in general are re-interpreted within an alternative paradigm of biological organization that is based on the concepts and empirical laws of nonequilibrium thermodynamics. In addition to resolving paradoxes and controversies, the proposed re-conceptualization of the cell and biological organization reveals hitherto unappreciated connections among many seemingly disparate phenomena and observations, and provides new and powerful insights into the universal principles governing the emergence and organizational dynamics of living systems on each and every scale of biological organizational hierarchy, from proteins and cells to economies and ecologies.

Kurakin (2009, Abstract)

[24]

Note to help you interpret the above quote, the definition of nonequilibrium refers to complex and dynamic non-static open systems which can sustain themselves and thermodynamics is given here: ***6.2: Thermodynamics and Equilibrium Chemistry*** *"Thermodynamics is the study of thermal, electrical, chemical, and mechanical forms of energy. The study of thermodynamics crosses many disciplines, including physics, engineering, and chemistry. Of the various branches of thermodynamics, the most important to chemistry is the study of the change in energy during a chemical reaction"*

Harvey (*n.d*)

[25]

The Tempo of Life – A Universal Scaling Law Applies?

The tempo of Life or the universal growth pattern applied to all living things would best summarise D'Arcy Thompson's discussion in his extended (1942) edition of his book: *On Growth & Form*, particularly in Chapter Three: *The Rate of Growth* [26]. In this, D'Arcy Thompson explores the very clear universal pattern with predicable ratios (equations), that he observes can be applied at every scale of development and growth over time.

In essence, what D'Arcy was discovering when assessing growth patterns, were predictable scales of growth/development that seemed, once again, universal to them all, but intrinsic and scalable according to the major types of organisms and their inherent complexity. He showed that growth was far from linear and incremental; but, instead it went in enormous leaps and then stabilised. Not only was this pattern to be seen in one life-time of say, a human being, but that this pattern repeated itself at key developmental stages of a human's life.

D'Arcy Thompson seen how this simple equation was proportional across different species; simpler organisms had the same growth pattern, just on a faster time scale, while more complex organisms reflected in their growth and development, a relatively slower timescale, but still followed the same fundamental pattern and tempo of growth in scaled proportion to its size or complexity.

In many ways, this growth pattern at every scale over time has a simple equation and can be represented as a growth curve and commonly referred to as Sigmoidal and again, in more recent times, D'Arcy Thompson's observations are finding confirmation and support, albeit indirectly, as seen in a statement made in Geoffrey West below regarding the universality of the sigmoidal growth curve:

Growth models based on first principles or phenomenology?

...Still largely missing, however, is a theoretical framework for understanding the mechanisms that affect whole-organism growth trajectories. So questions such as why growth curves are almost universally sigmoidal, what controls the final or mature body size, and what affects the allocation of energy and materials to growth and development remain largely unanswered.

West et al (2004, Introduction)

[27]

A clue to the sigmoidal equation being applicable at every scale of life, and therefore an 'almost' universal (invariant) shared by every living thing that has been studied thus far, is suggested below in an excerpt from a model proposed in the same paper above by West et al.

Note: ontogenetic is equivalent, or essentially means the same thing as morphogenesis (natural bio-chemically controlled egg to cellular differentiation to embryo development)

Is growth rate limited by resource supply or targeted adult size?

... Growth is fundamentally a dynamical process of energy and material transformation that must obey the first principles of physics, chemistry and biology. Across all organisms ontogenetic growth rates are directly tied to metabolic rates, because biosynthesis is fuelled by the biochemical reactions of metabolism.

West et al (2004, Coda)

[27]

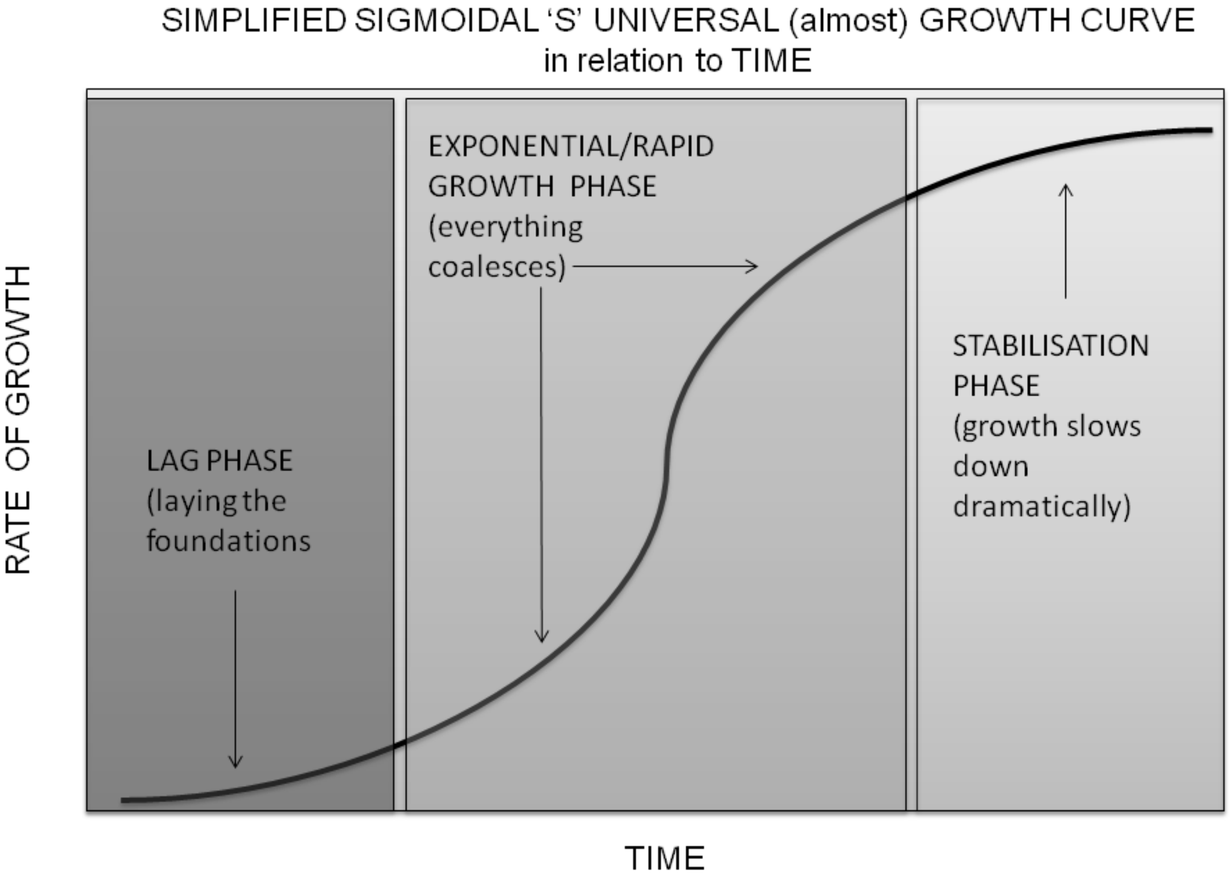

Fig. 3 Idealised chart showing the Sigmoidal growth/evolution over time curve. Left-hand section shows typical 'Lag Phase', the centre section where 'S' (Sigmoidal curve) rises rapidly and is sometimes referred to as the 'Exponential Phase' and finally, the third section (right) is the slow growth/evolutionary stage at the top of the 'S-Curve' which could be described as the 'Stabilisation Phase'.

Therefore, bearing in mind that the development of living organisms may be driven and guided according to resources and metabolic concerns (the energy requirements and regulation system that operates as an heat/energy/fuel exchange between an organism and its environment), we will now take a look at a number of examples of the Sigmoidal growth and development curve over time.

All natural phenomenon studied thus far, really do appear to scale according to complexity/size, as well as growth and development and function being ultimately guided by spatial and resource concerns and all of this is measurable and therefore predictable, as growth and development over time is seemingly, a universal, common to them all and discernible at every scale.

In other words, growth/development/evolution appears to obey laws of scale and all of this can be expressed via simple equations and probably stem from the dynamics and predictable properties of other thermodynamic systems (where cellular life and their constituent organs exhibit fundamentally similar characteristics, although, living systems are more like: cellular, whole metabolic networks/systems working dynamically in an energy exchange feedback-loop with their environments), just as D'Arcy proposed.

Essentially, the 'S' Curve or Sigmoidal growth curve over time, is the pattern followed by everything that we have observed and recorded growing or developing, colonising or multiplying in the natural world or systems created by us as you will see from the charts below:

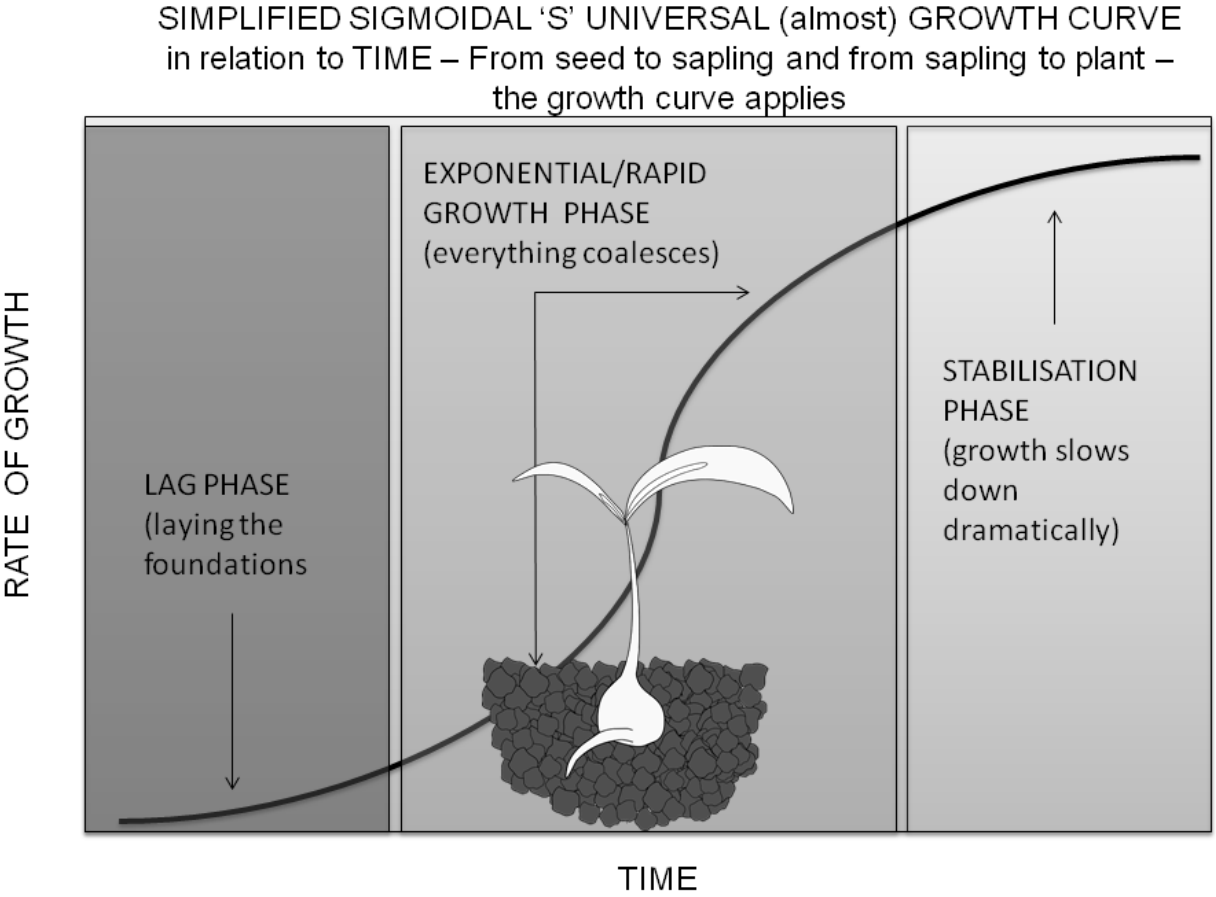

Fig. 4: Sigmoidal growth/evolution over time curve applies to the growth of a seed to a sapling to maturity. Plant biomass is Sigmoidal (Link).

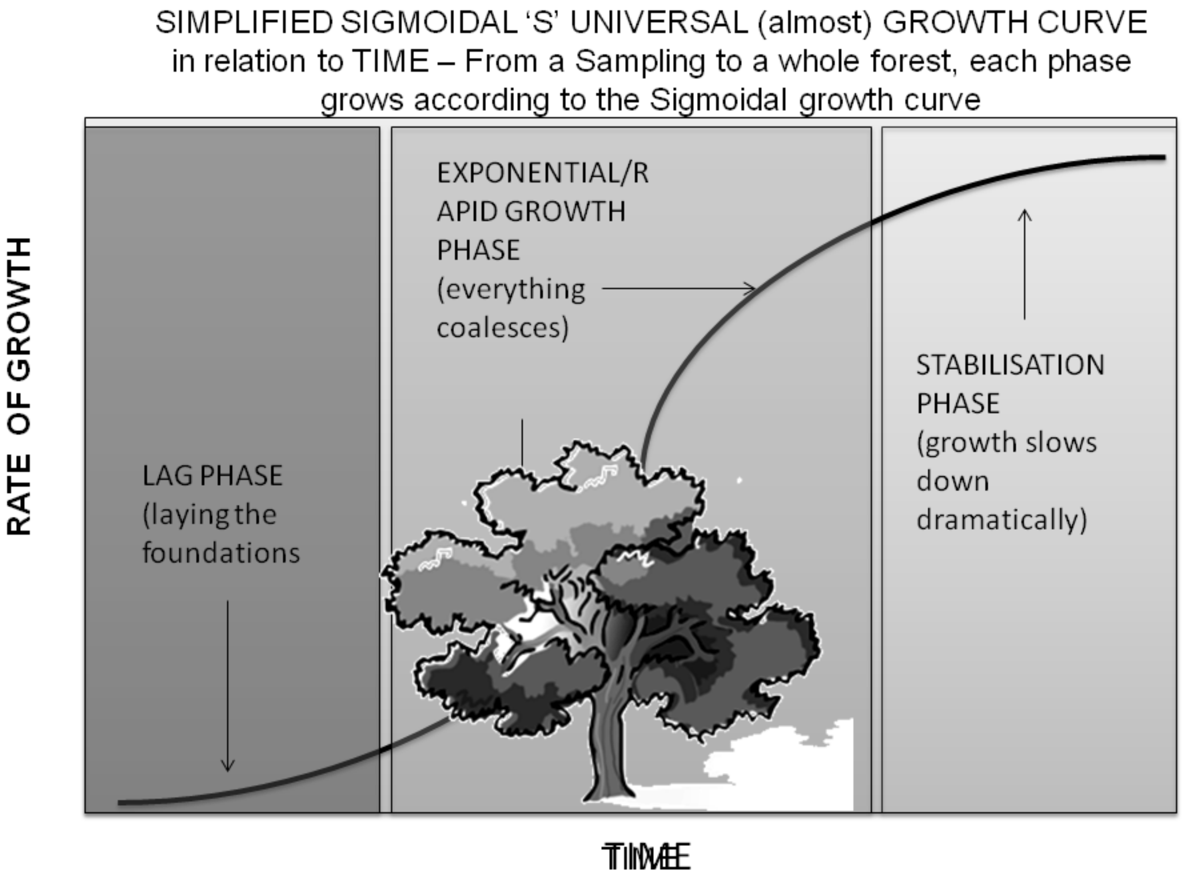

Fig. 5: Sigmoidal growth/evolution over time curve applies to the growth of an entire woodland. (See figure 11.5 Exponential growth of a colonizing population of Scots pine. Pinus sylvestris. Data from Bennen 1983).

From the seed to the sapling and from the mature plant to the entire colonisation and biomass, follow the same Sigmoidal growth pattern from a lag, exponential and stabilisation stage (Fig. 4) and the Sigmoidal growth pattern reflects the slow development of a woodland, to later (exponential) colonisation of an area and finally, stability (Fig. 5). Figure 6 below shows that the growth of yeast populations and their colonisation are no different, their growth rate is much faster, but this is relative to and proportional to their scale (size). Yeast follows a Sigmoidal growth curve.

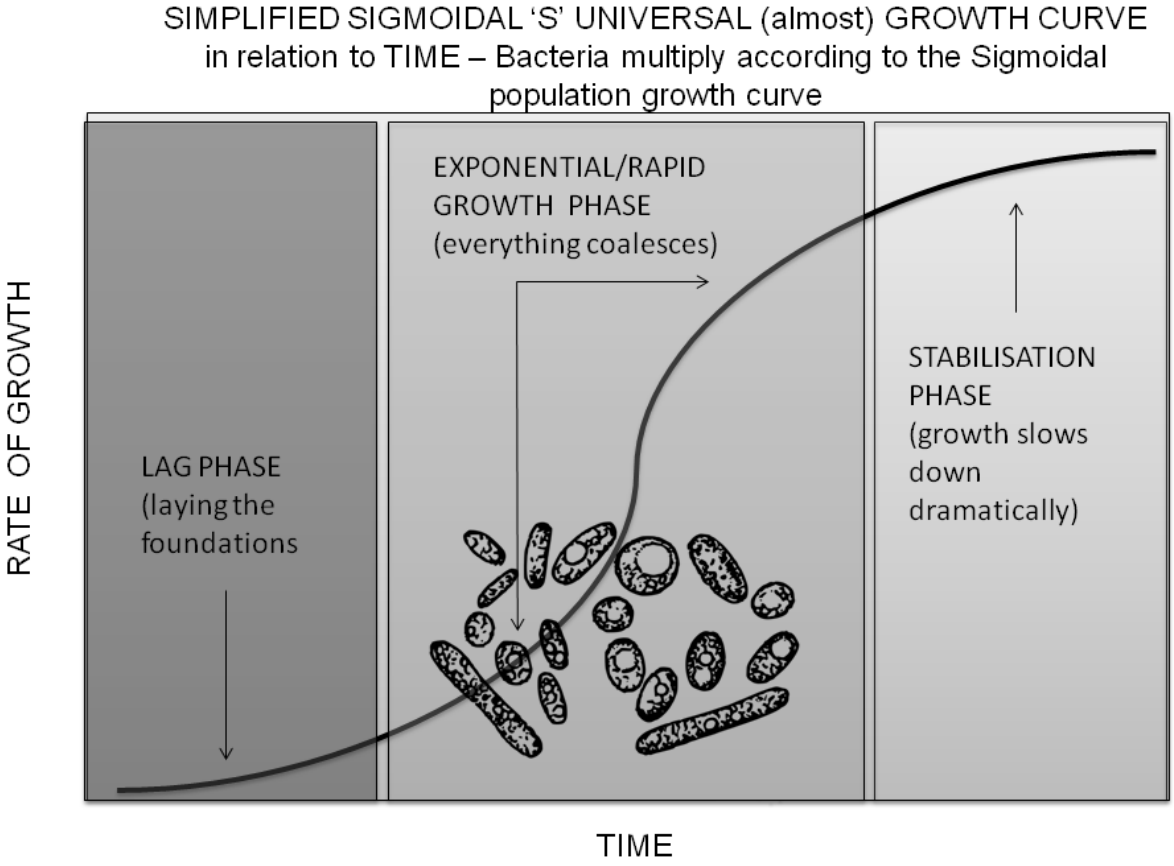

Fig. 6: Sigmoidal growth/evolution over time curve applies to the growth of colonies of yeast as seen in: figure 11.8 Sigmoidal growth by a population of the yeast Saccharomyoces cercvisiac . Data from Gause 1934.Or bacterial colonies is also Sigmoidal, but will rapidly decline in closed system such as a Petrie Dish (See: Link).

Embryological development has a lag phase, quickly followed by an exponential growth phase and stabilisation – it is one again Sigmoidal (Fig. 7). And I could fill a page with all the other instances, in other words, biological growth and development and even evolution is predictably Sigmoidal. Basically, as D'Arcy Thompson proposed: at every scale and level, things grow proportionally and in a predictable manner and can therefore be used to calculate otherwise unknown things in nature. This is the beauty of the mathematical formula.

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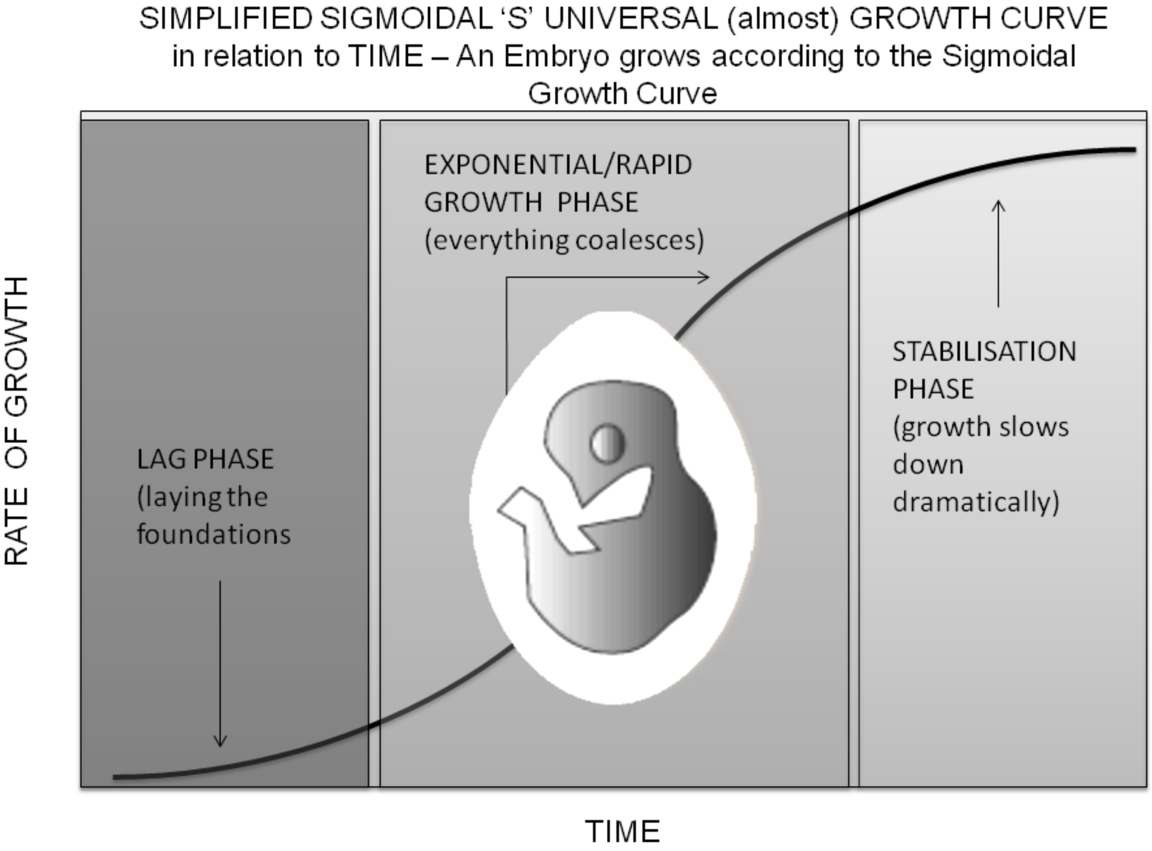


Fig. 7:Sigmoidal growth/evolution over time curve applies to the development and growth of an embryo (Link). Then the embryos grew up to develop social media and the internet that also followed a lag phase, an exponential phase and finally reached maturity and stabilisation.

Animals Growth Curve

Lag period

It is the first period during growth phase, where the curve rises gradually. The organism is getting prepared for growth by synthesizing enzymes and accumulating substances to metabolize protoplasmic components.

Exponential period

During this period growth begins slowly at first and becomes rapid later on. Hence the curve rises steeply. As a result the organism enlarges doubling and redoubling in size. This phase is also called as logarithmic phase.

Deaccelerating growth period

The exponential growth does not continue indefinitely. It is followed by a period when growth proceeds more slowly and finally ceases altogether. The curve therefore rises slowly and these become horizontal, signifying limit of growth. During this phase, the rate of acceleration is exactly equal to catabolism.

Growth rate in Animals

Growth in all higher animals including man, follow a specific rate and rhythm of growth, and stops long before death. The rate of growth is not uniform throughout life. If varies during different periods of life.

NCS Pearson (2016)

[28]

What makes the Sigmoidal curve, not only important as a model for seemingly all natural systems that grow under natural conditions and its application to the growth and development of broccoli to bacteria, is that the Sigmoidal curve being applicable at all scales to all natural systems studied, should therefore apply to other natural growth and development phenomenon that we cannot otherwise observe in real time. I.e. it should give us an insight into the growth and development of life itself, namely the tempo of evolution and the formation of the species.

As the Sigmoid growth/evolutionary curve appears to be a universal (or almost universal as noted above by West), it is therefore not perhaps that surprising that it could possibly reveal things that we couldn't otherwise know about Nature, such as the tempo and pattern of past evolutionary events. One very clear example of this can be seen in the application of the 'S' Sigmoidal growth curve to the tempo or eruption of life sometimes referred to as the Cambrian explosion of some half a billion years ago from seemingly no clear ancestral processors within the Pre-Cambrian period.

However, if we apply the Sigmoidal growth curve, we find that this illusive period of evolutionary history falls neatly unto this curve where the Pre-Cambrian represents the lag phase, the explosion of life itself (the exponential phase) happens tremendously rapidly and profoundly during the Cambrian period itself and finally, we can only assume that stabilisation has occurred as species do not change dramatically in our more modern era This is explored in more detail in Book Two and many of the means by which species could erupt rather rapidly will be reviewed particularly in the second half of this present book.

There is good evidence once again to support this principle of growth and form (evolutionary development) as you will see when it is applied to the embryological development as it mirrors on a much smaller and quicker timescale, the greater Sigmoidal tempo of the development (evolutionary) of the species itself. This will be discussed in more detail in Chapter Four of this book and will be fully applied in Book Two. Essentially, this indicates that the Sigmoidal growth equation may operate at all scales of life and complexity where, the shorter timeframes represent the growth curve in direct relation to quicker growth and conversely, larger timescales reflect much slower growth patterns and this is observable at every scale in between.

This proportional growth pattern according to natural scales of complexity begins to dovetail with D'Arcy Thompson's model of evolutionary change, where he proposed that the eloquent underlying cohesion of Nature and biological life is discoverable and predictable at all magnitudes (scales) and therefore can be applied to trying to figure out the processes of evolutionary development. Seemingly, the Sigmoidal growth curve is pointing very strongly to the fact that this is the pattern that Nature has followed in order to produce organisms as it is the most efficient, space-filling and time -saving way.

Is it really all a matter of scale?

This brings us to several other scalable aspects of life, but most specifically, metabolic rate to mass, and just like: growth over time the Sigmoidal pattern of life, which may be scalable as suggested above, due to metabolic concerns, this is also turning out to quantifiable, scalable and predictable across all levels of life. Interestingly enough, when we assess the entire spectrum of life from cold-blooded to warm-blooded animals, from amoeba-types, to reptiles, birds and mammals, discrete metabolic groups become apparent.

This begins to suggest that D'Arcy Thompson's proposal that there were intrinsically distinct "Types" or kinds of organisms may be discernible and by pursuing this pattern of discrete whole systems, we may be able to understand another fundamental regarding evolutionary development.

For instance, although there are underlying commonality between plants and animals being of a particular eukaryotic (cell with nucleus, which we will discuss in more detail further on) multi-cellular types, we could suggest that as plants use a fundamentally different energy/fuel exchange system in concert with its environment, that these are an obvious candidate for being a distinct group from animals; perhaps they had different trajectories and evolutionary life-histories due to even a small different in their early starting conditions, which of course forms an important aspect of D'Arcy Thompson's view of evolution where: initial conditions can make a very big difference in the end.

However, if we keep applying the principle of scale (the Matryoshka Principle) at every scale, which is the most logical approach, then, the discrete groupings should be identifiable, between and within, the plant and animal kingdoms at every scale and level of complexity from the least complex to the most complex (nested scales within scales within discrete sets).

This does appear to be the case as seen in the commonly shared metabolic system amongst animals and the overarching patterns emerging from studying this phenomenon in relation to size/mass. This is clearly shown in the work of an experimental agriculturalist Max Kleiber. His theory relates to the apparent predicable ¾ power laws where metabolic rate and mass are plotted for a diverse range of animals (see Link Kleiber, 1932 - *Body size and metabolism*). [29]

Note that all the images used in graphs within the following charts are my addition to existing graphs and data and are used to simplify and clearly illustrate the concept of scaling.

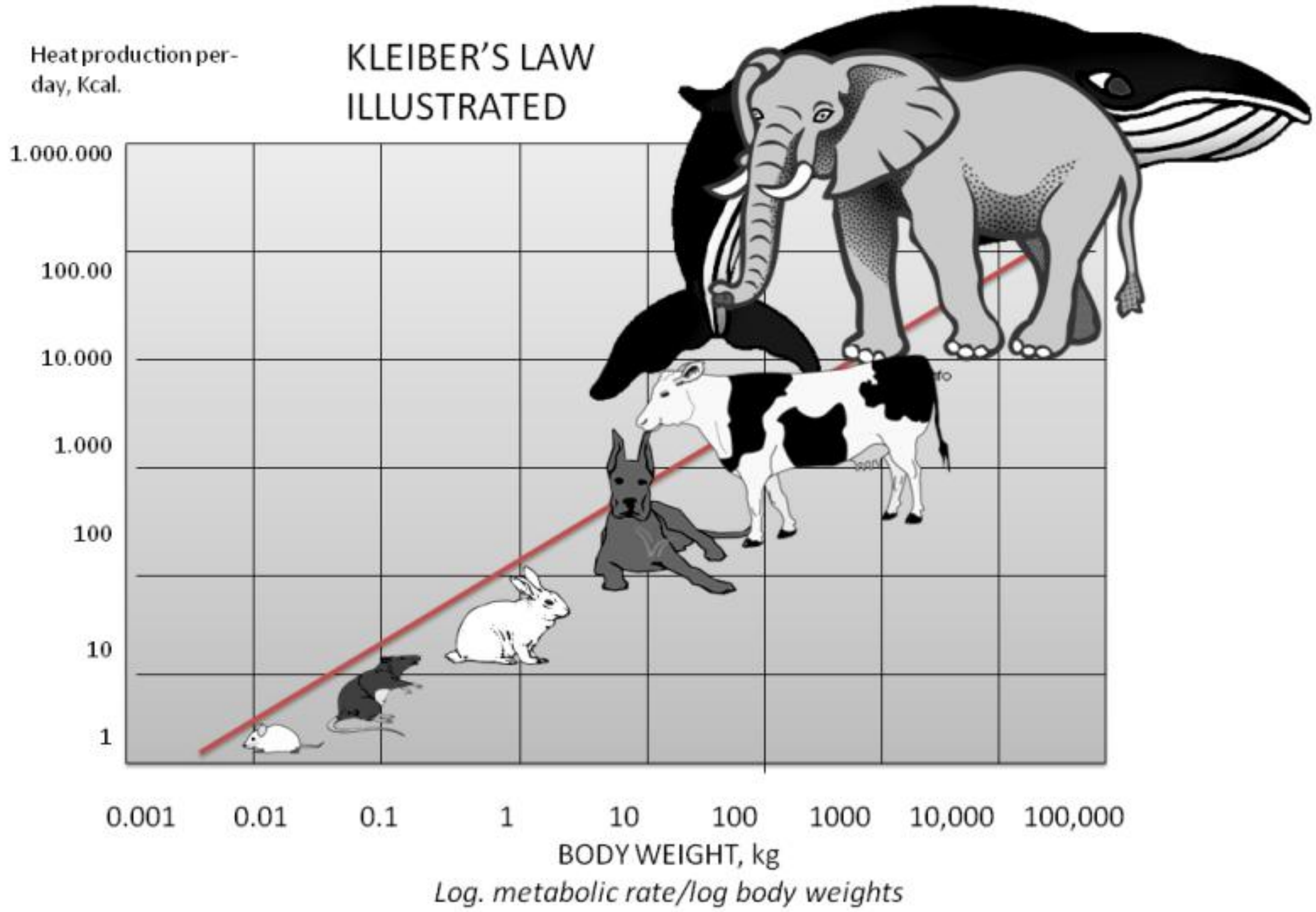


Fig. 8: Loosely based upon the metabolic rate to mass/surface area presented by Kleiber's ¾ scaling law. As mammal mass/surface area increases: so does its metabolic rate increase on a scalable gradient slope. Link

Applying Kleiber's laws in a more modern era has proved rather fruitful and more researchers have added on anything from amoebas to antelopes since his original proposal. Everything really would appear to scale in terms of metabolic rate to mass by factors of predictable magnitude. Now there has been hot debate regarding this law and the fact that it seems to apply almost universally and there are always exceptions to the rule. However, as seen in a science paper published in more recent years, this issue has been fully addressed by using actual living populations:

Experimental allometry: effect of size manipulation on metabolic rate of colonial ascidians

The allometric scaling of metabolic rate of organisms, the three-quarters power rule, has led to a questioning of the basis for the relation. We attacked this problem experimentally for the first time by employing the modular organism, the ascidian that forms a single layered flat colony, as a model system. The metabolic rate and colony size followed the three-quarters power relation, which held even after the colony size was experimentally manipulated. Our results established that the three-quarters power relation is a real continuous function, not an imaginary statistical regression

Nakaya et al (2005. Abstract)

[30]

The ¾ law is best explained using the information provided by A Van Aken (2014) from Brighton and Sussex medical school slide-share entitled: *Neuroscience made understandable* [31] which I have paraphrased as follows: When reading these charts where (body weight) mass is plotted against metabolic rate, the chart is showing a gradient and scalable linear relationship (obeying the ¾ power laws).

The numbers that you see above are transformed from the actual weights etc of different animals to a logarithmic scale. Base 10 is used in this case and the reason for this is that if you were to try and plot the actual range of magnitudes such as a mouse of less than 100 grams against elephants weight over 1000kg on same scale, these would be off the charts.

Therefore logarithmic scales are used so that we can view them on the same chart. However, it does not take away from the fact that these animals when body weight and metabolism are plotted reflect the seemingly universal scaling law or the ¾ power law as seen on the gradient slope. D'Arcy Thompson studied what he called logarithmic spirals for example.

Similar logarithmic patterns with predictable properties of scale have been identified as occurring across all of Nature and as a result of an increasing number of in-depth studies since both D'Arcy Thompson and Kleiber's time.

For instance, this seemingly universal pattern of the ¾ power laws as proposed by Kleiber and the applicability of scaling laws in general is highlighted in an interview with West and Brown in the *New York Times* below.

This is the same interview article referenced earlier in relation to the surprising universals underpinning life itself and the comments regarding the physicists approach versus the typically narrow and distracted approach of many, but not all, biologists:

Of Mice and Elephants: A Matter of Scale

For an amazing range of creatures, spanning in size from bacteria to blue whales, metabolic rate scales with body mass not to the two-thirds power but slightly faster -- to the three-quarter power.

Evolution seems to have found a way to overcome in part the limitations imposed by pure geometric scaling, the fact that surface area grows more slowly than size. For decades no one could plausibly say why.

Kleiber's law means that a cat's metabolic rate is not a hundred or 21.5 times greater than a mouse's, but about 31.6 -- 100 to the three-quarter power. This relationship seems to hold across the animal kingdom, from shrew to blue whale, and it has since been extended all the way down to single-celled organisms, and possibly within the cells themselves to the internal structures called mitochondria that turn nutrients into energy.

Johnston (1999, 'The New York Times' 12th January)

[32]

Interestingly, the research of West and others is being taken quite seriously even by biologists such as: Richard Dawkins as noted in an interview below:

A different mind set

The work has drawn praise from many biologists, including the popular science writer and Oxford professor Richard Dawkins, who describes it as "a theory of enormous power, explaining a huge range of facts with great economy".

Cartlidge (2001, 3).

[33]

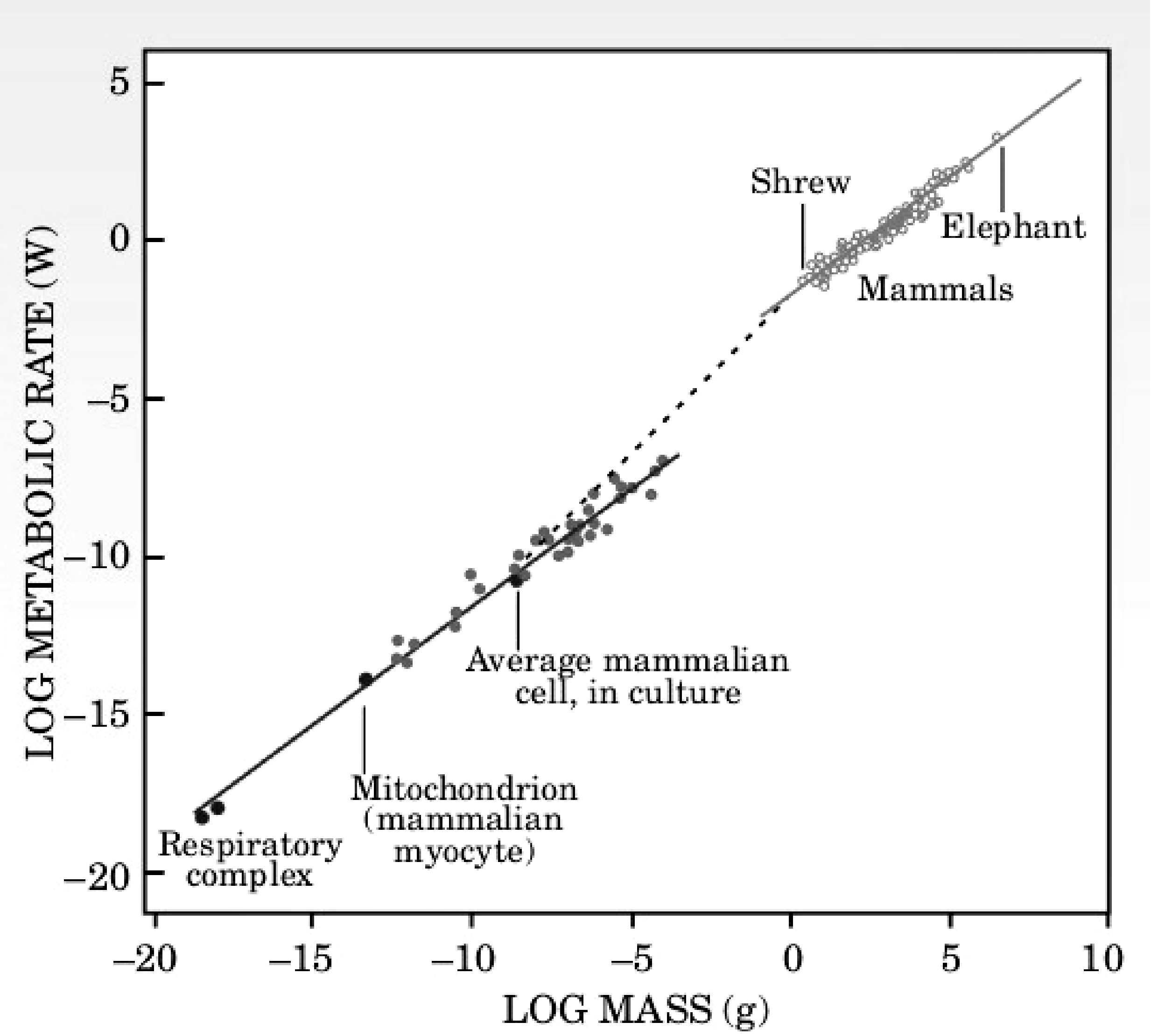


Fig. 9: Metabolic Rate: ¾ Power Law as it applies to mammalian Mitochondria to mammal cells in culture and the mammals themselves converted to greyscale After: Geoffrey B. West and James H. Brown 2004 in slideshow presented by: Faiza and Vineeth from What If Animals were Fractals? (2009), University of Utah Link

Although, the ¾ power law applies to mammals (See Figure 8) and as shown in Figure 9, is applicable also to the average metabolism in cells in culture and even the little fuel-driver of the mammal cell: Mitochondria, West and Brown encountered a problem which arose when they attempted to apply the same ¾ scaling law to the very different world of plants.

This is important to mention, as we are attempting to find universals for evolutionary complexity itself, but I also point to highlight the fact that even though plants and animals are essentially multi-cellular eukaryotic organisms, their solution to fuelling and sustaining themselves are quite distinct, implying a distinctive grouping of organisms (a set perhaps?) that may have diverged and diversified from their shared eukaryotic ancestral form according to environmental/resource concerns setting them on distinct developmental trajectories.

I also highlight the distinctive systems employed by animal and plant life respectively, as it demonstrates how science should work, if you encounter an unexpected problem with your model as exemplified below.

Of Mice and Elephants: a Matter of Scale:

> *What emerged closely approximated a so-called fractal network, in which each tiny part is a replica of the whole. Magnify the network of blood vessels in a hand and the image resembles one of an entire circulatory system. And to be as efficient as possible, the network also had to be ''area-preserving.'' If a branch split into three daughter branches, their cross-sectional areas had to add up to that of the parent branch. This would insure that blood or sap would continue to move at the same speed throughout the organism.*
>
> *The scientists were delighted to see that the model gave rise to three-quarter-power scaling between metabolic rate and body mass. But the system worked only for plants. ''We worked through the model and made clear predictions about mammals,'' Dr. Brown said, ''every single one of which was wrong.''*
>
> *In making the model as simple as possible, the scientists had hoped they could ignore the fact that blood is pumped by the heart in pulses and treat mammals as though they were trees. After studying hydrodynamics, they realized they needed a way to slow the pulsing blood as the vessels got tinier and tinier. These finer parts of the network would not be area-preserving but area-increasing: the cross sections of the daughter branches would add up to a sum greater than the parent branch, spreading the blood over a larger area.*
>
> *After adding these and other complications, they found that the model also predicted three-quarter-power scaling in mammals. Other quarter-power scaling laws also emerged naturally from the equations. Evolution, it seemed, has overcome the natural limitations of simple geometric scaling by developing these very efficient fractal-like webs.*

Johnston (1999, 'The New York Times' 12th January)

The other reason why I have highlighted the difference between the transport system of plants and animals is to reiterate the concept of the fundamental "Type" or theme of plant organisms compared to animals, even though they utilise their energy needs in the context of their environments differently, they are still seemingly governed by the same underlying universal scaling principles. The transport/energy systems used differently by these organisms are also scaled according to fractal networks and systems and this also calls to mind the fractal nature of Nature identified within D'Arcy Thompson's studies.

Fractal patterning in Nature is once again mathematically explicable as it is all about self-similar patterning on different scales. The smallest is reflected in the largest and at every scale of magnitude in between and all is reflected in the whole. This is how D'Arcy Thompson describes these systems of proportionally scaled repeating patterns of growth and form and he recognised that the veins of a leaf reflected the branching pattern of it outer twigs and the overall branching and root system was reflected on a much larger scale within the entire tree. Much research has been carried out on fractals in Nature and it seems that it is everywhere we look and everything truly is proportional to itself and the whole system.

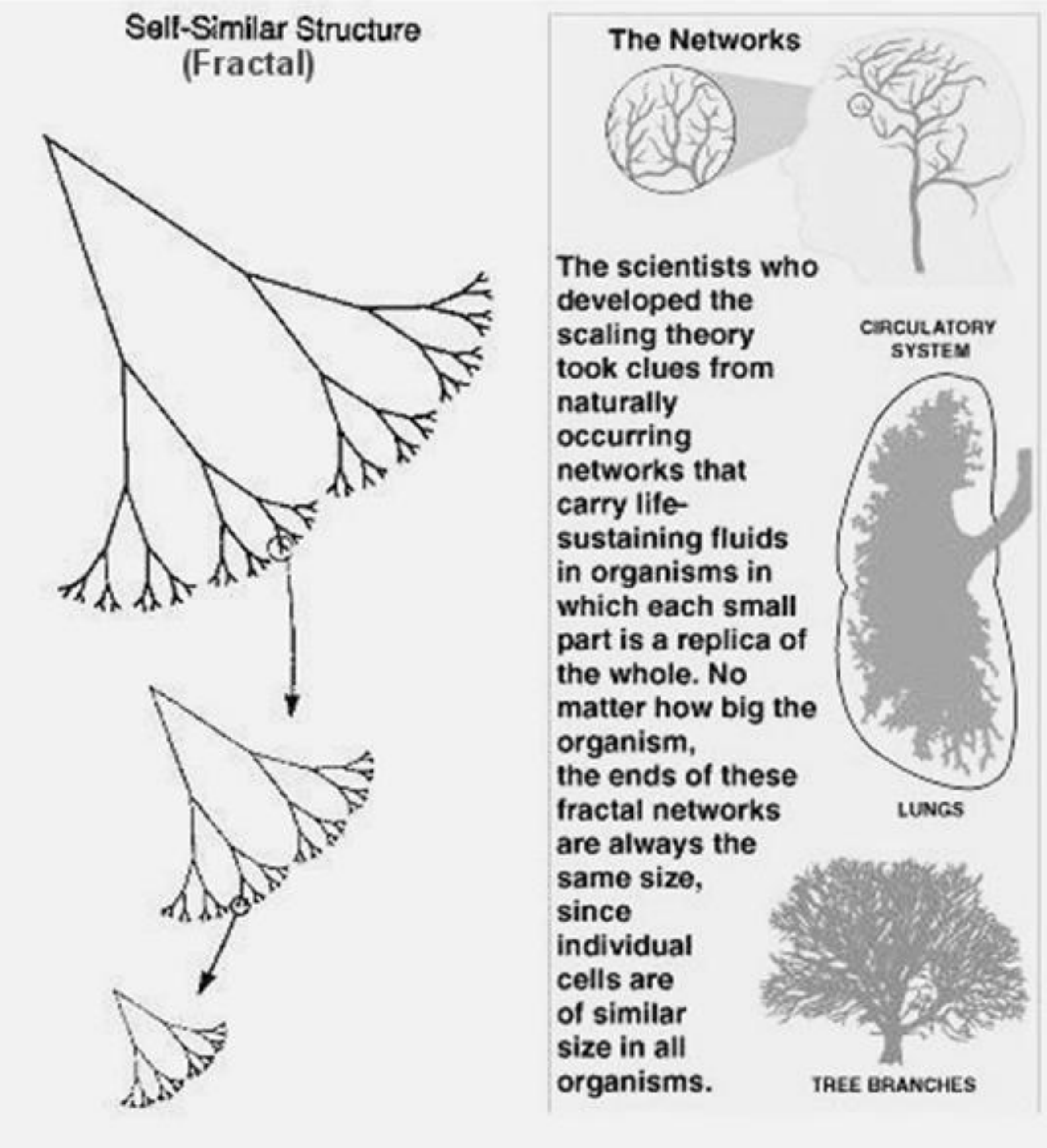
These fractal networks operating within such a diverse range of species are seemingly fundamentally similar, with the difference being that they use these fractal networks/systems in functionally different ways as indicated below in the *Universal Review*:

Metabolic Rate and Kleiber's Law

Mammals have richly branched air tubes, but they are confined to special organs, the lungs. Fish do a similar thing with gills. Trees use their richly dividing branches to supply their leaves with water and pump sugars back from the leaves to the trunk.

Universal Review (*n.d*)

[35]



The scientists who developed the scaling theory took clues from naturally occurring networks that carry life-sustaining fluids in organisms in which each small part is a replica of the whole. No matter how big the organism, the ends of these fractal networks are always the same size, since individual cells are of similar size in all organisms.

Fig. 10: Fractal networks that scale predictably across a diverse range of organisms. Source: Metabolic Rate and Kleiber's Law in Universal Review, Figure 3. Fractal in Nature https://universe-review.ca/R10-35-metabolic.htm

In other words, in principle, the observable and consistent patterns embedded in Nature may be partly driven by energy requirements (metabolism to mass) of an organism according to its environment. Or another way of saying it: Nature cuts her clothe to her measure (as the old tailor's saying goes). For instance, our internal networks are fractal-like and taking this to a universal scale, literally, they appear to have mapped the known universe and the image from what I can remember, looks indistinguishable from the neural networks that have been mapped in our brains.

You may not think about it, but even your digits on your hands and toes on your feet follow another type of fractal (self-similar repeating pattern at different scales). And as you might have guessed, there may also be a reason why our five fingers don't sprout five tinier fingers at the tips of our existing one. This may be because everything is a whole system within a larger whole system, just at different (repeating patterns) scales of complexity and as an efficient system needing to get resources to all extremities.

Just like Pinocchio's nose, there is a sensible limit for reasons of resources and proportion in relation to the whole and stability that stop his nose sprouting more branches. He is a wooden puppet trying to become a boy; not a wooden boy trying to become a tree. It is too late; his path has already been set in motion way back in the mist of time. So, just as a whole organism must grow in proportion to itself and its environment, it can only grow or evolve according to and proportion to its earlier developmental trajectory.

Recall that we don't suddenly change the whole set (Matryoshka) by later adding on bits, but take the underlying template (smaller and simpler scale) and develop and build and elaborate upon it at all possible scales and dimensions and thereby create more surface area to fill in the detail and elaborate the various themes; whilst the fundamental shape and form and function remains intact.

Therefore, perhaps the reason why we don't have five digit extremities and not many continuous branching and ever-decreasing multiple miniature digits, apart from the fact that they would look ridiculous and you would fall over a lot, it simply would be a very efficient way of getting blood circulating and everything else that you need around the whole body.

However, a tree would put on continuous branches reflecting the ratio of distance of the previous branches and the overall shape of the tree itself and the veins of some leaves can be seen to form this same branching pattern, on ever decreasing scales. But, even the tree will eventually stop branching and growing (or as might be the case during its species development) and stabilise to consolidate what it has, growing thicker and maturing (stabilising phase) according to its natural life cycle and the resources available within the context of the whole forest.

To emphasis this idea further, the following explanation for these principles of scale according to efficiency of the whole biological system is given below:

The origin of allometric scaling laws in biology from genomes to ecosystems: towards a quantitative unifying theory of biological structure and organization.

.., all organisms share a common structural and functional basis of metabolism at the molecular level. The basic enzymes and reactions are universal, at least across the aerobic eukaryotes. Additional general rules based on first principles determine how this molecular-level metabolism is supplied and regulated at higher levels of organization: from organelles, to cells, to organisms, to ecosystems.

The most important of these rules are those relating to the size of the systems, including the body size of the individual organisms, and the temperature at which they operate. Our theory of quarter-power scaling offers a unified conceptual explanation, based on first principles of geometry, biology, physics and chemistry for the size-dependence of the metabolic process.

The theory is based on generic properties of the metabolic distribution networks in simplified, idealized organisms.

West and Brown (2005, Introduction)

[36]

The above model very much begins to echo D'Arcy Thompson's own ideas of biological complexity and patterning as well as reiterating his concept of a shared generic system across seemingly most species that have been studied, albeit in an idealised form. And as you will see, our modern sciences are also beginning to identify the invariants that govern natural systems which, D'Arcy Thompson said we would find, if we took this approach.

For instance, although cells look and behave very differently to microbes and mice are very different to men, there is an underlying commonly shared system that relates to energy exchange relating to the complexity of the organism and their respective environments.

As indicated above, West and others have established these scaling laws for a wide range of biological phenomenon, and according to these researchers, it is all about distribution of resources which by their very nature form fractal-like (space-filling) networks, whether the system is directly biological or run by biological entities. (See: West and Brown 2005) *Life's Universal Scaling Laws*, [37] and for more information on these broader scaling laws follow this link to view a video [You Tube] where Geoffrey West gives a very good lecture on the topic, (see: Google Talks Archives, 2012) *Scaling Laws In Biology And Other Complex Systems* [38].

There is definitely something universally fractal going on if, as these scaling factors apply to anything from small business to big corporate entities and from the rail network to the whole infrastructure that supports big cities that started out as a one horse town, there is a universal growth/evolutionary pattern emerging. And of course biological systems are not that different as they are seemingly all about distribution of resources as well. Scaling laws certainly seem to apply predictably across a diverse range of biological phenomena that has been studied in this manner.

However, they do not always come out as ¾ scaling as seen in the mammals and their cells within or outside the organism when mass and metabolic rate are plotted as illustrated above, but they do scale predictably all the same as seen in the information presented below is taken from a slide show based on: *Life's Universal Scaling Laws*, Geoffrey B. West and James H. Brown 2004, and asks the question: *What if animals were fractals?* 2009, University of Utah, presented by: Faiza and Vineeth. Under the heading: *Allometric scaling exponents for various biological variables as a function of mass*, an interesting list of scaling emerges when a number of different systems are examined amongst a broad range of biological phenomenon [39]:

Allometric scaling exponents for various biological variables as a function of mass

Metabolic rate	**3/4**
Heart beat rate	**-1/4**
Life Span	**1/4**
Radius of aortas/ tree trunks	**3/8**
Genome length for unicellular organism	**1/4**
Brain mass	**3/4**

Link

For instance, another predictable phenomenon identified within biological systems is the concept that small organisms reproduce (multiply/replicate) much faster than larger organisms. Basically, as most of know from common knowledge, a small species like a mouse reproduce very fast compared to larger mammals such as elephants. This is referred to as intrinsic rate and it means that there is an intrinsic difference between the reproductive capacities over time according to size of the organism.

Mammals for instance with a self-regulating metabolic system- homeothermic, (warm-blooded) is rather different to a virus, but viruses predictably scale in relation to mammals in terms of their intrinsic rate being 100,000 times greater than a mammals! Essentially, as we know the rate and mass/size of one organism, we can predict according to size, the proportions or intrinsic rate in this case of any organism. (See Figure 11), note that this is running in the negative slope, but still abiding by the laws of scale:

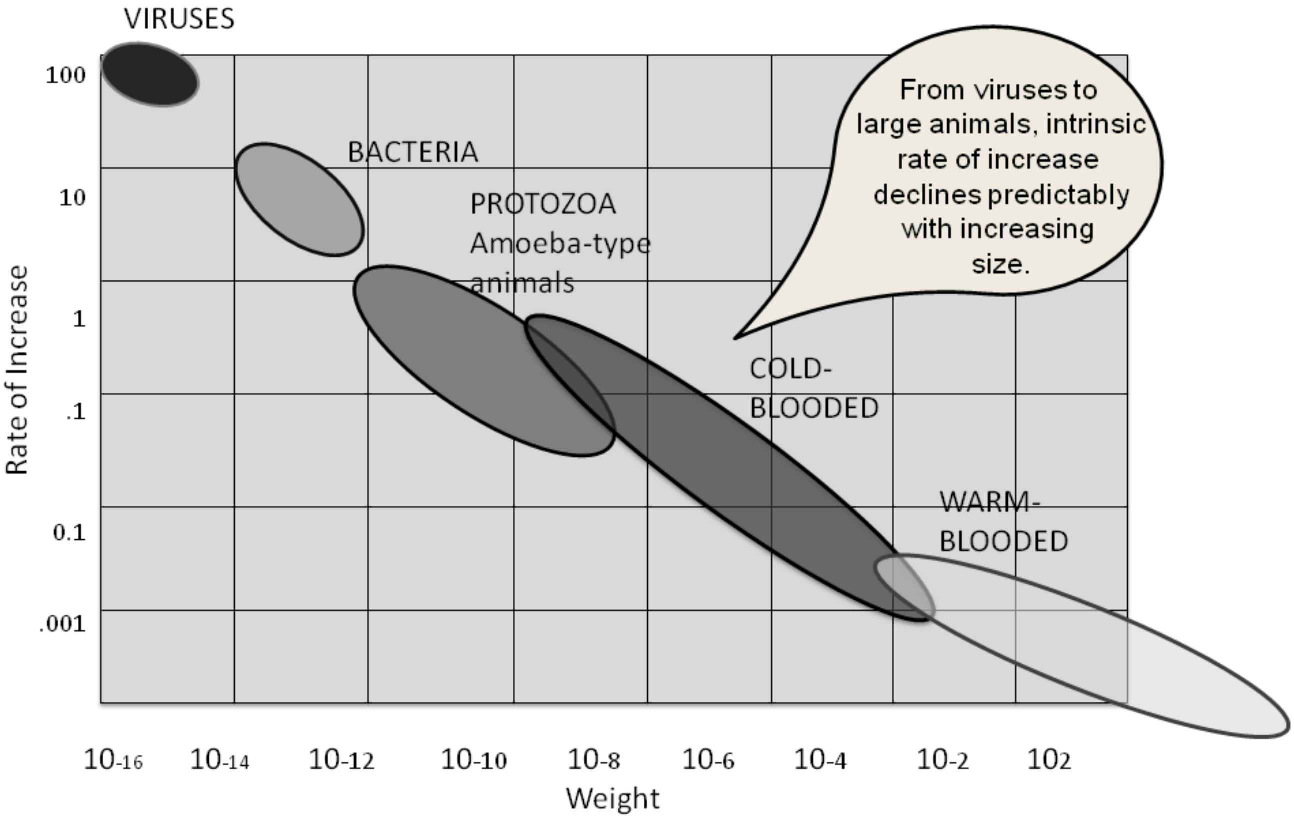


Fig. 11: Chart based upon rate of increase in relation to mass/weight of organism. Note the discrete groupings of fundamental forms /types with only a slight overlap between the more complex animal groups (Diagram based upon figure 11.21 Body size and intrinsic rate of increase - data based on Fenchel 1974, Link)

The charts for intrinsic rate for groups of major life-forms from viruses to bacteria and amoebas to monkeys are clearly clustering into discrete metabolic groups and indeed, from the protozoa (small animals that we can't see for the most part) single-celled organisms, to cold-blooded and warm-blooded species, the leaps of metabolic complexity between each group is worth drawing attention to as you will see in Figure 12 below.

In other words, the neat continuous grade seen exclusively for mammals and their metabolic rate to mass of ¾ naturally cluster with only a slight overlap when assessing such a broad range of organism beyond mammals or their cells according to their metabolic rate to mass, the slope and gradient clearly show an overall scaling exponent, but again clear species groupings, this time relating to metabolic complexity.

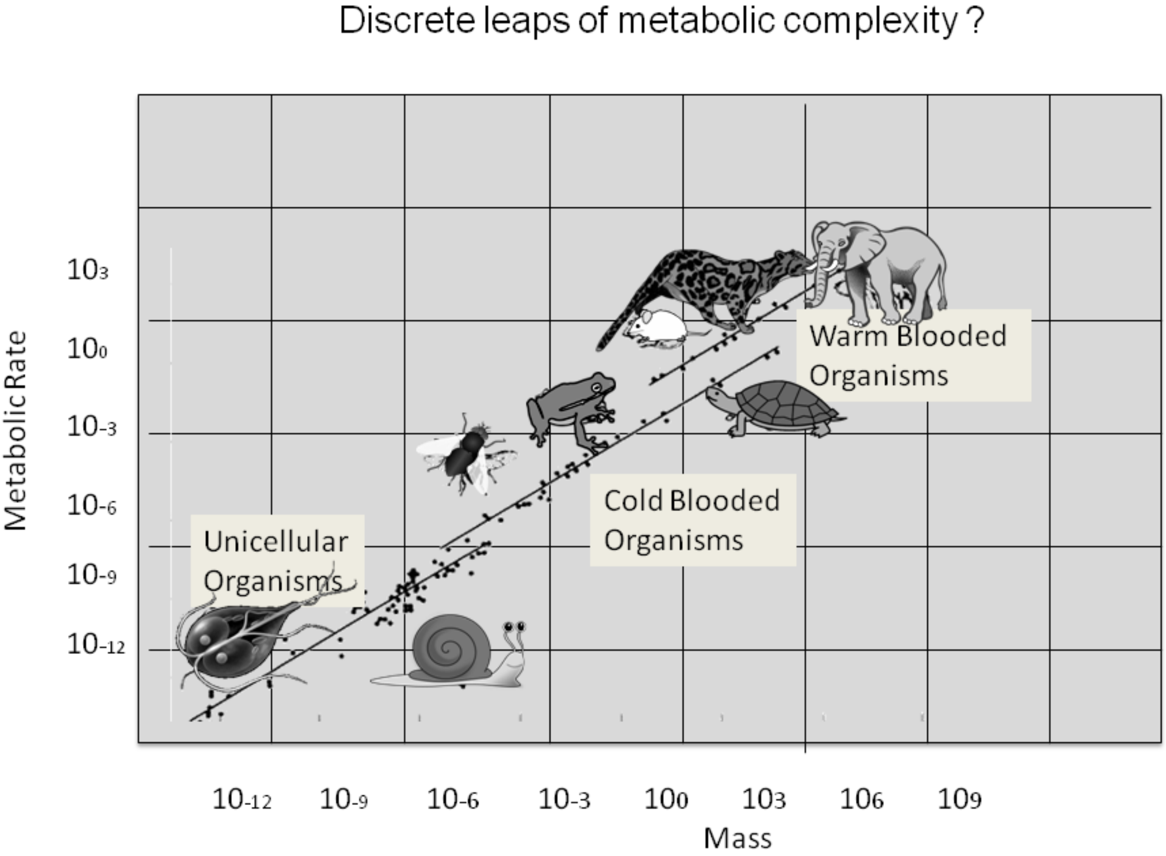


Fig. 12: Chart based upon metabolic rate to mass for diverse organisms ranging from unicellular to cold-blooded invertebrates and vertebrates and from warm-blooded vertebrates. Again note the discrete groupings of fundamental forms/types seemingly nested in scales of complexity. (Chart based upon data from Link and Tatsuo Motokawa, "Elephant's Time, Rat's Time" Link)

Just to highlight this proposal and reiterate these fundamental forms and their discrete groupings based, again, upon fundamental metabolic complexity, another chart (Figure 13) illustrated below, shows the scaling exponents of fish, amphibians, reptiles, birds and mammals; the latter forms are discrete from each other, but more dramatically divergent from the scaling exponent compared to the other main grouping, which have less divergence. In other words, there is no particular overlap between these major species groups and the chart actually shows fundamental leaps or 'discontinuous' groupings based on metabolism.

The images in the charts are used to literally to illustrate the point, but the chart itself is based upon the actual results of a study by White *et al* (2006, Abstract) [40]. Interestingly, this study is supposed to dispute the scaling laws as they sometimes show non-universals and it is these differences that are actually quite revealing from the perspective taken here.

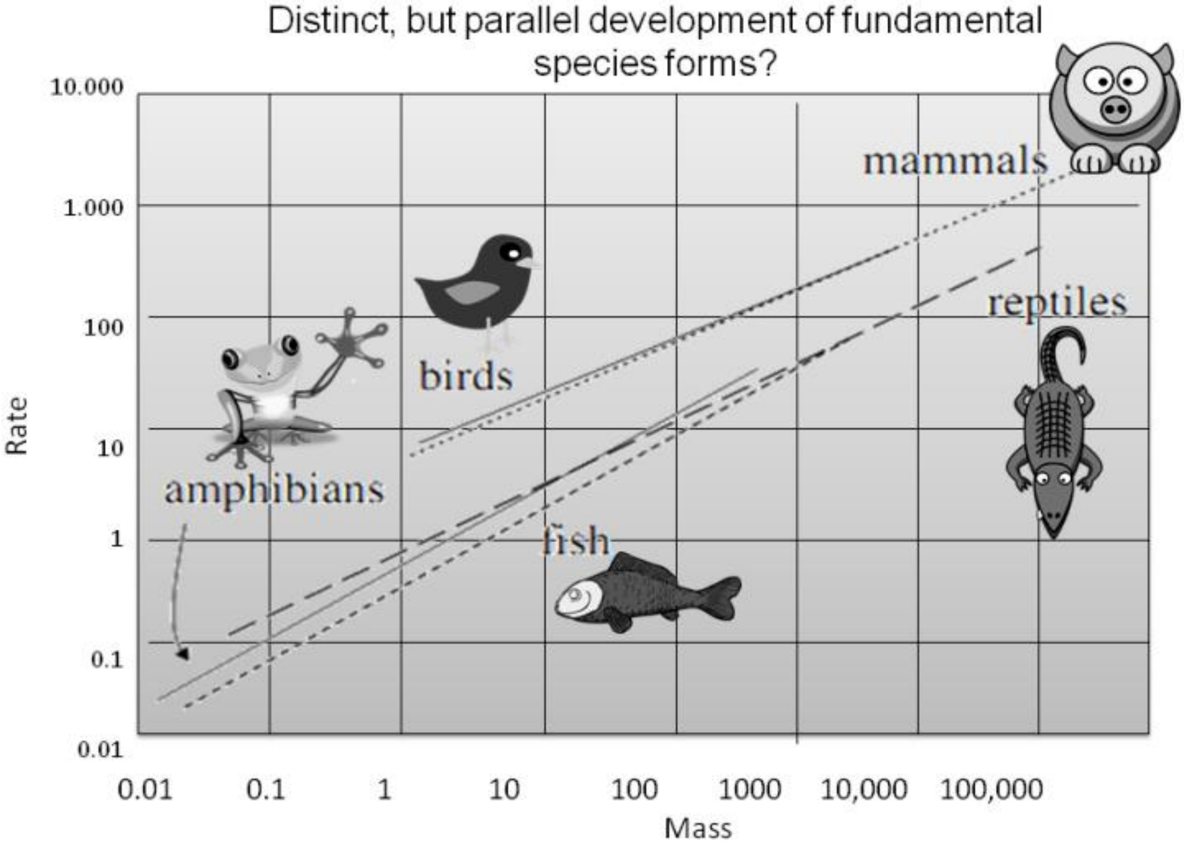


Fig.13: Chart of the fundamental 'types' of species that scale according to radically distinct metabolism according to their mass within discrete groups. (chart is based on figure 1 from White et al 2006, Link)

These metabolic (leaps or major shifts) between major groups of fundamental species forms which fall outside the ¾ scaling laws when applied to the whole range of complexity are highlighted in the following article. This highlights, I believe, what is most pertinent from the perspective of following D'Arcy Thompson's fundamental "Types" proposal using the same underlying systems common to them all.

Shifts in metabolic scaling, production, and efficiency across major evolutionary transitions of life

> *The 3.5 billion year history of life on earth was characterized by dramatic increases in the size, complexity, and diversity of living things. The first organisms were microbes with relatively simple body plans and metabolic networks. A few major transitions in form and function occurred during the subsequent evolution of life .... The resulting diversity of contemporary organisms ranges from minute, relatively simple unicellular prokaryotes to giant, complex animals and plants containing multiple differentiated organelles, cells, tissues, and organs.*
>
> *Two of the largest transitions were from simple prokaryotic to complex eukaryotic cells, and from unicellular to multicellular eukaryotes. Each transition required the integration of multiple individual organisms into a new higher-level unit of organization .... These transitions involved dramatic changes in structure and function, and several orders of magnitude in-crease in body size .... As all organisms share a common set of molecules and biochemical reactions..., the increases in size and organizational complexity were accomplished by assembling these universal components in new ways ....*

DeLong et al (2010, Abstract)

[41]

Essentially, it would seem that based upon the emerging data, that D'Arcy Thompson's concept of whole functional leaps of complexity on orders of magnitude between the fundamental 'Types' or divergent groupings (discrete sets) of organisms, using a similar underlying system, shared by all, but expressed in different ways according to spatial and energy concerns, may be essentially correct. However, we will fill out the evidence to support this assessment in more detail as we proceed through this book.

D'Arcy Thompson's laws of growth and form reviewed in light of the above

I thought the quote excerpt below would be appropriate in the summing up of D'Arcy's insights into biological complexity in the light of our more modern understanding of the same. It is from a highly respected biophysicist Stuart Kauffman, taken from his book:

At Home in the Universe: The Search for the Laws of Self-Organization and Complexity

...A few deep and beautiful laws may govern the emergence of life and the population of the biosphere...

Kauffman (1996, 23)

[42]

It may be as D'Arcy Thompson suggested that Nature works to scale at every possible level of complexity within the discrete/discontinuous groups. Thus, increasingly, D'Arcy Thompson's ideas of universal principles governing shape, pattern and form and dynamic processes in Nature seems to be gaining more and more support as we delve deeper into the complexities, but underlying mathematically describable and unifying scales of common complexity.

In combination, the charts presented above and the scaling principles in general, strongly suggest that the name of the evolutionary game is growth and innovation according to resources with a built-in drive to dynamic order and efficiency. Indeed, this aspect of this thought experiment is well supported as you will see in later chapters. D'Arcy Thompson's concept of space-filling and efficiency causing divergent forms from fundamental types, may actually apply. Again, I will expand on this with more supporting evidence as we proceed.

But returning briefly to the charts presented above, with regard to D'Arcy's concepts of discrete species, recall that he proposed that species did not descend linearly and continuously and progressively as the Darwinian model would claim, but, via common underlying patterning and common systems with many divergent and distinct forms arising from those fundamental forms of distinct (discontinuous) origins according to their developmental conditions, to ultimately produce all variations on the themes of life – the formation of the species.

Therefore, bearing this in mind, I do find it interesting that a mouse-sized lizard cannot be plotted within the higher scale of metabolism with a mammalian mouse of the same size, but remains fundamentally at the level of metabolic complexity seen in present-day lizard species. Does this indicate an intrinsic and fundamental metabolic organism type, where all the variation is just the filling in of the detail of the essential distinct themes of life?

Basically, this might be the case as, underlying all organisms, there would appear to be a shared metabolic system, but that this general system was used differently by different organisms, such as the difference between plants and animals, but still complying with Nature's fractal system and scaling laws according to metabolic requirements between the organism and its environment.

Furthermore, the closer metabolic systems shared between animals that still essentially scale predictably also scale, not just according to the size/mass of an animal organism and its metabolic rate, but fundamental leaps in metabolic complexity are clearly apparent between the warm-blooded and cold-blooded organisms and even within these groups. We may be looking at proportional scales within scales, each according to their own discontinuous set akin to the Matryoshka Principle.

Recall also from the charts showing discrete groupings, the fact that birds and mammals use a warm-blooded system, does not link these directly on a continuous linear metabolic gradient according to size/mass, but they have their own fundamental grouping, which does not link them to the group we refer to as reptiles.

Moreover, bear in mind that initial starting conditions, as we know from embryological studies and by inference, that metabolically discrete groupings could have been initiated much earlier, projecting even the most primitive types along distinctly different and increasingly divergent evolutionary trajectories as suggested by D'Arcy Thompson.

It could be that something as simple as the temperature of the primordial pond determined the level of metabolic complexity further down the line and this could have been a feedback mechanism, were more metabolic complexity begot more metabolic complexity in factors of scale and ultimately, produced discontinuous groups of cold-blooded systems that were more susceptible to environmental fluctuations in temperature than more sophisticated warm-blooded systems used by mammals and bird species today. As you will see throughout this book, there is good evidence to support this concept of evolutionary development.

Perhaps, the environment and resource availability and developmental conditions in general did inform the divergence of these shared metabolic systems and the organisms that could control their own energy regulation system by being more mobile would become more complex by virtue of having a greater range of environments to exploit. Perhaps organisms with less complex metabolic systems stabilised earlier and became fundamentally fixed using a slightly less sophisticated metabolic (cold-blooded) system. As strange as this may sound, all will become clear regarding the actual evidence for this form of evolution, particularly as more detailed and very real examples of this are given in Book Two.

All in all, it would appear that Nature runs things fractally and according to spatial, efficiency concerns and environmental conditions and in direct relation to resources and is not actually linearly hierarchical and actually nothing to do with Natural Selection, if you fully understand what this means in terms of the Darwinian model.

Nature doesn't appear to select anything, but sets up the conditions for species to adapt whatever the weather. So by understanding how fractal-like networks work and how natural systems evolve in real time, we can perhaps begin to understand how other complex systems (such as the species) evolved on greater timescales employing the same process.

We could, at this early stage suggest that as we know a little more about the fractal-like nature of intrinsic rate and metabolism to mass as well as the overarching growth principle of the Sigmoidal curve equation, as the charts presented above indicate discrete groupings of fundamental species types according to their inherent metabolism, these organisms being innately distinct metabolic groups of amoebas, amphibians, reptilia, mammalian, may have evolved at a predictable intrinsic rate according to their kind.

Presumably, simpler (metabolically-speaking) organisms would specialise earlier than innately more complex organisms (as whole space-saving and highly efficient metabolic exchange with their environment) just as simpler organisms such as bacteria will develop according to a much more rapid timescale and reproduce itself in significantly greater numbers (intrinsic rate) compared to a small mammal such as a mouse.

In other words, just as their real time development (growth pattern) corresponds directly to their metabolic complexity and size, can we scale this up and backwards in time to predict the rate at which these archetypes evolved (or developed as a species)? Similarly, if we apply the tempo of growth/development to evolutionary development and understand it to be Sigmoidal, we can infer that the species not only emerged slowly in the early stages and once everything was in place allowing a profoundly rapid explosion of life (exponential phase), but that the species must eventually have stabilised also, once they became fully developed; a mature species.

It is suggested that ancestrally, all species at every level of complexity, on every scale of life, eventually became fundamentally fixed (stabilised). This model dovetails very well with much of what you will read regarding other evolutionary theories further on and is strongly supported by the fossil record in Book Two.

In many ways, just as Nature doesn't grow one digit at a time, or put on a petal at a time on a flower, on another scales, presumably, Nature, wouldn't put all her eggs in one basket regarding the species either. This would express an essential aspect of D'Arcy Thompson's evolutionary concept of many origins and many ways to adapt these forms into all of life's diversity as whole systems and whole sets until their ultimate stabilisation and more micro-adaptations thereafter; or filling in the detail when the whole fundamental set is complete.

This stabilisation phase would seemingly come about as each reached the optimum level of their innate complexity: each tending to order and becoming energetically in a balanced exchange between organism and its environment, thus, fulfilling (at an evolutionary scale/level) their space-filling (carrying capacity) efficiency requirements within the whole eco-system.

This begins to fit neatly with the Matryoshka Principle at its most fundamental, but there is a great deal more scaling principles to introduce you too before the full nested sets concept will come into sharper relief. Obviously, we also need to discuss the genetic code and several other interrelated factors, materials, processes and genetic novelty that allowed Nature to shape and form the species in the first place.

Basically, as the evidence strongly suggests, and as you will come to see, evolution in the manner suggested by D'Arcy Thompson is beginning to offer a highly strategic piece of the evolutionary puzzle.

All in all, this is just an introduction to some of the main concepts and how they might begin to give us a foundational insight into a different form of evolutionary development. It also provides the overarching idea that is drawn from a larger perspective of the universals embedded in Nature that are observable and testable and give us the framework to work within.

We have only begun to scratch the surface of the alternative evolutionary model, but it is nevertheless, a fundamental foundational concept for all that is to follow as it establishes the groundwork for all the rest according to my own thought-experiment, guided by the investigation of equally novel and dynamic theories of evolution and of course supported by the most up-to-date scientific evidence.

Essentially, the evidence presented in the following chapters will begin to fill out the detail of this overarching concept and will drill down to the nitty-gritty of the processes and mechanisms involved that support D'Arcy Thompson's model and the Matryoshka Principle as applied as an aide to this exercise. I will now draw this chapter to a close by quoting D'Arcy below. The excerpt is taken from his 1917 book and I thought it apt as it leads directly to another interrelated mathematical theory of evolutionary processes outlined in the next chapter, giving us another important piece of the evolutionary puzzle.

On growth and form

> *And while I have sought to shew the naturalist how a few mathematical concepts and dynamical principles may help and guide him, I have tried to shew the mathematician a field for his labour- a field which few have entered and no man has explored...For the harmony of the world is made manifest in Form and Number, and the heart and soul and all the poetry of Natural Philosophy are embodied in the concept of mathematical beauty.*
>
> Thompson (1917, Epilogue)

[43]

CHAPTER TWO

Alan Mathison Turing

(1912-1954)

THE TURING ENIGMA

Morphogenesis and the other coding system of life

Alan Turing certainly did take his cue from D'Arcy Thompson's final statement in the previous chapter, because he was an amazing mathematician, apart from being a British pioneering computer scientist, logician and theoretical biologist amongst many other things [44].

Turing is perhaps better known for his pioneering work during World War II for cracking the Enigma Code than for his code cracking abilities as applied to biology as seen in his publication entitled: *The Chemical Basis of Morphogenesis* (1952) [45]. Where D'Arcy Thompson explained the underlying simplicity and universality of shape and form – transformations and scaled principles of the formation of the species, Turing showed how the bio-chemical properties and the context during development of the cells could create these meaningful patterns, shapes, forms and transformations of structures in the first place.

Turing's applications to growth and development and variation within biological organisms explores, using theoretical mathematics and the known behaviour of bio-chemicals under certain conditions for example, the reaction/diffusion of natural chemicals to explain the behaviour between and within cells during development. And on another scale, as organisms are a collection of trillions of highly specialised cells, it seems reasonable to suggest that Turing's formula and equations can be applied in principle, to help explain and account for much of the great diversity of life in the natural world.

For instance, if you follow this line of reasoning and apply the principles outlined in the previous chapter all the way from the chemical reaction scale, to the genetic molecule scale and beyond (DNA), to the cellular differential stage, to embryonic and all the way finally to the species scale, the result is quite profound, as it really begins to reveal something universal, yet, quite simple, that underlies even the most complex biological systems.

Turing was right all along

Turing, like D'Arcy Thompson's equations therefore, were not just mathematical abstractions, but could help explain the natural development processes as will be seen below. Indeed, just as D'Arcy Thompson's concepts of evolutionary processes are gaining wider acceptance due to a deeper understanding of biological complexity, so are Turing's ideas.

For example, the great diversity of complex patterning, shape and form seen within the animal kingdom may be underlain and explicable by simple principles of bio-chemistry operating within and between cells that can be expressed mathematically as highlighted in an article by Holehouse, dated to the 20th Feb 2012 in the Telegraph: entitled: *How did the leopard get its spots?* and with the subtitle: *Codebreaker Alan Turing was right all along* [46].

Turing's theory of morphogenesis validated

Scientists from Brandeis University and the University of Pittsburgh show how identical cells differentiate

Alan Turing's accomplishments in computer science are well known, but lesser known is his impact on biology and chemistry. In his only published paper on biology, Turing proposed a theory of morphogenesis, the process by which identical cells differentiate, for example, into an organism with arms and legs, a head and tail...

Turing was the first to offer an explanation of morphogenesis through chemistry. He theorized that identical biological cells differentiate and change shape through a process called intercellular reaction-diffusion. In this model, a system of chemicals react with each other and diffuse across a space – say between cells in an embryo. These chemical reactions need an inhibitory agent, to suppress the reaction, and an excitatory agent, to activate the reaction. This chemical reaction, diffused across an embryo, will create patterns of chemically different cells.

Burrows (2014, 10th March)

[47]

For further detail and increasing validation of Turing's theory of Morphogenesis, I would suggest viewing the video presentation given by Prof. Philip Maini and entitled: *Turing's Theory of Developmental Pattern Formation* from the University of Edinburg dating to 2012 [48].

Turing's mathematical equations can be applied directly to biological processes during early cellular and embryonic development known as Morphogenesis, recall all the while the morphogenetic field that guides the meaningful expression of shape and form and the proposal from D'Arcy Thompson, that with a simple shift in these invisible growing fields (axes), approximating our more modern understanding of the morphogenetic developmental field, the same underlying form can, via deformation, become radically different in the end as seen between a gorilla's skull and that of a modern human illustrated example.

As you will see below, Turing's model essentially explains how cells that start out as 'un-programmed' stem-cells or pluripotent cells, even though they all contain the same genetic code, can be 'programmed' chemically according to their growing environment. After programming, these cells would all have their specialised jobs relating to the function of a whole organism; it is this evolutionary process that actualises the meaningful proportions, patterning and formation of biological systems and seemingly has ultimately has helped modify, shape and form organisms according to their growing/developmental environment and therefore is implicated in the adaptation of the species itself.

For instance, Turing referred to the chemical interactions between cells as morphogens and proposed that cells patterned themselves according to the activation signal (diffusion) or, a deactivation signal (like a chemical off switch) causing a type of chain reaction (a certain sequence), which set up development patterns that once initiated, patterned itself repeatedly (reiteration/or committed to that developmental trajectory) accordingly.

In a sense, these chemical switches are one of the most fundamental processes for orchestrating, in a meaningful way, the differentiation of un-programmed cells into differentiated programmed and ultimately, highly specialised cells and on another scale, the undifferentiated organisms into differentiated species with their own specialisms via their own evolved bio-chemical programs.

It is important at this point to note that Turing's theory of development of the organism from undifferentiated cells is explicable via bio-chemical processes, does not directly involve the genetic code at this early stage, it is indirect and more complex as you will see further on. This is because the genetic code itself cannot be the cause of the different specialisations of the cells (bone, tissue, neurons etc) as there is nothing in the identical code in every cell that would allow them to become anything different.

For example, we know that when development begins that the pluripotent (stem-cells) are essentially cellular clones (same DNA sequence), which should look and act exactly the same if they are all genetically identical, but of course we know that the cells in the body become (during development) a multitude of different things. They end up extremely different to one another once they differentiate into highly ordered and specialised cooperative colonies of bone, tissue, organ and neuron type cells within an organism. In other words, cells need to have their own special programs to run and allow them to become something other than copies/clones of each other.

Having one and the same genetic code doesn't have the information necessary to allow these cells to express the genetic code differently and differentiate as yet. So how do these bio-chemical 'on' or 'off' switches proposed in Turing's model get triggered and ultimately help these undifferentiated (stem-cells) to become differentiated, highly specialised ones, if it isn't the genes directly?

Imprinting code and memorising it

A clue lies in a brief overview of the findings from a scientific study below. It is taken from the University of Wisconsin-Madison News website and entitled: *In directing stem cells, study shows context matters* and the results left the researchers rather puzzled, but by understanding that development and its context are inseparable it begins to make more sense, particularly as we proceed through further into this book.

In directing stem cells, study shows context matters

> *Figuring out how blank slate stem cells decide which kind of cell they want to be when they grow up — a muscle cell, a bone cell, a neuron —*
>
> *has been no small task for science. Human pluripotent stem cells, the undifferentiated cells that have the potential to become any of the 220 types of cells in the body, are influenced in the lab dish by the cocktail of chemical factors and proteins upon which they are grown and nurtured. Depending on the combination of factors used in a culture, the cells can be coaxed to become specific types of cells.... To fully explore the idea that surface matters to a stem cell, Kiessling's group created gels of different hardness to mimic muscle, liver and brain tissues. The study sought to test whether the surface alone, absent any added soluble factors to influence cell fate decisions, can have an effect on differentiation.*
>
> *Results, according to Kiessling, showed that a soft, brain tissue-like surface, independent of any soluble factors, was catalyst enough to direct cells to become neurons, the large elaborate cells that make up the central nervous system. Stiffer surfaces favored the stem cell state. "We didn't change anything but switch from a hard surface to a soft surface," Kiessling says. "They all started looking like neurons. It was stunning to me that the surface had such a profound effect."*

Devitt (2014, Sept. 8th)

Perhaps when we ask the big evolutionary question: What and how do organisms know what to become when they grow up, we could attempt to answer it by looking at another scale of life that we can test in the lab by asking: what and how do genetically identical cells know what to become when they grow up? In both instances, it simply may be a matter of scale.

As suggested in the experiment above carried out with stem-cells (pluripotent cells) the key points being that initial conditions are seemingly triggered and directed according to context and environment and the shift to a particular form - a differentiated state (in the case of the study above, neuron-like cells began to form when grown on a softer surface) and once this was triggered, this would appear to commit the cells to a particular state.

This begins to reflect Turing's bio-chemical cascades during the process of Morphogenesis. In a sense, the cells are being programmed differentially by their environment and the chemical cocktail in which they develop in. They are chemically and environmentally triggered into finding their identity.

Moreover, the above article also gives us a clue to the trigger and a strong indication that somehow cells have memory. How else would they know what to be once the bio-chemical process triggered by the surface type they began to differentiate in, began its cascade committing the cells to a particular form? For example, cellular memory is indicated in the following study:

Evidence Of 'Memory' In Cells And Molecules

New research provides evidence that some molecular interactions on cell surfaces may have a "memory" that affects their future interactions...

"Positive memory increases the likelihood of having two interactions in a row, which generates long strings of interactions," said Zarnitsyna. "The negative memory, conversely, decreases the likelihood of having consecutive interactions, which results in more solitary interactions in the sequence... "This may represent a way for cells to regulate their adhesion and signaling".

Georgia Institute of Technology (2007, 3rd November).

[50]

Therefore, the 'positive memory' can seemingly forge links and chains, while 'negative memory' seems to avoid them and eventually, via interactions, a long string of positive bio-chemical bonds can emerge, implying that cells have the ability to learn and remember these interactions. Presumably Nature would have gotten very efficient at making the information patterns and perhaps on another level, this principle of forming meaningful biochemical bounds could be applied at a more complex and larger scale to the interactive macro-molecules that bond into meaningful sequences that we call coded DNA or genes.

I will discuss this possible evolutionary principle of scale embedded within the potential first code of life within the context of cells in the next chapter. Also, this concept of the 'negative', or 'positive' interaction and meaningful bonding is akin to the negative and positive attraction of the bar magnet analogy for the developmental Morphogenetic field during Morphogenesis as discussed in the previous chapter and of course, the process explained by Turing's model in bio-chemical terms relating specifically to the chemical processes involved in Morphogenesis.

And specifically, these biochemical bonds of attraction and/or non-attraction (a type of chemical memory perhaps analogous to memory foam) also mirror directly, the 'on' or 'off' biochemical switches proposed in Turing's model and this in turn, is analogous to the electro-magnet field.

This brings us to another related piece of the puzzle involving Turing's theory which should help explain how the genetic code itself is only one layer of this overall system, where the other code involving chemical switching and the context of the code within the cell is the key to understanding the differential programs of the differentiated cells.

Modification via other genetic means

The article below explains the role of epigenetics in relation to what could be described as the second, and perhaps, lesser known code of life, which operates, above, beyond and upon the genetic code by changing its expression without changing the underlying DNA code itself as seen in the article excerpt below:

Deciphering the Second Code – Computational Epigenetics

> *The 3 billion letter code known as the human genome comprises the blueprint for the molecular building blocks of life. There exists a large variety of different tissues in the human body, all of whose cells share the same genome but run individual genetic programs. The epigenome provides a code for the operation of these programs: DNA does not float around naked in the cell's nucleus, but is packed more or less tightly around molecular scaffolds (chromatin). The density of this packing controls how accessible the DNA is to the molecules reading off the genomic information. This packing is controlled by chemical modifications to the DNA itself (methylation) or the histoneproteins which comprise the scaffold. Consequently, epigenetics plays an important role in orchestrating the entire organism: Complex tissue structures can arise only if, after countless cell divisions, each cell follows its program, which is configured by the accessible regions in the genome.*

Assenov et al (2014 Abstract)

[51]

The key point from the above quote is that there is differential programs that seem to run using this underlying genetic code to orchestrate the development of the cells and cellular organisms (via the cellular packaging and processes of epigenetic bio-chemical switches that can turn genes 'on', or 'off' leading to even identical genome being expressed differently at different times and stages of development).

This suggests that you cannot have genetic expression outside the context of the cells and genes are essentially inert until triggered into a meaningful expression (running specific programs) via epigenetic processes that appear to code according to their biochemical interactions and environment within the context of the cell. In other words, just as D'Arcy Thompson suggested, we may be looking at a whole dynamic systems where each part depends entirely upon the other and that the whole system co-evolved from the beginning.

The clue to the primitive beginnings of biochemical sequencing and firing leading to cell differentiation is indicated via the study above where pluripotent (un-programmed) cells, 'remembered;, not unlike memory foam, what to be (neuron-type etc) as they were triggered (nudged) along this trajectory (their initial starting conditions) via something as simple as surface hardness or softness within their chemical Petrie-dish.

The cellular memory aspect is profoundly important to begin grasping how cells actually do remember what to be as they are triggered via their controlled environments during embryological development, which typically happens within a egg, or womb or seed of some description rather than a Petrie-dish.

Below, the excerpt explains the means by which the vastly understated role of epigenetics in orchestrating the expressive programs of the existing genes (of the identical genome replicated throughout a cellular organism) within the cells memorises past modifications and different expressions by imprinting via bio-chemical markers or tags upon the epigenome. The epigenome is inherited along with the more obvious genome and it can change throughout the life time of an organism according to life-style and environmental factors.

The Epigenome learns from its experiences

Epigenetic tags act as a kind of cellular memory. A cell's epigenetic profile -- a collection of tags that tell genes whether to be on or off -- is the sum of the signals it has received during its lifetime.

Genetic Science Learning Center (2014, 22nd June)

[52]

I will just reflect on the epigenetic aspect of evolution in principle as it aligns with Turing's own model. Essentially, just as bio-chemical 'on' and 'off' switches are triggered and generate cellular differentiation and all patterns and forms of cellular processes as proposed in Turing's model, epigenetic processes during development and cellular differentiation work according to bio-chemically induced processes within and between the cells that are conditioned by environmental factors and all of this is seemingly guided and orchestrated by the properties of the morphogenetic field during morphogenesis.

This begins to hint at the possible scenario that cellular chemical 'positive' memory bonding, creating informational chains, may be a primitive forerunner of the genetic code itself. I will discuss the origin and primitive evolutionary beginnings in the next chapter, but it does begin to give us a clue as to how the genetic coding system came into being at a chemical bonding or macro-molecule level in the first place to co-evolve into a scaled up version of a complex memory storage, coding and retrieval systems that we call the genes.

The epigenetic orchestration of this code, being the more flexible of the two, is perhaps a more fundamental system that later became conserved in parts. It may have taken its cue from the cellular system that are seemingly shaped and formed via chemical triggers and cascades, aiding the differentiation of cells into the particular specialisations which do not in principle require the conserved code in order to adapt.

For instance, essentially, Turing's Morphogenesis model is one and the same thing as epigenetic processes as these operate according to the very same principle using 'on' or 'off' chemical switching. Only in the case of epigenetics, the chemical tags, switches that can act like a dimmer switch – biochemically instructing the genes to express, or not to express or when and to what degree to express the relatively fixed genetic code. The process of morphogenesis is clearly an epigenetic phenomenon as seen in the title of the partial abstract given below:

Epigenetic control of skull morphogenesis by histone deacetylase 8

Mammalian development is an intrinsically epigenetic process in which a zygote generates hundreds of different cell types, which show vast differences in their phenotype, behavior, and function, despite being genetically identical... Epigenetic modifications, generally defined as the outcome of processes that lead to inheritance that is not reflected in the sequence of the nuclear DNA, are broadly divided into two categories: modifications of the DNA itself by methylation ... [and] Histone modifications

Haberland et al (2009 Abstract)

[53]

Therefore, it would appear that it is epigenetic processes (bio-chemically-driven) in the context of the developmental environment (morphogenesis) that orchestrates the differential expression of DNA sequences (genes) by changing its expression (running different programs) without changing the code (DNA) sequence itself, that gives the cells their unique identity, or individual epigenetic program.

Seemingly, we may be looking in evolutionary terms, at the co-evolution of whole context dependent systems where the interplay between developmental chemistry and environment, context dependent cellular memory and epigenetic processes and inheritance (bio-chemical switching and epigenome imprinting) that dynamically run the individual programs from the DNA source code, are all implicated in the differentiation highly organised cellular organisms operating at every possible scale that became increasingly specialised (just like cellular networks) and expressed every possible variation upon fundamental templates (or themes) of life to become what we call a species to-day.

Ultimately, this begins to offer us an explanation of the differentiation of the species itself from an analogous shared common condition which could be called a pluripotent un-speciated state to become a highly specialised species form, modified and developed (shaped and moulded) in accordance with their environment and being committed to their ultimate species trajectory by the context (chemical and environmental) of their initial starting conditions and the accumulation of their epigenetic tags picked up along the way.

Obviously, there is more to the genetic story and its role in helping to shape the species, (as it seemingly wasn't by Darwinian means), which should become more transparent as we proceed to present all the other scientists and their theories who have equally tantalising pieces of the evolutionary puzzle.

In many ways, the understanding of epigenetics in terms of context/environment and bio-chemical switching, has given us the second code of life and a much better understanding of the first one (genetics). So Alan Turing, seemingly, not only contributed significantly to cracking the Enigma code, but his research has potentially helped us to decipher a fundamental and foundational scale of evolutionary complexity by identifying the bio-chemical basis of the code of life itself.

This in essence, is what I have simply attempted to update in the context of Turing's model and by way of a brief introduction to the critical role of epigenetic processes and its implications our current genetic basis of evolution and species formation and relatedness which, I will return to in more depth particularly in Chapters Four and Five. The following chapter will address the possible origins of this entire coding system (genetically and epigenetically) within the context of cellular life.

CHAPTER THREE

Alexander Graham Cairns-Smith Turing

(Born 1931)

THE POSSIBLE ORIGINS OF NATURE'S FIRST CRYSTALINE (QUANTUM) COMPUTERS

Cairns-Smith is a Scottish molecular biologist and organic chemist and his crystalline origins theory leads on naturally from the previous chapters, as it corresponds to the fundamental and inherent properties of patterns of scale, self-organisation, replication: 'remembered' patterning and modification according to environmental factors, that can be essentially, scaled up to possibly account for the evolution of the cells and the complex molecules of life - its code.

Smith-Cairns' concept is not an alternative to the Darwinian model, as are many of the others presented in this book, but rather, it deals with the origins aspect of cellular life along with the code of life, that our current model has never fully addressed. Below is a short excerpt that should give an insight into his main hypothesis.

Life's Crystal Code

To Alexander Graham Cairns-Smith, that glimmer may owe something to the sparkle of a crystal.

Cairns-Smith, an organic chemist at the University of Glasgow, sees a significant relationship between the structure of DNA molecules and the structure of certain kinds of mineral crystals. He says that while patterned structures that replicate themselves are common in the inorganic world of crystals, it is a rare quality in the organic world — DNA and RNA are the only organic molecules we know of that strongly exhibit this characteristic.?

Mullen (2009,'Astrobiology Magazine' March 19th)

[54]

Essentially, Cairns-Smith's novel proposal can be seen from the 1960s onwards via his many books and numerous articles on the topic of the self-replication of clay crystals in solution as a precursor to molecular life and its ability to replicate itself. Some of the main publications are listed as follows: *The life puzzle: on crystals and organisms and on the possibility of a crystal as an ancestor*, 1971, by A.G., Cairns-Smith, Toronto University Press [55]; *Genetic takeover - and the mineral origins of life*, 1982, by A.G., Cairns-Smith, Cambridge University Press [56]; *Clay minerals and the origin of life*, 1986, by A. G. Cairns-Smith and Hartman, H., (*eds.,*), Cambridge University Press. UK [57] and, *Seven Clues to the Origin of Life - a scientific detective story*, 1990, by A.G. Cairns-Smith, Cambridge University Press [58].

Essentially, Cairns-Smith's concept, as it specifically applies to the clay crystalline matrix origin of coding complexity, not only proposes a useful model to account for rather humble beginnings of life from non-life, but he takes this one step further and suggests we may be looking at an actual ancestor when we observe the complex growth processes of such crystalline forms as stated in: *Origin of Life*, (ed.,) C. H. Waddington, Transaction Publishers, 2009 in the chapter entitled:

An approach to a blueprint for a primitive organism

> *We might think of the replication of the unit cell of a crystal, or better the replication of a pattern of dislocations, during the growth of a crystal...Rather than consider theoretical models of replication processes that closely mirror those of modern organisms we should perhaps look very hard at the simple processes of replication which already exist in profusion in the physico-chemical world, and to consider these not simply as models, but as potential ancestors.*
>
> Cairns-Smith (2009, 58)
>
> [59]

Now, I would propose an ancestrally shared condition or system, rather than a literal ancestor, as discussed previously where evolution appears to be a process of simpler and more primitive systems that tend towards complexity and organisation on every possible scale, but Cairn-Smith's model is certainly more than a simple model, and does, indeed appear to have a very real and tangible link to organic life as you will see further on in this chapter.

Peeling back the Crystal-Coded Onion

... Life's First Barcode?

> *..., clay mineral layers not only attracted certain chemicals from the environment to their surfaces, the mineral layers also acted as the first genetic information carriers, much as the base pairs in DNA do today.*
>
> *"The objects that I'm particularly interested in are mixed-layered crystals, in which the crystal structure consists of beautifully formed layers packed on top of each other, but with an arbitrary sequence," says Cairns-Smith. "In that respect, they're like a DNA molecule, which has base pairs, little platelets inside it which are stacked on top of each other. It is the sequence of this stacking which creates the information."*
>
> *Cairns-Smith doesn't think the clay mineral crystals were "alive" anymore than a DNA sample is thought to be alive. Instead, by acting as the first genetic materials for early life, clay mineral crystals created a link between the worlds of inorganic and organic chemistry.*
>
> *At some point, life launched free of its inorganic genetic origins — the organic substances that evolved from chemical interactions on the mineral layers became stable enough to live apart from their birthplace, and complex enough to replicate themselves into the future.*
>
> *Some mineral layer combinations probably worked better than others when it came to marshalling the organic molecules that were to eventually become genetic materials.*

Mullen (2009, 'Astrobiology Magazine' March 19th)

[60]

Basically, I have outlined the main characteristics of crystal growth below, and emphasised, what I think are the most interesting facts regarding crystals as they correspond to Smith-Cairn's hypothesis. This should help to get a broad feel for his concept. For instance, for anyone that doesn't already know the fascinating properties of crystal growth (but I'm sure you do, this is just a brief overview reminder). I will start with the snow-crystal or snow flake structures as they, like biological life, need a starter seed, a trigger to start growing (some inorganic material, just as a snowflake has to be first seeded from a speck of dust in the clouds). Then their growth pattern follows a very clear and predictable molecular (molecule bonding etc) pathway via hydrogen bonds in the case of snow-crystals.

A snowflake starts out as a basic geometric prism (always six-sided in the case of snowflakes or cubes as in salt crystals) and this informs the underlying pattern in every direction along the main axes in proportion to itself. Each level of growth is a complete scale of growth and this pattern will be repeated over and over again on all the finer scales until the crystal has reached the full capacity of its sustainable system. And all of this is in direct relation to its environment, temperature and surface conditions, water molecules and float rate etc.

Then of course they melt and the whole process can start over, if the conditions are right. Their final shape and form (even though they all follow the same fundamental principles of growth) there are modifications made according to the fluctuations in the growing conditions and hence: the expression *no two snowflakes look the same* comes to mind.

However, the type of crystal growth and form that Cairns-Smith uses such as rock crystals in a clay solution as outlined in the quote above, does highlight the rather amazing properties of memorised and replicated patterning, where, if a small part of the whole crystalline structure becomes dislodged as it forms; the parent matrix/lattice from which it came directs the growth and development matrix pattern of the daughter crystalline structure, this will vary slightly if its growing conditions/surface is different or changed in some way – modified.

Recall the concept emerging within the nested scales of complexity model, where a small change at the beginning can ultimately have quite a large effect further down the line, well, clay-crystal growth in solution is fundamentally similar and ultimately, conditioned in its overall shape and form by rules that are seemingly applicable and universal to almost all living structures as far as we can tell; just as much as to crystalline ones as well.

I should also point out that Nature does not grow one snow-crystal arm at a time, any more than a snow drop puts on one petal at a time. Each stage of fractal-like growth is a whole phase or stage and completes this stage before taking the self-similar repeating pattern to another more elaborate and complex (and typically larger) scale. In combination then, crystal growth gives us all the essential processes and principles embedded within life itself.

It has the properties of fractal-like growth at different complete scales, patterned memory and its modifications according to environmental factors during growth that can be ‘remembered’, via imprinting that can be replicated ‘inherited’ allowing further divergent growth and has fundamental properties of predictable, measurable, fractal-like (self-similar patterns repeated at all scales) shape and form.

In other words, crystal growth also mirrors at its most fundamental level, all the main characteristics embedded within the genetic code, epigenetic modification processes, cellular memory and adaptation according to environmental conditions discussed in the previous chapters, only on a much more primitive scale of complexity.

Once again, it seems that we may be looking at building upon the same principles of earlier systems to evolve much more complex systems: nested scales of complexity. Therefore, in order to explore this concept fully, particularly with regard to the genetic code itself, we need to rewind the possible evolutionary scenario for the evolution of the genetic code within the context of the cells and as complex organisms are made up of lots of interacting cells - this should begin to reveal the nested scales of complexity embedded within the evolutionary development process which is clearly in evidence from the very small and primitive to the very complex and large.

We will therefore start with a brief overview of what we can establish as the essence of how the current DNA and the genetic code operates (bearing in mind the fact that the epigenome operates above this code and is also inherited with continuous finer modifications, and the fact that these modifications may have been much more dramatic, rapid and profound during earlier evolutionary development as strongly indicated from the scientific literature which will become clearer as we proceed).

By peeling back the coded onion and working our way down to the level (scale) of the crystal code itself, and maybe even go a little deeper than this, this will help us to identify and assess the entire spectrum of scaled complexity operating. So beginning with our first and most complex level, when we think of DNA, it boggles the mind how such a system could itself have evolved.

However, if we try to not get distracted by all the details of complexity and look for simpler versions of forms of the DNA molecules, then we can begin to see the underlying principles that are common to more primitive (less specialised and presumably earlier scales of complexity) versions of the system.

The following excerpt just scratches the surface of the outer layers of genetic scales of complexity. It is taken from a science paper on ancestral pre-cursers to DNA is highlighted in the slightly different chemical composition of a more primitive version of DNA molecule known as TNA.

The TNA world that came before the RNA one

Once it was recognised that DNA is key to the molecular self-replication that underpins life, chemists have sought to understand the origins of this double-helical molecule in that primordial age. It was quickly assumed that RNA, a single-stranded nucleic acid, may have been the precursor genetic material to DNA, and the RNA world hypothesis was born. But what gave rise to RNA? Chemists in the US are starting to home in on another nucleic acid, TNA: threose nucleic acid. ..

Bradley (2012, 8th January)

[61]

Another article exploring this recent discovery of the TNA molecule expands a little upon the interesting properties of this molecule in terms of an ancestral (more primitive) form of DNA and its key features of self-organisation, (self-assembly – fold into meaningful shapes via molecular bonding) and replication is given below:

Did an Earlier Genetic Molecule Predate DNA and RNA?

One approach to identifying molecules that may have acted as genetic precursors to RNA and DNA is to examine other nucleic acids that differ slightly in their chemical composition, yet still possess critical properties of self-assembly and replication as well as the ability to fold into shapes useful for biological function...According to Chaput, one interesting contender for the role of early genetic carrier is a molecule known as TNA, whose arrival on the primordial scene may have predated its more familiar kin. A nucleic acid similar in form to both DNA and RNA, TNA differs in the sugar component of its structure, using threose rather than deoxyribose (as in DNA) or ribose (as in RNA) to compose its backbone.

The TNA world that came before the RNA one...Threose, which has one fewer carbon atoms than ribose, is simpler than RNA not because it has fewer atoms, but rather because it can be synthesised from a single starting material,' explains Chaput.

... The researchers have now demonstrated that these selected TNA molecules can fold into complex shapes with discrete ligand-binding properties...Fundamentally, the work demonstrates a property of TNA that was not clear before the team began but was known, of course, in RNA and DNA. 'This provides evidence that TNA could have served as an ancestral genetic system during an early stage of life,' Chaput tells Chemistry World.

Astrobiology (2012, 13th January)

[62]

Now, this begins to reveal at least three scales of genetic complexity that are all built upon the previous system, starting with TNA, a more complex molecule: RNA and finally our more familiar DNA: the most complex of them all. The other important point within the above article excerpts relating to the TNA as a DNA precursor is that it works from simpler systems and builds upon these whole systems operating at a more primitive level to essentially do the same thing in more complex and later systems. And this is exemplified in the fact that TNA, apart from having lesser carbon atoms than ribose (RNA constituent), but it could be synthesised from a single starting material to get going.

This clearly demonstrates how Nature tends to start with simpler processes and then elaborates upon these recipes according to the ingredients available such as molecular complexity of sugars used. In other words, Nature seems to have evolved systems (that are ancestral to all) building upon the principle of earlier versions on increasing scales of complexity. But in order to begin understanding this level of complexity, even at the TNA scale, we need to go a little deeper still and see some of the systems that may have led to the coded complexity of life that brought it to the TNA level in the first place. I will therefore, briefly introduce you to some of the main players of the whole genetic system, if you are not already familiar with the whole system, via the review below:

How Do Genes Work

> *... each gene is really just a recipe for making a certain protein.*
>
> *And why are proteins important? Well, for starters, you are made of proteins. 50% of the dry weight of a cell is protein of one form or another. Meanwhile, proteins also do all of the heavy lifting in your body: digestion, circulation, immunity, communication between cells, motion-all are made possible by one or more of the estimated 100,000 different proteins that your body makes.*
>
> *But the genes in your DNA don't make protein directly. Instead, special proteins called enzymes read and copy (or "transcribe") the DNA code. The segment of DNA to be transcribed gets "unzipped" by an enzyme, which uses the DNA as a template to build a single-stranded molecule of RNA. Like DNA, RNA is a long strand of nucleotides.*

The Tech Museum of Innovation (2013)

[63]

We may therefore, be looking at different recipes and increasingly elaborate processes involving several players that have specialised functions in the present form of the genetic system. And as you can see, proteins and special proteins (enzymes) do the lion's share of the work, once the DNA code (recipe) is unzipped, transcribed/translated. Therefore, if RNA existed as a precursor to DNA and even RNA may have had a precursor and more primitive and direct interpretative system in relation to proteins, it might be useful to investigate proteins a little further within the context of the cell.

Protein Structure

> *Proteins are the end products of the decoding process that starts with the information in cellular DNA. As workhorses of the cell, proteins compose structural and motor elements in the cell, and they serve as the catalysts for virtually every biochemical reaction that occurs in living things. This incredible array of functions derives from a startlingly simple code that specifies a hugely diverse set of structures.In fact, each gene in cellular DNA contains the code for a unique protein structure. Not only are these proteins assembled with different amino acid sequences, but they also are held together by different bonds and folded into a variety of three-dimensional structures. The folded shape, or conformation, depends directly on the linear amino acid sequence of the protein.*
>
> *... Within a protein, multiple amino acids are linked together by peptide bonds, thereby forming a long chain. Peptide bonds are formed by a biochemical reaction that extracts a water molecule as it joins the amino group of one amino acid to the carboxyl group of a neighboring amino acid. The linear sequence of amino acids within a protein is considered the primary structure of the protein.*
>
> *Proteins are built from a set of only twenty amino acids, each of which has a unique side chain. The side chains of amino acids have different chemistries...*

Nature Education (2014)

[64]

What is particularly interesting about the above excerpt, as it might apply to the nested scales of complexity model, is that proteins would appear to have their own direct, primary code (even though the modern genetic system now triggers and codes for these protein templates) that gives them their unique identity and function. It is also interesting that at one stage in evolutionary terms, DNA didn't exist, and RNA did, while at another level, RNA may not have existed and only the simpler system of TNA existed and something similar in terms of coding must have existed before that. The only clear candidate is the amino-acids with their ability to chemically bond (memorise these bonds – recall the previous discussion in chapter two and Turing's Model of the chemical basis of Morphogenesis and cellular differentiation?) and it may therefore, be simply a matter of scale.

As noted above, it is amino-acids which give proteins their primary structure and seems to point to an evolutionary preserved condition and therefore suggests a more primitive coding system (an amino-acid code perhaps) for shape, form, organisation and function of the protein system that emerged from environmental factors triggering chemical bonding sequences that remembered, a bit like memory foam?

It is this potentially more primitive and direct coding system of amino-acids that, in its most direct and primitive form, provided the primary information of 'How to Build a Protein' where, the DNA now does this in a fairly indirect way and on several levels, seemingly, using all of the elements of amino-acids, enzymes, proteins, cellular functions, biochemical and molecular sequences, DNA code, epigenetic processes adapted to run the fully optimised and efficient genetic system we recognise today.

Visual account of protein investment in cellular functions

Proteins and, by extension, genes perform numerous biological functions ranging from the catalysis of chemical reactions to the formation of physical cell structures and the processing of environmental signals.

Liebermeiste et al (2014, 8488)

If we excluded the reference to genes from the above excerpt and substituted it with a sequence of bio-chemical bonds, and taking into account the bio-chemical and context dependent epigenetic system that also operates above and beyond this essential coding, we could say that the system of producing differentiated proteins, each with their own little string of amino-acid code, expressing the underlying amino-acid code according to environmentally-triggered and adaptive responses, is a self-contained environmentally sensitive primitive genetic/epigenetic coding that co-evolved within the context of the cells and itself is a precursor to the TNA/epigenetic-type coding system.

For instance, the key point of the excerpt below is that proteins possess the same fundamental properties of self-organisation as does DNA, RNA or TNA.

Protein Self-Organization: Lessons from the Min System

One of the most fundamental features of biological systems is probably their ability to self-organize in space and time on different scales. Despite many elaborate theoretical models of how molecular self-organization can come about, only a few experimental systems of biological origin have so far been rigorously described, due mostly to their inherent complexity. The most promising strategy of modern biophysics is thus to identify minimal biological systems showing self-organized emergent behavior.

Loose et al (2011, Abstract)

[68]

This article goes on to describe the best and least complex examples that they thought useful to experimentally assess, being a particular type of protein (noted in the title) which self-organises according to its environment. To reiterate this fundamental property of proteins to self-organise according to their environment and to memorise their state (not essentially requiring DNA code to form themselves into meaningful shapes), the excerpt below highlights these differential behaviours of enzyme/proteins below in an article entitled: *Scale-free flow of life: on the biology, economics, and physics of the cell*

Ambiguity in protein localization, interactions, structure, and function

> *Taking into account the fact that a protein's conformational landscape depends on environmental context and on the protein's own state (e.g., posttranslational modifications), one can envisage that different environments and different protein states may elicit different "behavioral routines" in the same protein. In other words, it is very likely that any given enzyme/protein possesses, in fact, a whole repertoire of context- and state-dependent behavioral routines rather than a single routine, the repertoire that has been "hard-wired" into protein structural dynamics as a set of useful sequences of coupled conformational transitions selected and "remembered" in the course of the co-evolution of a given enzyme/protein and its host.*
>
> Kurakin (2009)
>
> [66]

If proteins can seemingly arrange and shape themselves and make connections in space and time depending upon the context and interactions as they begin to assemble themselves, just as the cells themselves appear to do via their own biochemical switching program and remember their state, then, it could be suggested that proteins within the context of the cells are forerunners or a more primitive systems of genetic memory conservation and the interface between the outside and inside biochemical world, pattern sequence formation and epigenetic imprinting.

It is also of interest that proteins form families or networks of their own kind as you will see in the next article excerpt and this is perhaps akin to the cellular families that can be triggered into becoming differentiated neurons, bone, and the soft-tissue cells in direct response to environmental factors via chemical diffusion/fusion systems discussed in the previous chapter. Are we looking at differentiated proteins just like their differentiated cellular kin? Is this another scale of the primitive genetic whole system? Recall that the differentiation of cellular families is epigenetic in nature (it operates above and beyond the coded sequence of genes and expresses them differentially).

What Are Protein Families?

All proteins bind to other molecules in order to complete their tasks, and the precise function of a protein depends on the way its exposed surfaces interact with those molecules. Proteins with related shapes tend to interact with certain molecules in similar ways, and these proteins are therefore considered a protein family. The proteins within a particular family tend to perform similar functions within the cell. Proteins from the same family also often have long stretches of similar amino acid sequences within their primary structure. These stretches have been conserved through evolution and are vital to the catalytic function of the protein. For example, cell receptor proteins contain different amino acid sequences at their binding sites, which receive chemical signals from outside the cell, but they are more similar in amino acid sequences that interact with common intracellular signaling proteins. Protein families may have many members...

Conclusion

Proteins are built as chains of amino acids, which then fold into unique three-dimensional shapes. Bonding within protein molecules helps stabilize their structure, and the final folded forms of proteins are well-adapted for their functions.

Nature Education (2014)

[67]

This system (amino-acid chains and molecular bonding to form unique families of proteins), could have easily been the precursor system of the cellular differentiation according to biochemical processes described in the previous chapter. In many ways, the protein/amino-acid system provides a genetic precursor to even TNA as although it may have a different chemical composition: essentially it possesses the crucial properties of self-assembly with its ability to fold into useful shapes for biological function and these states are triggered environmentally, are context dependent and can be memorised and these critical properties seemingly operate at all scales as indicated below.

Self-Assembly at All Scales

Self-assembly is the autonomous organization of components into patterns or structures without human intervention. Self-assembling processes are common throughout nature and technology. They involve components from the molecular (crystals) to the planetary (weather systems) scale and many different kinds of interactions. The concept of self-assembly is used increasingly in many disciplines, with a different flavor and emphasis in each... In dynamic self-assembly ... the interactions responsible for the formation of structures or patterns between components only occur if the system is dissipating energy.

The patterns formed by competition between reaction and diffusion in oscillating chemical reactions ... are simple examples; biological cells are much more complex ones. The study of dynamic self-assembly is in its infancy. We define two further variants of self-assembly. In templated self-assembly ... interactions between the components and regular features in their environment determine the structures that form. Crystallization on surfaces that determine the morphology of the crystal is one example [...]; crystallization of colloids in three-dimensional optical fields is another ... The characteristic of Biological self-assembly ... is the variety and complexity of the functions that it produces.

Whitesides and Grzybowski (2002, 2418, 'Science Magazine' 29th March)

[69]

Apart from the obvious reference to the self-organising ability (and memory imprinting) of crystalline structures (which we will return to in relation to Cairns-Smith's model further on) and the reference to the diffusion system well-known in chemistry and applied in Turing's model for cellular differentiation as outlined previously, the information within the article referenced above, goes into the many different means by which natural systems can self-organise. To simplify this, I suppose the best way perhaps of describing how natural non-living systems can self-assemble, is that we could say there is a polarity between 'N' and 'S' of a magnet and certain particles would be attracted, or not attracted and orientated and arranged accordingly (iron filings in the presence of a moving magnet would be self-assembled).

Now to apply this to biological self-organisation using one example, we could equate this to biological cells as we know that cells have little polar-type attractors and non-attractors which relate to water-loving molecules and water-hating molecules (hydrophilic and hydrophobic respectively). Because of this property, cells do amazing things. It is a little like oil and water, where the oil in water will form whole droplets to avoid getting wet; so obviously, the oil is full of hydrophobic molecules which are more like the oily lipid membrane that protects the inner watery cellular environment that has seemingly been conducting chemical catalyst – bonding and chain building as well as molecular synthesis experiments for a very long time to get as sophisticated as cells are today.

As for coding, we could say that this can be understood, even at its most primitive and simple scale as akin to our modern use of the binary code system for computer languages. Binary code is simply '0s' and '1s' but look how much code can be written from the arrangements and ordering of this code. It is either on or off/activated or not. For instance, in the biological or magnetic system, every negative is a non-bond '0' and every positive polarity is a positive bond '1' or 'on' or 'off', which would be a foundational and simple code. However, if we bring the ability to memorise these 'on', 'off' coded sequences, into the equation, eventually, molecules will find each other a lot quicker and these chemical reactions and diffusions will get very efficient at firing together if they are triggered into doing so, akin to Turing's biochemical 'On', 'Off' switching.

The article excerpt above: *Self Assembly at All Scales,* demonstrates that self-assembly is observable within many natural systems at a molecule level, so it is not surprising that chemical bonds of attraction or non-attraction can eventually form chains of bonds that in turn, build proteins or become special proteins (macro-molecules) that self-assemble (or self-fold three-dimensionally according to temperature, negative or positive polarity etc) as you will see below, proteins have very similar characteristics to cells and their building blocks: the amino-acid chains have their own code. The article excerpt below is rather technical and long, but I thought it was worth highlighting, so that you get an idea of the protein/amino-acid system and its code.

Introduction to protein structure and structural bioinformatics

The 20 Amino Acids and Their Role in Protein Structures

The amino acids are put together into a polypeptide chain on the ribosome during protein synthesis. In this process the peptide bond, the covalent bond between two amino acid residues, is formed. There are 20 different amino acids most commonly occurring in nature. Each of them has its specific characteristics defined by the side chain, which provides it with its unique role in a protein structure. Based on the propensity of the side chain to be in contact with polar solvent like water, it may be classified as hydrophobic (low propensity to be in contact with water), polar or charged (energetically favorable contact with water).

The charged amino acid residues include lysine (+), arginine (+), aspartate (-) and glutamate (-). Polar amino acids include serine, threonine, asparagine, glutamine, histidine and tyrosine. The hydrophobic amino acids include alanine, valine, leucine, isoleucine, proline, phenylalanine, tryptophane, cysteine and methionine. The amino acid glycine does not have a side chain and is hard to assign to one of the above classes.

However, glycine is often found at the surface of proteins, often within loops, providing high flexibility to these regions. Proline has the opposite effect, providing rigidity to the protein structure by imposing certain torsion angles on the segment of the polypeptide chain. The reason for these effects is discussed in the section on torsion angles. These two residues are often highly conserved in protein families since they are essential for preserving a particular protein three-dimensional fold...

...Most protein molecules have a hydrophobic core, which is not accessible to solvent and a polar surface in contact with the environment (although membrane proteins follow a different pattern). While hydrophobic amino acid residues build up the core, polar and charged amino acids preferentially cover the surface of the molecule and are in contact with solvent due to their ability to form hydrogen bonds (by donating or accepting a proton from an electronegative atom).

Very often they also interact with each other: positively and negatively charged amino acids form so called salt bridges, while polar amino acid side chains may form side chain-side chain or side chains-main chain hydrogen bonds (with polar amide carbonyl groups). It has been observed that all polar groups capable of forming hydrogen bonds in proteins do form such bonds. And since these interactions are often crucial for the stabilization of the protein three-dimensional structure, they are normally conserved.

Karadaghi (2015)

[70]

What is of particular interest here, I believe, is that when we look for the precursor system of protein/cellular and amino-acid/TNA/RNA/DNA coding system, this brings us right down to the level/scale of Cairns-Smith's clay crystals in solution hypothesis and the inherent self-organising properties embedded within it. We have looked at self-organisation principles, self-patterning/folding and chemical/molecular bonds in response to environmental factors and interactions and ability to memorise (akin to memory foam) patterns, bonds and connections and how these might equate with the crystalline coding with modification pattern of growth and development, but we haven't yet looked at another key feature of the crystal code within cellular structures which is clearly inherent in biological cellular systems and that is self-replication.

It is actually quite difficult to pin-point this characteristic within biological life, but we can infer that as crystalline formations can replicate, with slight modification, from their parent matrix/lattice, a daughter formation that can grow and break off, thus cloning itself, that this method may underpin a more complex and more sophisticated means of reproduction seen within living systems today. So it may be useful to go back as far as possible on the borderlands of life itself, and see what we can deduce about replication beyond (and on a more complex scale) the inert crystalline patterns that may have given their cue to first life.

Virus Structure

> *All viruses contain nucleic acid, either DNA or RNA (but not both), and a protein coat, which encases the nucleic acid. Some viruses are also enclosed by an envelope of fat and protein molecules. In its infective form, outside the cell, a virus particle is called a virion. Each virion contains at least one unique protein synthesized by specific genes in its nucleic acid. Viroids (meaning "viruslike") are disease-causing organisms that contain only nucleic acid and have no structural proteins. Other viruslike particles called prions are composed primarily of a protein tightly integrated with a small nucleic acid molecule.*
>
> Davidson (2015)
>
> [71]

As indicated above, in many ways, proteins are actually akin, albeit seemingly a much more primitive and potential precursor to the modern type cell, and have become a major part and function of the cell itself. Well, in the context of viruses, this primordial code-carrier dressed in a protein sheet, may be significant. The key characteristic of viruses is that they are the great replicators and are not that dissimilar in function to computer viruses, as they don't have the ability to replicate and make lots and lots of copies of their own code and little programs to spread virally outside the context of your computer any more than biological viruses being effective outside the context of the modern cell.

But I have to say that Nature's viruses are actually not all bad and indeed, viruses are seemingly essential to life and life itself would not have evolved much further if viruses hadn't have developed such a cozy relationship with cells. Or, perhaps their little protein coats, with all the main characteristics of cells in a much more primitive form, became more sophisticated and elaborate code-carriers.

For instance, some researchers prefer a cellular metabolism first hypothesis and have come up with ingenious means of how this could have occurred under natural conditions. Others have suggested the virus first hypothesis, but based upon the model used here, I would be inclined to see the viral coded critters protected by a protein sheet as a whole system which later became another scaled-up level of complexity of the whole system and some versions of that cellular/metabolic and amino-acid coding and primitive protein system became mobile (what we would call a free-living virus, which thankfully doesn't seem to exist or it might be rather scary and big at this stage. Now viruses seem to be fairly restricted and only effective in the context of cells). But, as you will see below, it may not have always been this way.

Could Giant Viruses Be the Origin of Life on Earth?

The ancestors of modern viruses may have laid the groundwork for cellular life as we know it.

In the world of microbes, viruses are small – notoriously small. Pithovirus is not. The largest virus ever discovered, pithovirus is more massive than even some bacteria. Most viruses copy themselves by hijacking their host's molecular machinery. But pithovirus is much more independent, possessing some replication machinery of its own.

Pithovirus's relatively large number of genes also differentiated it from other viruses, which are often genetically simple – the smallest have a mere four genes. Pithovirus has around 500 genes, and some are used for complex tasks such as making proteins and repairing and replicating DNA.

"It was so different from what we were taught about viruses," Abergel said

Arnold (2014, 'Quanta Magazine' 17th July)

[72]

The prospect of viruses being the ancestral condition for the complex of proteins to cells, and as I have suggested for the complex to have evolved as a whole coding system as well – scaling from amino-acids, to more complex molecules such as TNA, RNA and finally DNA, (this does not mean that viruses were our actual ancestors), becomes even more intriguing when we explore another key feature of viruses, namely the fact that they are assembled from a two-dimensional crystalline structure as outlined in the excerpt below. This certainly brings Cairns-Smith's hypothesis into sharp relief.

Two-dimensional crystalline structure assembled from outer shells of a virus

In a paper published in Soft Matter, September 2013, scientists announced their discovery of a two-dimensional crystalline structure assembled from the outer shells of a virus. A virus consists of a protein shell protecting an interior consisting of either DNA or RNA.

"We are excited about the potential of virus-like particles as building blocks for creating new nanostructures," said the paper's lead author, Masafumi Fukuto, a physicist in the Condensed Matter Physics and Materials Science Department at Brookhaven National Laboratory. " For the particular virus that we studied, we discovered two new forms of 2D crystals that are distinct from previously observed hexagonal and square crystals."

Rowe (Physics.Org 21st February 2014)

[73]

As amino-acids are the primary (primordial) code and assembled (chemically-bonded by natural organising principles) of the proteins with self-similar organisational properties, we now have a further clue to the sophistication of this system in terms of the crystalline nature of the protein/coding system itself. The underlying crystalline nature of this system is further supported in the next section where just about everything in the body, from the proteins in your eye lens, to whole protein systems, and from DNA and the formation of the double helix is crystalline.

We could be seeing the emergence of the software and the hardware required to carry out fundamental coding (chemical bonding, chemical 'on', 'off' switching, which have all the hallmarks of the more developed coding and cellular system allowing for macro-molecular synthesis via special proteins – enzymes etc); and we now have the basis of an environmentally sensitive and controlled system for the reproduction/replication of the primary coding format in the form as a crystalline organism itself – as seen in the virus-type entity.

The gives us an insight into how the crystalline hypothesis can be taken to a completely distinct new, but related level, as you will see in the following section. This is where the whole system would appear to take an unexpected quantum leap in crystalline complexity and perhaps it is this level of sophistication that makes it alive as you will see below.

Quantum Liquid Crystalline Life

From the most primitive crystalline clay-crystal in solution hypothesis of Cairns-Smith, perhaps a smaller scaled-down version of the whole cellular/genetic/epigenetic coding system, is only possible to begin grasping if we can first understand the highly sophisticated role of crystalline structures in their non-solid - liquid crystalline form/phase. For instance, could we say that the eyes alive, as we can begin to appreciate just how sophisticated this system of crystalline protein coated coding got when we consider something as complex as the crystalline proteins within the lens of our own eyes as alluded to in the excerpt below?

Soon, sight-saving treatment to protect eyes from cataract

It has long been known that human eyes have a powerful ability to focus because of three kinds of crystalline proteins in their lenses, maintaining transparency via a delicate balance of both repelling and attracting light.

ANI (2013, 'Zee Health News' 6th December)

Furthermore, to give you an idea of the powerful efficiency of liquid crystals as a highly responsive information system, the following application to technology is outlined below, where Nature has seemingly been encoding and using the dynamic properties of liquid crystals within cells and organisms for a very long time. Note that LCLCs stand for lyotropic chromonic liquid crystals.

Scientists to Advance Biology-Liquid Crystal Research

Liquid crystals represent the fourth phase of matter…

Certain organic materials exhibit the liquid crystalline state as they transition between the solid and the liquid states, known as mesophases. Though liquid crystals are best known for their application in displays, they also are an essential part of all life. Liquid crystals in organisms include the amphiphilic lipids of cellular membranes, the DNA in chromosomes, all proteins, especially cytoskeletal proteins, muscle proteins, collagens and proteoglycans of connective tissues. These adopt a multiplicity of mesophases that may be crucial for biological structure and function at all levels of organization, from processing metabolites in the cell to pattern determination in development, as well as the coordinated locomotion of whole organisms.

Kent State University (2005, 'Physics.org' 11th October)

[75]

As noted above, the liquid crystal phase is also important to DNA in the chromosomes which, is elaborated upon in a little more detail in another science excerpt below:

Liquid crystalline phases of ultra-short DNA and RNA sequences

The ability of long, hydrated, double-stranded DNA to form liquid crystal phases has been known for more than 50 years and played a key role in the initial deciphering of its structure...Recent collaborative work between the Boulder group and the Complex Fluids and Molecular Biophysics group of the University of Milan has shown that self-pairing, or complementary, DNA oligomers as short as six base pairs can exhibit chiral nematic and columnar LC phases ...

Zanchetta and Nakata (*n.d.* Colorado Education)

[76]

The chiral pairs they are talking about refer to right or left-handedness, meaning the orientation of how structures line up. So therefore, the more recent data is pointing to very powerful memory systems and ordering of molecular sequences – not to forget the ability of these molecules to fold in meaningful ways and self-organise and perhaps this begins to give us an insight into the shape and form of the double helix structure of the DNA code itself. This is described below:

Polymers and Liquid Crystals

chiral molecule

A molecule that is not identical to its mirror image. This gives a chiral substance its characteristic twisted shape, due to the fact that its molecules do not line up when combined.

cholesteric liquid crystals

Also known as Chiral Nematic. Similar to the nematic phase, however, in the cholesteric phase, molecules in the different layers orient at a slight angle relative to each other (rather than parallel as in the nematic). Each consecutive molecule is rotated slightly relative to the one before it. Therefore, instead of the constant director of the nematic, the cholesteric director rotates helically throughout the sample. Many cholesterol esters exhibit this phase, hence the name cholesteric...

cholesteric mesophase

Nematic liquid crystals with chiral centers form in two dimensional nematic-like layers with directors in each layer twisted with respect to those above and below so that the directors form a continuous helix about the layer normal.

Case Western Reserve University (2004).

[77]

This suggests an explanation for how the distinct double helix structure with its meaningfully arranged molecules may have bonded. This twisted ladder effect as a property of certain liquid crystalline behaviour in solution is indicated in the excerpt below. It also begins to give you an insight into the more dynamic properties of self-organising, shaping/forming and patterning within solution with different polarities (context dependent) when observed within certain liquid crystals.

Liquid Crystal Droplets gemstones

In a study published in the Proceedings of the National Academy of Sciences, researchers from the University of Pennsylvania and Swarthmore College describe new research into a type of liquid crystal that dissolves in water rather than avoids it as do the oily liquid crystals found in displays. This property means that these liquid crystals hold potential for biomedical applications, where their changing internal patterns could signal the presence of specific proteins or other biological macromolecules.

The researchers placed these liquid crystals into water droplets, which in turn were placed in oil, producing an emulsion. At high enough concentrations within the droplets, the liquid crystals exhibit a twisting pattern visible under an optical microscope.

Lerner (2014, 'Phys.Org' January 21)

[78]

Moreover, another property of liquid crystals which, may account in some way for the coded complexity of the DNA molecule - propelling the whole genetic system unto a highly sophisticated level (but still employing the services of the earlier and critical systems), is the extremely efficient way that liquid crystals can store vast amounts of information in some novel technological applications as indicated from the excerpt below.

Liquid crystals light way to better data storage

As cell phones and computers continue to shrink, many companies are seeking better ways to store hundreds of gigabytes of data in small, low-power devices.

A special type of liquid crystal, similar to those used in computer displays and televisions, offers a solution. Unlike CDs and DVDs, which store information only on their surface, lasers can encode data throughout a liquid crystal. Known as holographic storage, the technique makes it possible to pack much more information in a tiny space.

American Institute of Physics (2010, 24th June)

[79]

The liquid crystalline phase transition properties allows for not only incredible information (coding) storage, but a level of dynamic flexibility that would have allowed a whole new scale of complexity to emerge that seems to have originated as a symbiotic relationship to the environment - as a whole system irrespective of how rudimentary it was in its crystalline form.

As suggested all along and indicated above and as you will see below, with regard to protein liquid crystalline behaviour, the genetic code cannot be seen in isolation to the protein and/or cellular system. Therefore, if we now look at the cell itself with its self-similar properties of ordering and meaningful structuring in direct relation to its interactions and biochemical/molecular environment, polarities in solution and temperature, we can gain an insight into the fundamentals of the whole interactive system.

Lipids and Membrane Structure

> *Membrane fluidity: The interior of a lipid bilayer is normally highly fluid ... In the liquid crystal state, hydrocarbon chains of phospholipids are disordered and in constant motion.*
>
> *At lower temperature, a membrane containing a single phospholipid type undergoes transition to a crystalline state in which fatty acid tails are fully extended, packing is highly ordered, and van der Waals interactions between adjacent chains are maximal.*
>
> *Kinks in fatty acid chains, due to cis double bonds, interfere with packing of lipids in the crystalline state, and lower the phase transition temperature.*
>
> *Cholesterol, an important constituent of cell membranes, has a rigid ring system and a short branched hydrocarbon tail. Cholesterol is largely hydrophobic. But it has one polar group, a hydroxyl, making it amphipathic is the ability...*
>
> Rensselaer Polytechnic Institute (2015)
>
> [80]

Now when you hear about taking care of your cholesterol levels and taking your fatty-acids, you might think differently about what this actually means. This excerpt also brings to mind the discussion of the oil and water type attraction and repulsion system (polarity and charge) or the water loving molecules and those trying to avoid water, working much like a magnetic field, akin to the Morphogenetic field well known by its effects to anyone studying cellular and embryological development? As the excerpt above outlines, the liquid crystalline behaviour is very much context depend. .

The all-important behavior of certain proteins is further explored in the excerpt below in terms of the liquid crystalline properties and the fundamentally similar behavior and equally context dependent nature of cells and the fundamental properties of the code itself. However, when this next article talks about mutants, they mean a change occurring from a different solution (environment). Although quite a difficult science paper to follow, it does highlight a few key points about proteins and their underlying self-organised amino-acids (there are only 20 combinations and these are ubiquitous on the planet and beyond – apparently).

The self assembly of proteins; probing patchy protein interactions

Conclusions

> *This work suggests a mechanism by which protein ...interactions can be probed in a systematic manner. This type of data is critical if good molecular models to predict protein behavior are to be developed. .., we created a protein, which forms two different crystal types, one that melts when the solution is heated and one that melts when the solution is cooled, with co-existence of the two crystal forms at 303 K, the point at which the individual liquidus lines for the single mutant variants overlap.*
>
> *This observation is unprecedented. On a broader level, this work is a starting point which will require a combination of further experiments and complementary simulations to more clearly understand the interplay between the complex, competing forces controlling protein self-assembly and crystallization. However, it is clear that the surface characteristics of the protein, defined by the surface amino acids, can lead to a variety of condensed phases for the same protein. A change in the external environment, e.g. temperature, results in some amino acids contributing more to the protein self-assembly behaviour than others, leading to the variety of structures that we observe.*

James et al (2015, 5419)

[81]

What I believe is most significant from the point of view of the nested scales of complexity model as it is employed throughout this present book, is that the article excerpt above states that it is clear *"that the surface characteristics of the protein, defined by the surface amino acids, can lead to a variety of condensed phases for the same protein"* which directly reflects the nested doll principle, where the surface features of the more primitive amino-acid system informs the main characteristics of the next level up: proteins. It is the spaces in between the nested dolls that give us the most information, rather than getting distracted by all the detail of variations from these interactions that lead us in the wrong direction when trying to peel back the scaled layers of this genetic onion.

As discussed in Chapter Two, we know that cells, particularly pluripotent cells (unprogrammed), are highly sensitive to their environment/temperature/chemical landscapes and that this can cause a chemical chain reaction that programs the cells to become differentiated. Therefore, looking at evolution in terms of levels and scales of complexity, it is perhaps not that surprising that, proteins and at another scale: enzymes are similarly sensitive to their environments and interactions with each other and this can inform their shape and form and ultimately function. On another scale, this mirrors the crystalline growth system and with the added phase transition and dynamically responsive and fluid system of liquid crystalline growth and development we now have the foundation for speciation (the differentiation of the pluripotent) organisms themselves.

The self-assembly properties are therefore a complex interplay of molecular interactions in solution and at different temperatures, proteins surface interactions and differential polarities and tensions and memory bond via natural attractors or polarity factors than bind particular chemicals/molecules leading to self-assembly at an atomic level and later (on another scale), a chemical and then molecular and macro-molecule scale. This complex interplay between the interactions such as the liquid crystalline condensed phase and a very dynamic system indeed as you will see below, leads us back to the idea that D'Arcy Thompson proposed that the most interesting discoveries are to be made on the borderlands of disciplines, where one science meets another as discussed in Chapter One. Similarly, the excerpt article above indicates that it is the interplay of the different forces on the borderlands of amino-acid and protein surfaces in the context of their environment that creates dynamic and very interesting results.

This of course brings us to the scaled up version of cellular systems and its interplay with the coding system and the organisms themselves. As we have been going from the bottom up and scaling each of these systems all the way, it is natural to see if the dynamic fourth phase of matter of the crystalline system: liquid crystal phase, is actually in evidence during the latter stages of embryological development or indeed, after the cellular differentiation stage. Indeed, as seen below, there is evidence to support the important role of liquid crystal phase during an organism's development.

The study below is by MengMeng Xu and Xuehong Xu (Affiliations: Duke University School of Medicine, Department of Physiology Centre for Biomedical Engineering Technology, Centre for Stem Cell Biology and Regenerative Medicine, University of Maryland Medical School and Shaanxi Normal University School of Life Science, USA/China).

The patchy history of this much neglected area of this type of fascinating research is outlined below in the introduction, followed by the more recent conclusions based upon a number of studies. There is a little bit of scientific terminology which may not make a great deal of sense, but the main idea from this article is that there is very good support for the presence of the liquid crystal stage (dynamic phase transition) during early development (embryogenesis) and I have presented it here to reiterate the fact that all of these interacting systems appear to have co-evolved in relation to environmental factors and interactions, that it is reflected at every scale of life and this has implications for how the species itself came into being in the first place.

Liquid-Crystal in Embryogenesis and Pathogenesis of Human Diseases

In 1979, a systematic publication summarizing the state of research on liquid-crystals in biological organisms was published [Brown GH et al 1979]. After this historic publication on liquid-crystals and biology, the field remained largely dormant for more than two decades. However in 1978 and 1979, Haiping He and Xizai Wu, who had continued pursuing this field despite international disinterest, reported their findings on liquid-crystal involvement during chicken development. For the first time, they revealed that massive quantities of liquid-crystals in the liver, yolk sac, blood, and many other developing tissues and organs of chicken during embryogenesis. Their later studies also reported similar liquid-crystalline structures during fish development.

In 1988, another group reported the existence of vaterite CaCO3 within the liquid-crystals found in yolk fluid, identifying the spherical calcified structures first reported in 1979 as one of three iso-forms of calcium carbonate [Feher G 1979, Li M et al 1988]. Subsequent studies have identified liquid-crystalline structures to be omnipresent in the liver during avian development [Xu XH et al 1995a, 1995b, 1997]. Recent studies have revealed that liquid-crystals play a critical role in the preservation of calcium and other trace elements required for embryo development [Xu MM et al 2009, 2010, 2011; Xu XH et al 2009, 2011a]...

General characteristics of embryonic liquid-crystal

During embryogenesis, liquid crystals are widely distributed in the tissues of vertebrates and invertebrates, including Apis cerana chrysalis, fish, reptile, avian and mammal early embryo in vitro [X XH et al 1993, 2009, 2011a, Xu MM et al 2009 2011]. In chicken development, more than twenty different organs and tissues exhibit liquid crystal droplets including liver, meso and metanephros, lungs, blood in heart, and brain. The presence of liquid crystal normally appears at different developmental stages depending on the tissue type, and lasts until early postnatal stages. The earliest liquid crystal droplets appear on the inner embryonic disc during the second day of development [He H et al 1978]. Regardless of their distribution, however, the liquid crystal droplets eventually vanish within three to four weeks into the postnatal period, also depending on tissue type maturation [X XH et al 2009, 2011a]...

Conclusion

Based on current discoveries obtained via XRD, SAXS, confocol microscope, and polarization microscopy in combination with cryo-section, push-release procedure for fluidity measurement, and thermal stage for phase transition progress has been made in the field of liquid crystal function in embryogenesis and pathogenesis of human diseases. With this methodology, the research has proved that, during the embryo development, liquid crystals are readily identifiable in the embryo through their Maltese Crosse birefringence texture. Liquid crystals with this configuration display strong fluidity accompanied with shape-changing properties under direct pressure conditions.

Xu and Xu Xu and Xu (2012, 637, 643 and 649)

[82]

This much neglected field of study became a focus for the research of Mae-Wan Ho who began to take a multi-disciplinary approach as you will see below, and discusses the process of Morphogenesis and pattern formation (recall Turing's model of the Chemical Basis of Morphogenesis). According to the excerpt above, and the following excerpt, Ho and her collaborators certainly do seem to have discovered the most interesting phenomenon on the borderlines or the interface between different fields of science (just where D'Arcy Thompson said we would find the most interesting answers).

The science paper is entitled: *Organisms as Polyphasic Liquid Crystals*, in Bioelectrochemistry and Bioenergetics 41, 81-91, 1996 [83] and its authors are: Mae-Wan Ho, Julian Haffegee, Richard Newton, Yu-ming Zhou, John S. Bolton and Stephen Ross and reflects the collaboration between the fields of biology, bio-electrodynamics and physics and the sub-field of quantum mechanics to name but a few.

Liquid crystals and pattern determination

One of the first generalizations to emerge from developmental biology is that early embryos and isolated parts of early embryos show a strong tendency to form whole organisms. This gave rise to the notion of a morphogenetic field - a spatiotemporal domain of activities organized globally to form the whole organism...

At the start of embryogenesis, the morphogenetic field exhibits 'pleuripotency' or 'totipotency', where all parts has the potential to develop into any structure. In the course of early embryogenesis, however, determination occurs in which the different parts of the embryo become more and more restricted in their developmental potential. The determined state can be demonstrated by transplantation and grafting experiments. If a piece is removed from an embryo before determination and transplanted to a different location, or grafted to another embryo, then the piece will develop in harmony with its surroundings. If the same experiment is carried out after determination, the graft will develop into the structure it was determined to be, irrespective of its surroundings. Thus, the graft may develop into a limb on the back of the host, for example. The process of determination was discovered a century ago, but its basis remains largely unknown despite impressive advances in the molecular genetics of morphogenesis in recent years.

The significant feature of pattern determination is that the determinative influences not only possess dynamic field-like characteristics, but are material and transplantable. ...

A vital clue to the basis of determination may have been provided by Totafurno and Trainor ... who successfully interpreted classical experiments on transplanting and grafting limb-buds in salamander, in which supernumery limbs were often induced, in terms of a non-linear vector field. This vector-field is precisely the sort that is embodied in liquid crystal phase alignments. ... liquid crystals go through in transitions from the liquid to the solid state, which are comparable to the successive stages of determination of the limb-buds in amphibians...

There is indeed a wide range of liquid crystalline mesophases from the most dynamic and liquid - possessing orientation order in one dimension without any translationnal order - to the most solid - with orientation order in 3-dimensions and also a large measure of translational order. It is conceivable that in the course of development, the relevant liquid crystalline mesophases do undergo transitions from the dynamic and fluid to the relatively more (meta)stable, patterned regimes...

Ho et al (1996, Liquid Crystals and Pattern Formation)

[83]

More of this research can be found in the book, noted above and entitled: *The Rainbow and the Worm: The Physics of Organisms* (2008, extended 3rd edition) by Mae Wan Ho [84]. Essentially, Mae-Wan Ho, from her deep research and experimental work and observations, led her to propose that the liquid crystalline phase and its high precision and holistic resonant molecular ordering during Morphogenesis, could be explained in terms of quantum coherence, a well-known phenomenon within the tiny atomic world describable by quantum mechanics and its intrinsic link to another branch of physics which studies the dynamic properties of the liquid crystalline complexity as seen in her talk below. Her observations also dovetail with and are pertinent to the study outlined earlier by Xu and Xu (2012) [85].

What it Means to be Quantum Coherent

Quantum coherence and the liquid crystalline "rainbow worm"

The "rainbow worm" is this little fruit fly larva I first encountered in 1992 as it was hatching from its egg. We placed a batch of eggs in a continuously irrigated chamber on a microscope slide under the polarizing microscope and waited. The microscope was set up so we can see the organism developing and getting energized, right through to the arrays of molecules that make up its tissues and cells. ...But what do the colours mean?

Geologists use the polarising microscope to identify rock crystals. We have slightly modified the setting, but the principle is the same. The rainbow colours are generated by crystals with orderly arrangements of atoms and molecules. We were puzzled at first. In rock crystals or liquid crystals outside the organism, molecules and atoms certainly have an orderly arrangement that stays ordered because there is no movement. But in the living organism nothing is static, the molecules and atoms are moving all the time. So how can they maintain the molecular order required to generate the brilliant crystal colours? ...

The only explanation is that the molecules are moving coherently together, so much so that they appear as ordered as a static crystal. To cut a long story short, the molecules, especially the big ones, macromolecules like proteins and nucleic acids, thoroughly infiltrated with water, are in a dynamic liquid crystalline state. To begin with, they are completely aligned with their electrical polarities to form a continuum that links up the whole body, permeating throughout the connective tissues, the extra-cellular matrix, and into the interior of every single cell. More importantly, all the molecules, including the water, are dancing together as a whole, and the more active they are, the more coherent, hence the brighter the colours...

So, these beautiful images of living organisms are direct evidence of their high degree of coherence. And this high degree of coherence itself depends on the liquid crystalline matrix that enables every single molecule to intercommunicate, synchronize and syncopate with every other. The water, making up some 70 percent by weight of the organism, is the most important part of the living liquid crystalline matrix, without which it cannot form. Many molecules, DNA and proteins, would not be stable; and would not function without water; water is also crucial for the intercommunication that enables the organism to work as a coherent, perfectly coordinated whole ..Mainstream biology has steadfastly ignored the liquid crystalline organism and all its implications.

Ho (2008, Institute of Science and Society 1st October)

[86]

Mae-Wan Ho's theory becomes even more compelling when we understand that Nature, apparently, has been using quantum mechanics for a very long time and it has been sitting under our noses all this time – a way to beat the laws of thermodynamics (a closed system tends to deteriorate over time by becoming an open dynamic system that finds a way to sustain itself and develop). It is positively "jaw-dropping" says Johnjoe Mc Fadden (working on the quantum nature of Nature) in a recent article seen in Discover Magazine entitled: *Solving Biology's Mysteries Using Quantum Mechanics.*

> *"Physicists had been battling for years to build a quantum computer – and now it seemed that all that time they may have been eating quantum computers for lunch, in the leaves in their salad!"*

Merali (2014, 17th December)

[87]

One key principle of the quantum world is that the word quantum itself basically means a discrete packet with irreducible parts - i.e. it is all about whole systems and it is a tiny world as otherwise things get too noisy and busy for the quantum effects to operate. This is elaborated upon and echoes some of Mae-Wan Ho's conclusions in a science paper in the Journal of Physics conference papers (2011) by Seth Lloyd in the following:

Quantum Coherence in Biological Systems

> *Nature is the great nano-technologist. The chemical machinery that powers biological systems consists of complicated molecules structured at the nanoscale and sub-nanoscale. At these small scales, the dynamics of the chemical machinery is governed by the laws of quantum mechanics. Quantum mechanics is well known to exhibit strange and counterintuitive effects. Accordingly, it makes sense to investigate the extent to which peculiarly quantum effects such as coherence and entanglement play an important role in living systems. Quantum mechanics and quantum coherence play a central role in chemistry.*
>
> *Quantum coherence and entanglement determine the valence structure of atoms and the form of covalent bonds. Quantum mechanics fixes the set of allowed chemical compounds and sets the parameters of chemical reactions. Indeed, the very fact that there are only a countable, discrete set of possible chemical compounds arises from the fundamentally discrete nature of quantum mechanics. Chemistry, in turn, lays down the rules for what biological structures are possible and for how they function. Biomolecules can contain many atoms (billions in the case of DNA). As molecules become larger and more complex, quantum coherence becomes harder to maintain. Vibrational modes and interactions with the environment tend to decohere quantum superpositions. Consequently, most biomolecular mechanisms have traditionally been modeled as essentially classical processes...*

Lloyd (2011, 1)

[88]

Once you start to become a quantum computer in Nature's scheme of things: you will become the best quantum computer possible, as you are not just one giant complex cell, driven slavishly and randomly by your genetic code, you are made up of a whole fractal network of trillions of interacting and cooperative, communicating nano-scale liquid crystalline quantum computer cells. Using this ingenious system of making miniature copies of the original system of patterning and being able to continually modify the program, updated it according to adaptive needs and in direct relation to the environment, is the ultimate biological quantum computer.

Returning to Mae-Wan Ho's research on quantum liquid crystalline organisms, she also continues to discuss the quantum properties of the biological organism and contrasts this with our current attempts to develop quantum computing in the article excerpt below.

The quantum coherent organism and quantum computation

> *...Quantum superposition and quantum entanglement are the signatures of quantum coherence, and they have been attracting a lot of attention with regard to the possibility of a quantum computer, as opposed to the conventional classical computer now in use.*
>
> *A quantum computer operates on the quantum bit or 'qubit' instead of the ordinary bit in a classical computer. While the ordinary bit is a simple binary 1 or 0, the qubit can hold 1, 0, or crucially, a quantum superposition of 1 and 0. In fact, it can hold anything up to an infinite number of values in superposition ... .A quantum computer can in theory do computations that are intractable with a classical computer or achieve exponential speedup in solving certain problems. And building an actual quantum computer has become the holy grail of a new breed of quantum information technologists...*
>
> *To my mind, the perfect quantum computer already exists: it is the quantum coherent living organism, ...*
>
> *Consider the elementary process of a protein folding into shape, a difficult problem even for the fastest classical computer. It takes about 300 years for a classical computer to simulate a small peptide of 23 amino-acid residues (with associated water molecules) to fold into shape. By running simulations simultaneously on some 140 000 individual computers around the world, researchers took over three weeks ... Real proteins, however, fold to perfection in several microseconds ...*
>
> *It is very important for proteins to fold correctly. Incorrect folding makes proteins aggregate into insoluble, inflexible clumps associated with wasting diseases such as mad cow disease, Alzheimer's Diseases, Huntington's and Parkinson's Disease...The model of the quantum coherent organism depends on reciprocity and cooperation, rather than relentless Darwinian competition as in the mainstream model ...*
>
> *Hopefully, this is a new paradigm that will support a new world order that's much closer to how nature is, that will enable us to live sustainably within her...*

Ho (2008, Institute of Science and Society 1st October)

Using this system, it is therefore perhaps not that surprising that life got so complex, but it is quite astounding that we may now be looking at quantum evolution that is a polar opposite and several billion light years from our current Darwinian model. Furthermore, now having used the Matryoshka principle to look at the coding system at every possible scale, maybe we should begin taking a salad leaf out of Nature's recipe book and use this to build our future technology in accordance with hers. At least the nano-technologists are beginning to recognise this, perhaps the biologists will begin to catch up – but I'm afraid they will have to let go of their pet theory first or they will completely miss the point.

For instance, I came across an excerpt which seems to be at least looking in the right direction. It is a bit technical, but hopefully, you'll get the idea. The solution would appear to be those liquid crystals again and I like their idea of scalability:

Nuclear magnetic resonance quantum computing using liquid crystal solvents

> *Liquid crystals offer several advantages as solvents for molecules used for nuclear magnetic resonance quantum computing (NMRQC). The dipolar coupling between nuclear spins manifest in the NMRspectra of molecules oriented by a liquid crystal permits a significant increase in clock frequency, while short spin-lattice relaxation times permit fast recycling of algorithms, and save time in calibration and signal-enhancement experiments.*
>
> *Furthermore, the use of liquid crystalsolvents offers scalability in the form of an expanded library of spin-bearing molecules suitable for NMRQC. These ideas are demonstrated with the successful execution of a two-qubit Grover search using a molecule (13C?1HCl3) oriented in a liquid crystal and a clock speed eight times greater than in an isotropic solvent. Perhaps more importantly, five times as many logic operations can be executed within the coherence time using the liquid crystalsolvent.*

Yabbibu (1999, Abstract)

Final Thoughts on the Evolution of Computer Technology and its Nature's Bio-Chemical/Crystalline System

Just as another little thought experiment, picture how the abacus was once, and indeed, still is useable as a self-contained counting system for tens of centuries before Babbage's first computation machine or, the punch-card system used to code for the first IBM computers and the same principle of coding that allowed the great textile mills to pattern their linens and clothes, where the same design could be repeatedly produced from the same underlying pattern of a series of holes in a card, even in different factories. If one card got damaged; you could always make copies from the original or modified copies.

The telegraph system used another type of code, producing information that could be passed between vast distances; then came the telephone and we now have mobile phones. The typewriter was used mechanically and eventually we got the electric one, once we had electricity of course, but it was still a typewriter. And from the camera, to moving film and eventually sound, we all ended up with viewable boxes in our homes that we call televisions. And of course, the internet once the typewriter technology merged with the television to become your keyboard and monitor; the coded punch-cards were put on floppy discs and the computing machine became a super computing device and when the phone came into the equation and merged with the computing system, well, we know that the whole system became greater than the sum of its parts, in fact it is going quantum, yet each part was once a whole system, and you can still see whole functional systems within the greater whole. All the systems, irrespective of how primitive it may seem to us today, were once fully functioning technologies in their own right.

The main difference between this analogy and Nature is that Nature would appear to be highly efficient at using all the available resources and is the great recycler and adapter. At every level of life, even the microbial world, still have critical jobs to do. From the bottom feeders up: to ourselves and everything in between which is essentially made of stardust anyway, are part of one whole sustainable natural system. And perhaps instead of thinking of literal ancestors, i.e. the computer keyboard descended directly from the old Imperial Typewriters, and trying to find the missing link for what gave rise directly to the mouse and its imminent demise (nearing extinction apparently) and it has become an endangered species due to the superior advances of the touch-screen, we should perhaps see that the systems behind these innovations are fundamentally the same at every scale and it is this that is ancestral to them all.

CHAPTER FOUR

Karl Ernst Von Baer

(1792-1876)

EMBRYOLOGICAL DEVELOPMENT MIRRORS DEVELOPMENT OF THE SPECIES ON DIFFERENT SCALES

Von Baer Karl Ernst, Ritter von Baer -Prussian-Estonian embryologist (sometimes referred to as the Father of Embryology), proposed a theory regarding vertebrate development from egg to cell differentiation to embryos and by rewinding its developmental stages, their evolutionary species developmental stages could be inferred as outlined by Elizabeth Barnes (2014) from the Arizona State University, Center for Biology and Society working on the Embryo Project Encyclopedia [91] and her interpretation of Von Baer laws of embryology in both editions of his book *Über Entwickelungsgeschichte der Thiere* [*On the Development of Animals*], 1828. link to German editions [92]. The essence of Von Baer's model formulated in a pre-genetic era is given below:

> *Von Baer's first law states that the general characters of an animal group appear earlier in the embryo than the specialized characters do, which contradicted preformationist theories. Von Baer's second law states that embryos develop from a uniform and noncomplex structure into an increasingly complicated and diverse organism. For example, a defining and general characteristic of vertebrates is the vertebral column... This feature appears early in the embryonic development of vertebrates.*
>
> *However, other features that are more specific to groups within vertebrates, such as fur on mammals or scales on reptiles, form in a later developmental stage. Von Baer argued that this evidence supporting epigenetic development rather than development from preformed structures. He concluded from the first two laws that development occurs through epigenesis .., when the complex form of an animal arises gradually from unformed material during development.*

Barnes (2014)

[93]

Von Baer's laws reflect D'Arcy Thompson's alternative evolutionary concepts at their most fundamental and although, D'Arcy Thompson would have been fully aware of the highly popular work of Von Baer, his conclusions were seemingly independently derived as far as I can tell from reading D'Arcy Thompson's concepts.

Essentially, as Von Baer was first and foremost a vertebrate embryologist, his observations led him to propose that development reflects on another scale the fundamental stages of evolutionary development of the species. Therefore, in principle the alternative view of evolution proposed by D'Arcy Thompson is quite similar in that both theories seen fundamental (archetype) forms diverging and becoming increasingly different from the main group. Both seen that the context of the developmental environment and therefore, the context for the development and diversification of the species according to natural laws was paramount in their extrapolations of present-day species, where the modifications would be passed on via inheritance.

These two scientists also objected to the main tenants of the Darwinian literal form of descent (fish type to frog-type) and instead proposed that the species went from the generalist (archetype forms) to the more diversified and specialist species over time. I will explain Von Baer's objections further on and I have already alluded to D'Arcy's issues with Darwin's theory above. Finally, where D'Arcy Thompson proposed natural scaling laws according to efficiency and resource constraints rather than natural selection and non-linear descent, Von Baer's research, although specific to embryology, in principle proposed something similar to D'Arcy Thompson, in that evolution of the species was non-linear and discrete: a scaled up version of embryological development, where the former could be inferred from the latter and he also emphasised the growing/developmental context and/or environment being implicated in the formation of the species instead of natural selection.

Von Baer essentially presented an alternative form of evolution to the Darwinian linear common descent concept, just as D'Arcy Thompson had and indeed, it is worth revisiting the fact that in: *On Growth and Form*, Volume 1, (1942 Edition) [94], where D'Arcy Thompson discusses under the heading: *Of Physics and Embryology*, the main issues with Darwin's model and proposes that the research of Von Baer and morphology according to shape and form proposed in his own research, would go some way to resolving the formation of the species issues embedded in Darwin's model, i.e. how the species changed as he could not possibly see how selection would actually bring this about. Google Books

(Genetic) Pre-formation versus Epigenesis/Epigenetic Development

The context in which Von Baer developed his theory is important as it was in an era when biologists and embryologists were just beginning to demonstrate the process of epigenesis during development, a concept that had been around for some time, but could now be observed as cellular and embryological development was becoming better understood. Essentially, it was Von Baer's research that played a significant role in the overturning of the old concept of pre-formation (Richards, *nd. p*.2) [95].

In other words, the long entrenched belief that species were preformed in miniature in a fundamental type and grew to become a species was now explicable by epigenesis or its interchangeable term: epigenetics as it was used later in the context of genetics and embryological Morphogenesis (O'Hare 2014) [96], where an organism as seen from the development of the egg and sperm to the cellular differentiation and the assembly of these organised cells into meaningful shapes in the context of their developmental environment, pointed to something quite the opposite.

For instance, the old pre-formationist view of evolution and embryology is highlighted in contrast to the epigenetic/epigenesis understanding as deeper investigations of the later 18th and throughout the 19th century unfolded (particularly as the means of genetic inheritance became better known – referred to as the germ or germ plasm) as outlined in the following except taken from a study dealing with pre-formation versus epigenesis by Oscar Hertwig (University of Berlin) with an authorised translation by P. Chalmers Mitchell (2011).

1896

The Biological Problems of to-day: Preformation or Epigenesis? The Basis of a Theory of Organic Development

> *It is only because the minute constitution of matter is no longer a secret to us that the theory of germ within germ now touches the absurd.*
>
> *It was very different in earlier days; the acutest biologists and philosophers were evolutionists, and an epigenetic conception of the process of development could find no foothold alongside the apparent logical consistency of the theory of preformation.*
>
> *Wolff's Theoria Generationis (1759) failed to convince his contemporaries, because he could bring against the closed system of the evolutionists only isolated observations, and these doubtful of interpretation; and because, in his time, on account of the rudimentary state of the methods of research in biology, men attached more importance to abstract reasoning than to observation. His effort was the more praiseworthy in that it was observation bearing witness against abstract and dogmatic conceptions. By means of actual observation he tried to expose the fallacy in preformation, to show that the organism was not fully formed in the germ, but that all development proceeded by new formation, or epigenesis; that the germ consisted of unorganised organic material, which became formed or organised only little by little in the course of its development, and that Nature really was able to produce an organism from an unorganised material simply by her inherent forces.*

Hertwig (1896, 3-4)

[97]

The epigenetic concept as highlighted below or the organisation of unformed matter via epigenesis clearly offered the hard proofs of an alternative to pre-formation. Von Baer's own field of study came to be defined by epigenesis as it forms the basis of how species changed. In other words, this is the fundamental focus of Von Baer's theory in that organisms were indeed shaped and ordered into meaningful forms by their developmental environment – or via epigenetic factors.

> *Drawing a number of conclusions from his work on developing embryos, von Baer emphasized that development is epigenetic, proceeding from homogeneous to heterogeneous matter, which he felt made preformationist ideas no longer plausible.*

Buettner (2007)

[98]

However, there are fairly specific historical reasons as to why this concept does not form the basis, or even, typically inform the Neo-Darwinian Modern Synthesis version of evolutionary development today. This is a whole story by itself which I will not go into here, but it is worth pointing out that Charles Darwin came to understand the epigenetic principle of environmentally-driven modification of the species/developing organism alongside a softer form of selection (prior to the genetic era) (O'Hare 2014, 2015a) [99]; [100]. This of course contrasts significantly with the later understanding of epigenetics in the context of genetics adhered to so stringently by the Modern Darwinian Synthesis.

For instance, the staunchest proponents of the modern version of Darwinian theory, not only rejected Darwin's own epigenetic understanding of evolutionary change combined with a much softer form of selection, but they have also returned to a pre-formationist view of life in the belief that everything ever required to build and maintain an organism already exists in its genes, albeit in a more sophisticated form of latent development hidden in the so-called germplasm (*ibid*) as you will see as this, and particularly the following chapter, unfolds.

For instance, as discussed in Chapter Two in relation to epigenetic cellular development (biochemical 'on'. 'off' switches and the distinct cellular programs), we know, and have known for a very long time, that cellular differentiation and therefore embryological development cannot be accounted for by the same code that is within each undifferentiated cell. We know that it is epigenetic processes within the context of the development environment that primarily guides this differentiation of cells (expressing the genes differently and providing a diversity of programmed functions for the cellular processes).

This is no better illustrated than by highlighting the role of Von Baer's fellow country man, the early geneticist August Weismann whose work back in the late 1800s forms one of the main foundational pillar stones of the Darwinian Modern Synthesis which proposes that genes are closed off from their environment and each cell and organism comes with a preformed set of genetic instructions (*ibid*) which is highlighted in the quote dating back to Weismann's own era below:

1896

The Biological Problems of to-day: Preformation or Epigenesis? The Basis of a Theory of Organic Development

> *Weismann[...] leads the van for preformation; for the last ten years he has occupied himself with the theoretical discussion of the questions set forth above; and now, in a recent treatise, The Germplasm, he has combined his views, already many times modified, in a coherent theory. Now he explains candidly that he has been driven to the view that epigenetic development does not exist.*

Hertwig (1896, 8)

[101]

Note the use of epigenetics as far back as 1896, this is certainly not the first use of this term dating to this period and it is therefore not a new term or concept as many believe. Epigenetics, like epigenesist is the opposite of pre-formation which Weismann accepted at the expense of epigenetics. Indeed, in more recent years in particular as the evidence has become so overwhelming, the understanding of the epigenetic factors in the role of gene expression and cellular expression is turning out to be of paramount importance as an evolutionary driver as you will see particularly in the following chapter. Conversely, the genetic-only route promoted by Weismann and adopted whole-heartedly by our current Neo-Darwinian model of evolution and pre-formation idea (everything required is in the genes) is not.

The above overview has hopefully helped to some extent to give you a brief historical context for Von Baer's own theory and go some way to lay the foundation to begin showing you that it wasn't the lack of scientific understanding that led to his laws and theory of embryological development and its processes mirroring on another scale, the evolution of the species itself and driven by epigenetic factors, becoming essentially forgotten and historically obscured, it was other factors relating to misinterpretations, even on Charles Darwin's own part, as well as other historical factors that drove our current model of linear descent into prominence that led to its relative obscurity and fundamental lack of understanding of the model itself which I will discuss further on. So bearing all of this in mind, we will return now to the main principles of Von Baer's model.

Scales of Evolutionary Development from the Archetypal Form – Generalist to the Specialist

In the context of species diversification (differentiated programs) via their multi-cellular and metabolic systems working in tandem as these seem to be whole interactive systems from the get-go, evolving on many increasingly sophisticated scales of complexity, as discussed in the earlier chapters within this book, this dovetails extremely well with Von Baer's model. Von Baer proposed four main fundamental groups from which all modifications and divergence arose within the group as described below:

Karl Ernst von Baer

> *von Baer held that the animal kingdom could be separated into four distinct archetypes: the radiata (e.g., starfish and sea urchins), the mollusca (e.g., clams and octopus), the articulata (e.g., insects and crabs), and the vertebrata (e.g., fish and human beings). He denied recapitulation theory – the idea that the embryos of more complex animals passed through morphological stages comparable to those of the adult forms of organisms lower in the hierarchy of life. He maintained that the embryo of an animal exemplified from the beginning of its gestation only the archetype or Urform of that particular organism "The embryo of the vertebrate," he asserted, "is already at the beginning a vertebrate" (1828-1837, 1: 220).*
>
> *So a human fetus, he held, would move through stages in which it would take on the form of a generalized vertebrate, a generalized mammal, a generalized primate, and finally a particular human being. The form of the growing fetus moved from the general to the specific. The human embryo, in its early stages, therefore, never assumed the mature form of an invertebrate or of a fish.*

Richards (nd. 2)

[102]

Von Baer's concept of principle (his laws) are reflected in recent research involving the study of brain development in vertebrates and its implication for our simplistic linear and continuous view of evolutionary development by A.B. Butler and others The quotes below are taken from 'Evolution of Vertebrate Brains:

EVOLUTION OF VERTEBRATE BRAINS

> *....The simplistic ... concept of evolution ranks organisms on an ascending scale that is presumed to reflect evolutionary history ... While this concept is unfortunately widely and deeply embedded in the public consciousness, it is completely unsupported by the massive amount of data on evolution, not only for the brain but for all characters across the board.*
>
> *...That brain enlargement and elaboration has occurred four times independently presents a very different reality of how brain evolution has operated than is perceived in the widely held folk-belief...*

Butler (2009, 57)

[103]

> *… reptiles did not give rise to mammals any more than mammals gave rise to reptiles. In regard to embryological development, it likewise generally proceeds from the general (common ancestral features) to the specific (specializations of the taxon) ... What is clearly established is that all taxa have their own specializations. Each taxon has a mix of primitive features.*

Butler (2009, 64)

[104]

Basically, as you can see above, this brain study really begins to support a theory proposed over 180 years ago in a pre-molecular/genetic age and strongly supports the concept that species converge on ancestral features (shared ancestral condition) and then, later become specialists and they diverge from a shared (common) ancestral CONDITION, not a literal descent as the independent origins of brain types strongly suggests.

> *The first law says that the general features of a large group of animals appear earlier in the embryo than the special features. The second law says that less general characters are developed from the most general, and so forth, until finally the most specialized appear. The third law is that instead of passing through the stages of other animals, each embryo of a given species departs more and more from them. Finally, the fourth law concludes from the previous three that the embryo of a higher animal is never like the adult of a lower animal, but only like its embryo.*

Buettner (2007)

[105]

It also highlights the independent evolution of brains and essentially a non-linear model which also dovetails very well with D'Arcy Thompson's discontinuous model. This begins to open up an alternative, less literal form of evolutionary development of the actual species and of course begins to support older principles of development and evolution by epigenetic principles of shape and form according to natural scales of complexity.

What made Von Baer's model distinct from the Darwinian perspective was the means by which these commonly associated ancestral organisms had changed so dramatically through time. The Neo-Darwinian perspective sees it as a fishy-pod to walking amphibian/reptile to mammal progression as highlighted above in Butler's study, whereas, Von Baer seen the complex patterning of embryological development as a scaled down version (not a literal recapitulation) of species formation itself (akin to D'Arcy Thompson's view – see Chapter One of this present book).

Von Baer extrapolated the patterns of development to infer that evolution had preceded from the unorganised cellular world, to the undefined generic (generalist) forms and from fundamental forms, diversified into a myriad of species (specialists) from these commonly shared templates, to put his theory in more modern language.

Von Baer's Laws and Evolutionary Descent Model Misconstrued

Now, Von Baer's model became rather misconstrued as time went by and one insight into this can be seen in the comments from one of the staunchest Neo-Darwinist's views on Von Baer's laws. It certainly wasn't that Mayr had misunderstood Von Baer's theory as Mayr was able to read his works in the original German language (as he himself was also German). For instance, Ernst Mayr refers to Von Baer as "emphatically anti-evolutionary" as seen in the quote below taken from Harvard University Press, 1997, in *Evolution and the Diversity of Life: Selected Essays:*

> *When such an emphatically anti-evolutionary author as von baer (1828) defines the species as "the sum of the individuals that are united by common descent," it becomes evident that he does not refer to evolution.*
>
> Ernst Mayr (1997, 498)
>
> [106]

Perhaps Mayr thinks that Von Baer's evolutionary theory of life on scaled levels of complexity is anti-evolutionary because Neo-Darwinist's almost always refer to any alternative model of evolution as anti-evolutionary and besides, Von Baer was often highly critical of the Darwinian descent model itself: perhaps, then, this was a type of intellectual counter attack on Mayr's part? Furthermore, Mayr himself strongly adhered to the simplistic linear common descent model and being a particularly staunch believer in the Weismann preformationist genetic doctrine, had to be anti-epigenetic in his views and publicly defend the Neo-Darwinian position on this matter – he was after all, one of the main authors and official commentator of the movement itself as his prolific writings clearly show.

However, the support for the Weismannian or pre-formationist genetic view is historically unsupported by many of his contemporaries and particularly by embryologists as the historical record clearly shows. This is well documented in Peter J. Bowler's book: *The Eclipse of Darwinism: Anti-Darwinian Evolution Theories in the Decades* (1992) [107].

And there is an historical reason why Von Baer's alternative scaled model of descent got demoted in favour of the Neo-Darwinian model of descent as you will see below. Again, it isn't because Von Baer's model and his epigenetic concept of the development of the species being scientifically unfounded, it was more a case that things become somewhat misconstrued, misinterpreted and distorted along the way.

All in all, prior to the solidification of the Modern Synthesis, Von Baer's pre-Darwinian theory was taken seriously and well respected, even before and during Darwin's own time and was considered pertinent by Darwin himself as noted by Barnes (2014) [108]. However, Barnes also suggests that, Von Baer's model was somewhat misunderstood in its finer details and became historically obscured, in large part due to the fact that it became overshadowed by Haeckel's embryonic similarity charts across many different species – this ended up being abandoned as they were just a bit exaggerated and the result is that Von Baer's more subtle and less direct common descent model from several different origins fell into obscurity; below is an insight into this rather convoluted, but important tale..

Most of us have heard of Ernst Haeckel and his famous – now infamous, drawings of different animal embryo drawings, still used in some biology text books today? Well, only seven years after Darwin wrote *Origin of Species*, as noted on the Embryo Project Encyclopaedia website, Von Baer's laws ran into Haeckel's recapitulation theory known as biogenetic law. Ernst Haeckel's early suggestion that ontogeny (development) recapitulates phylogeny (evolution) is outlined below which should give you some historical context:

Ernst Haeckel's Biogenetic Law (1866)

The biogenetic law is a theory of development and evolution proposed by Ernst Haeckel in Germany in the 1860s. It is one of several recapitulation theories, which posit that the stages of development for an animal embryo are the same as other animals' adult stages or forms. Commonly stated as ontogeny recapitulates phylogeny, the biogenetic law theorizes that the stages an animal embryo undergoes during development are a chronological replay of that species' past evolutionary forms.

– "the Biogenetic Law" "Ontogeny recapitulates phylogeny."

.... Despite von Baer's objections to Haeckel's biogenetic law and recapitulation in general, the biogenetic law persisted in biology until the turn of the twentieth century when new experimental and comparative evidence rendered it untenable.

Barnes (2014a)

[109]

Moreover, Von Baer actually used his laws to rebut such recapitulation theories that had widespread appeal in his day as noted below:

Karl Ernst von Baer's Laws of Embryology

Von Baer used the third and fourth laws to counter the recapitulation theories of [others] which became increasingly popular in Europe throughout the eighteenth and nineteenth centuries.

Barnes (2014)

[110]

Basically, even though Haeckel's theory was dismissed, his concept lives on despite the efforts of Von Baer to point out the obvious flaws in the theory: i.e. it wasn't what actually happened during developmental processes (a non fish species never resembles a fish) and even with his popular theory of a fundamentally different view of both developmental and evolutionary processes, something literarily got lost in translation as you will see below and this begins to reveal how Haeckel's laws somehow got muddled up with Von Baer's which proposed two entirely different patterns of descent and how this informed the Origin of Species, which in turn formed the anti-Von Baerean attitude amongst the strictest Darwinists who understood the difference.

Finally, I began to realise what had happened; it was more than a misunderstanding of Von Baer's laws, Darwin had fundamentally missed the point and was rather enthusiastic to employ embryological evidence to support the theory of common descent from a single origin in a branching pattern according to gradual natural selection, as becomes apparent when you read the different editions of *Origin*. And this is supported in the quote below: taken from *Individual Development and Evolution: The Genesis of Novel Behaviour*, by Gilbert Gottlieb (2001):

Charles Darwin on the Evolution of Species and the Role of Embryological Development.

Jane Oppenheimer (1967, 338) "Darwin got his wrongheaded idea about the testimony of embryology from the naturalist Louis Agassiz, and he could not be dissuaded from it even by the arguments of Thomas Huxley, one of his most ardent and dedicated supporters" as quoted in page 25 individual development... "As Oppenheimer points out, Darwin did not have any of von Baer's works in his library at the time of his death in 1882. We also know from various sources that Darwin did not read German easily or with great understanding, thus von Baer's writings would have been quite a chore in the original. But German was Ernst Haeckel's mother tongue and still he managed to stand von Baer on his head,..."

Gottlieb (2001, 25)

[111]

Thomas Henry Huxley (Darwin's so-called Bull Dog and greatest defender of the theory of selection) as detailed in Barnes' 2014 in Scientific Memoirs verbatim was fully acquainted with Von Baer's embryological laws in the original German as reiterated below:

... the more general characters of a large group appear earlier in the embryo than the more special characters. From the most general forms the less general are developed, and so on, until finally the most special arises. Every embryo of a given animal form, instead of passing through the other forms, rather becomes separated from them. Fundamentally, therefore, the embryo of a higher form never resembles any other form, but only its embryo.

Barnes (2014)

[112]

Anyway, the Darwinists went with the Haeckel model and Von Baer's theory fell into obscurity. So it didn't matter that Haeckel was a little over artistic in his representations or literal in his concept of linear descent, for by this time, the Darwinist version took hold and their linear descent is the one we adhere to dogmatically to this day. They also dismissed everything epigenetic and therefore Darwin's own views on the matter as you will see in the next chapter. And another dimension to all of this is the fact that: *"Following the publication of Darwin's Origin of Species, in 1859, biologists were eager to apply the theory of evolution to the paleontological record."* as noted by Aulie (1975, 21) in The American Biology Teacher, 1975, National Association of Biology Teachers. [113].

Haeckel's form of common descent became the Darwinian doctrine, helped by a whole plethora of fossil hunters who had a particular passion for giant lizards (dinosaurs) and used the Weismannian (pre-formationist) view to guide their interpretation. To-day we are categorically told without a doubt that we shared a common ancestor between fish and a fishy-pod species that gave rise to amphibians, the reptiles and then, somehow mammals emerge from these reptilian ancestors and so on and so forth. Yet these proposed ancestors remain entirely illusive in the fossil record as it happens when you drill down to it. You'll see what I mean when you get to Part Two of this book and offer more detail on the actual mechanisms of speciation as we continue throughout this present book.

A More Modern Evolutionary Developmental Model and Revisiting Von Baer's Alternative

Von Baer's alternative model of evolutionary development akin to D'Arcy Thompson's view, are however, beginning to find support, but I doubt with all the wrongheadedness and the anti-Von Baerean views regarding the theory, that even our modern embryologists/evolutionary developmental biologists, as they are referred to in modern times, are grasping the full implications of Von Baer's laws. For instance, the following excerpt explains how many of Von Baer's concepts are beginning to be supported by more recent studies as seen below:

Von Baer's law for the ages: lost and found principles of developmental evolution

> *With advances in multiple fields, including paleontology, cladistics, phylogenetics, genomics, and cell and developmental biology, it is now possible to examine carefully the significance of von Baer's law and its predictions...185 years after von Baer's law was first formulated, its main concepts after proper refurbishing remain surprisingly relevant in revealing the fundamentals of the evolution–development connection, and suggest that their explanation should become the focus of renewed research.*
>
> Abzhanov (2013 Summary)
>
> [114]

Von Baer's laws are coming into clearer focus in the light of our more modern understanding of embryological development and how it may relate to species development. This is perhaps best illustrated via what has come to be described as the hourglass model. Do bear in mind the all-to-little reference to epigenetics in the studies below, as epigenetics, as you will clearly see, particularly in the following chapter, is implicated in one of the main causes (according to environmental factors) in the species divergences away from their more generic and unspecialised primitive embryonic-type forms. Therefore, the hourglass model should be viewed with these factors in mind (See Figure 14). The developmental hourglass model is summarised in the excerpt below. (*note embryogenesis means the origin of the embryo as a species and phylotypic means the phylo type where phylo refers to the shape and form of an organism):*

The developmental hourglass model: a predictor of the basic body plan?

The hourglass model of embryonic evolution predicts an hourglass-like divergence during animal embryogenesis – with embryos being more divergent at the earliest and latest stages but conserved during a mid-embryonic (phylotypic) period that serves as a source of the basic body plan for animals within a phylum. Morphological observations have suggested hourglass-like divergence in various vertebrate and invertebrate groups, and recent molecular data support this model. However, further investigation is required to determine whether the phylotypic period represents a basic body plan for each animal phylum, and whether this principle might apply at higher taxonomic levels.

Naoki and Shigeru (2014, Abstract)

[115]

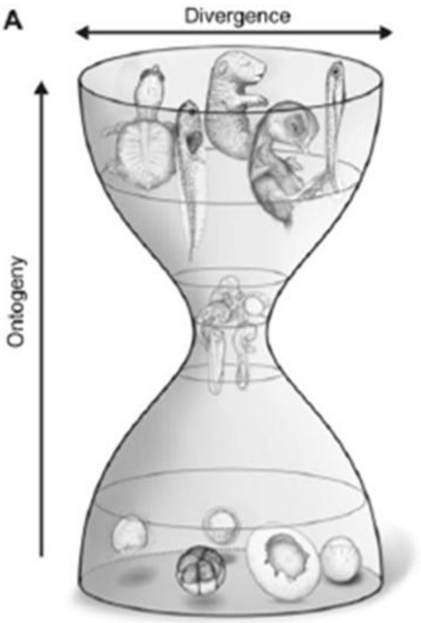


Fig. 14: Part of diagram sourced from: Naoki, I., and Shigeru, K., 2014, The developmental hourglass model: a predictor of the basic body plan? Development, Vol. 141, [24], Fig. 2, p. 4651 (adapted from Wang et. al. 2013) Link

Below is another excerpt relating to the hourglass model and directly links recent molecular investigations to the pattern predicted specifically in Von Baer's third law that corresponds with the latter phase of the embryological developmental hourglass model.

In search of the vertebrate phylotypic stage: A molecular examination of the developmental hourglass model and von Baer's third law

In 1828, Karl von Baer proposed a set of four evolutionary "laws" pertaining to embryological development. According to von Baer's third law, young embryos from different species are relatively undifferentiated and resemble one another but as development proceeds, distinguishing features of the species begin to appear and embryos of different species progressively diverge from one another.

..According to the hourglass model, ontogeny is characterized by a starting point at which different taxa differ markedly from one another, followed by a stage of reduced intertaxonomic variability (the phylotypic stage), and ending in a von-Baer-like progressive divergence among the taxa. ...The molecular evidence for the later parts of the hourglass model, i.e., for von Baer's third law, was stronger than that for the earlier parts.

Hazkani-Covo, et al (2005 Abstract)

[116]

The hourglass model is idealised to show the type of convergence (on a shared ancestral condition, I would like to stress, rather than a literal ancestral common ancestral form) and this is where the following excerpt becomes interesting.

There is no highly conserved embryonic stage in the vertebrates: implications for current theories of evolution and development

Embryos of different species of vertebrate share a common organisation and often look similar. Adult differences among species become more apparent through divergence at later stages...Our survey seriously undermines the credibility of Haeckel's drawings, which depict not a conserved stage for vertebrates, but a stylised amniote embryo. In fact, the taxonomic level of greatest resemblance among vertebrate embryos is below the subphylum.

Richardson et al (1997, Abstract)

[117]

This bottleneck of the hourglass does not therefore correspond to the 'conserved stage' employed by the literal and linear model of common genetic descent, but to a stylised amniotic embryo stage, which is important as this describes not only a more primitive and less defined stage in the amniotic organisms (these include all vertebrates that are not fish or amphibian types), but it implies a much earlier stage in evolutionary development akin to when Butler's study established a fundamental ancestrally shared generalist shared condition amongst the vertebrate groups .

This will become clearer further on in this book and particularly relevant in Book Two when we examine the actual fossil record, but in the meantime, it corresponds much more closely with Von Baer's actual laws of going from the generic generalist forms (archetypes) and diverging into increasingly independent and more specialised forms that we might call an adult species, than I believe even the scientists re-examining his model realise.

This model in turn, supports D'Arcy Thompson's view of the same (different primitive generalist form becoming increasingly diversified and ultimately becoming specialised species). And of course reflects the study carried out by Butler on the evolution of vertebrate brains where the results suggest independent evolution of the brains within the broader vertebrate groups and descent from a commonly shared ancestral condition rather than the simplistic linear model of fish to amphibian, to reptile and mammal etc we currently employ today, even if we say it was from a common ancestor that then split.

Therefore, I have retained the principle of the hourglass model as it corresponds to Von Baer's Third Law and the latter phase in particular, with the narrower waist (bottleneck) showing convergences prior to divergence. The earlier phase of the hourglass may represent diversity amongst types, but this would not necessarily show in a molecular (gene) study, but we might assume that organisms were diverse and perhaps fundamentally distinct with independent origins as D'Arcy Thompson indicated, as the evidence seems to support this idea which should become clearer as further on in this book.

Essentially, the hourglass model, if applied in accordance with Von Baer's actual laws and principles, gives us a fairly major piece of the evolutionary puzzle where, if Nature does operate on increasingly sophisticated scales of complexity using the same fundamental method of self-similar patterns of growth and form as indicated throughout this and the previous chapters, then Von Baer's developmental model for vertebrates can be easily scaled up to an evolutionary level of speciation and when restated in the light of our most up-to-date understanding of epigenetics, as you will see in the chapter that follows, this becomes a very dynamic model indeed and has the potential to unlock the otherwise unknown course of the evolutionary past.

We will attempt to apply, more broadly, so as to incorporate other scales of life beyond vertebrates in the light of their present-day modes of reproduction and development to ascertain their ancestral evolutionary developmental modes as suggested in Von Baer's model to, non-vertebrate species and the highly diverse and almost experimental world of microbial life to ascertain the same underlying scales of complexity and perhaps origin of these reproduction/developmental modes. If we can begin to grasp the profound difference between literal linear descent and the concept of scales of complexity model embedded within Von Baer's laws. The hour glass model should operate at all scales and seemingly, as you will see as we proceed, it does.

However, we should not lose sight of the means of developmental and/species change and the all important context dependent developmental process also embedded in Von Baer's model. In order to grasp the whole alternative evolutionary concept proposed by Von Baer, we cannot ignore the fundamental and profound implications of the epigenetic phenomenon.

As discussed previously, essentially, it is epigenetic factors that change the epigenome, which in turn causes the differential expression of the genetic code giving cellular communities and their organisms their distinctive programs. This epigenetic process can express the same genes in the same or identically related organisms and give cells their identify, and is implicated in being the a major modifying force during the evolutionary past.

Recall that it is epigenetics that explains how the trillions of cells in your body with the same genetic code, know what to be when they grow up. And by extrapolation of Von Baer's scaling principle in a more modern interpretation, means that epigenetic regulation and differential expression of the genomes even within the same species implies that species may have similarly come into being as their collective colony of cells knew what to be when they eventually grew up and differentiated into final specialised species forms, and presumably following the Sigmoidal growth curve as embryological development does on a much shorter timeline and less major scale.

This now brings us to a name that is virtually synonymous with epigenetics: Jean Baptiste Lamarck, but again like Von Baer's concepts of evolution, these were developed within a pre-genetic age, but is being confirmed and supported by our most up to date studies that have explored the nature of genetics and molecular biology in particular.

CHAPTER FIVE

Jean-Baptiste Lamarck

(1744-1829)

THE ORIGINAL NATURAL EVOLUTIONARY THEORY OF DESCENT – BY EPIGENETIC MODIFICATION

The evolutionary ideas of Jean-Baptiste Lamarck French Naturalist (early biologist) and *Founder of Evolution* as indicated in Packard's publication title (1901) [118] go back to over 200 years and are most commonly associated with his fully comprehensive publication *Philosophie Zoologique* ("*Zoological Philosophy: Exposition with Regard to the Natural History of Animals*") [119]. This comprehensive theory was informed by his deep anatomical study of a vast array of species, as indicated below:

**Lamarck As Founder of the Theory of Descent*

> *Lamarck had acquainted himself with an astonishingly large number of animal and plant species, and it had not escaped him that the individual members, by changing their environment, under the influence of changed feeding requirements with regard to their body proportions, underwent many changes in their physical appearance and organization.*
>
> Claus (1888, 11)
>
> [120]

Claus, Carl, **Lamack als Begrunder der Descendenziehre (*Lamarck As Founder of the Theory of Descent) Alfred Holder, Vienna, 1888, p. 11. (trans., H. Gershenowitz 1983, 146).

Interestingly, Lamarck's main treatise on the topic of evolution came out the same year of Charles Darwin's birth – 1809, but wasn't translated into English until 1914 [121] and, as you will see throughout this chapter, Lamarckian evolutionary principles are finally beginning to return from their long, arduous and scientifically unwarranted exile.

However, in order to gain a better insight into what some scientists thought of Lamarck's theory back in the day, particularly prior to the installation of modern Darwinism, I believe Ernst Haeckel, who we discussed in the previous chapter, writing at the end of the nineteenth century summarises Lamarck's evolutionary theory succinctly below:

The Evolution of Man

1897

To enable my readers to judge of the great value of the Philosophie Zoologique, I shall here briefly mention some of the most important of Lamarck's ideas. According to him there is no essential difference between animate and inanimate nature; all nature is a single world of connected phenomena, and the same causes which form and transform inanimate natural bodies are alone those which are at work in animate nature.

Hence, we must apply the same methods of investigation and explanation to both. Life is only a physical phenomenon. The conditions of internal and external form of all organisms-plants and animals, with man at their head-are to be explained, like those of minerals and other inanimate natural bodies, only by natural causes... The same is true of the origin of the various species...

Haeckel (1897, 83)

[122]

Apart from the fact that Haeckel reveals in the overarching concept of Lamarck's theory concepts that parallel much of what was discussed in Chapter One on universal scaling laws and embedded patterns of growth and form that Nature employs and the discussion in Chapter Three of the principles and processes of systems from the inanimate to the animated being one and the same thing only on different scales of complexity, I think Haeckel also reflects in his view of Lamarck's theory a relatively untainted understanding prior to the rise of the Neo-Darwinian synthesisers and their staunchly gene-centred evolutionary theory, which as indicated earlier, is an anathema to epigenetics and epigenetics is virtually synonymous with another very important and most known aspect of the Lamarckian form of evolutionary species formation, and therefore, it is important to highlight where Lamarck's theory stands today.

In the deep reading of Lamarck's work (for most of his publications and related works in both English translation and original French) [123], it becomes clear that what he meant by acquired characteristics is that species (particularly as they were themselves developing) could be modified in accordance with their ancestral/evolutionary environmental conditions/interactions and all of this was driven by natural laws that shape, form and mould and ultimately adapt each species – going from the generalist to the specialist – to be all that it can be according to its intrinsic or innate complexity.

In other words, Lamarck's theory is underpinned by the fundamentals of epigenesis/epigenetic processes of non-preformation of the cells and embryo (as also advocated by Von Baer's study and scaled-up to the species level) as it particularly extends out to the species scale of formation. Lamarck's expertise came from his deep anatomical research with extensive collections of specimens along with his insightful understanding of the nature of Nature.

As far back as 1907, in the publication entitled: *Evolution and Animal Life...* Lamarckian environmentally-driven evolutionary concepts were clearly linked to epigenetics, (and the term is explicitly used) in the context of an emerging understanding of genetics and advances in embryology and that this

Lamarckian-form of evolution which is highlighted as being widely supported around the turn of the late nineteenth and early 20th Century Jordan (1907, 56) [124].

Historically there was a growing body of evidence to support the epigenetic/Lamarckian view of evolutionary change, particularly around the end of the 19th Century and earlier part of the 20th Century as seen below:

MIT Press chapter seven The Notions of Plasticity and Heredity among French Neo-Lamarckians (1880-1940): From Complementarity to Incompatibility

During the 1880s "Pasteur and his colleagues showed that some bacteria could be transformed by vary in culture conditions." …

"However, the most spectacular and clear results were obtained in botany. ..They performed numerous experiments in order to establish that the morphology, anatomy, and physiology of plants were dominated by abiotic parameters such as luminosity, temperature, and humidity."

Beginning in the 1880s (e.g. Bonnier) "Many characteristics of the plants were rapidly affected by the new environment: their size, color, general shape, for example, were changed. The results showed clearly that by changing growing conditions, it was possible to directly (i.e., without the need for natural selection) transform living plants."

..."it was possible to transform one organ into another by imposing drastic changes in growing conditions. Indeed, by cultivating a stem under a mass of thick soil, one could observe transformations which slowly made the stem look like a root (Constantin 1883). He also obtained interesting results by pushing land plants into the water during their growth, which led to the disappearance of stomata (Constantin 1886).

Whatever the trait, at every possible level and on every scale; it seemed that living organisms were capable of conforming to the requirements of their environment. All these results strengthened the idea of the transformability of life, and were widely discussed in France at the end of the nineteenth century.

Loison.(2011, 68 – 69).

[125]

Again, within the early period between the end of the 19th and early 20th Century, Lamarckian concepts continued to find empirical support as detailed in an excerpt from a science article by Yongsheng Liu, where we can see clearly that inherited traits (acquired characters) were demonstrated and even explored by Darwin himself.

Like father like son. A fresh review of the inheritance of acquired characteristics

> *There are also many records of graft-induced inheritable changes in plants and Darwin was the first to compile the available information on graft hybrid individuals produced from the cellular tissue of two different plants (Darwin 1868). Several famous plant breeders, including Luther Burbank (1849–1926) and Ivan Michurin (1855–1935), created plants with inheritable characteristics that were acquired from the tissues of both original plants.*
>
> *In addition, about 500 papers on these types of hybridization experiment were published in the Soviet Union during the 1950s, although Western geneticists largely ignored the literature and dismissed the work as based on fraudulent results. Over the past decades, however, independent scientists have repeatedly shown that graft-induced variant characteristics in plants are stable and inheritable (*
>
> *...Oscar Hertwig in the late 19th century discovered a number of examples of phenotypic plasticity – the ability of an organism to alter its development, hence phenotype, depending on environmental conditions – such as that underlying the sexual dimorphism of the echiuroid worm Bonellia viridis.*

Liu (2007)

[126]

But indicated above and further supported below, Non-Preformationist and epigenetics operating above and beyond the gene level along with their environmental-drivers (updated Lamarckian evolutionary principles) were never dismissible on scientific grounds; it was much more to do with a Neo-Darwinian ideology; a story for another day perhaps? Moreover, epigenetics and its direct association with Lamarckian evolutionary concept of acquired characteristics is finally beginning to see resurgence again as indicated above as a result of our more modern era of molecular and genetic understanding as also seen below:

A Comeback for Lamarckian Evolution?

Lamarckian Evolution confirmed 200 years later in Epigenetic studies

Two new studies show that the effects of a mother's early environment can be passed on to the next generation. The findings provide support for a 200-year-old theory of evolution that has been largely dismissed: Lamarckian evolution, which states that acquired characteristics can be passed on to offspring. MIT article on Lamarckian Evolution's comeback continued...

In contrast to natural selection, in which organisms that are born well adapted to their environment survive and reproduce, passing down those successful traits, Lamarckian evolution suggests that animals can develop adaptive traits, such as better memory, during their lifetimes, and pass on those traits to their offspring. The latter theory was largely abandoned as Darwin's, and later Mendel's, theories took hold. But the concept of Lamarckian inheritance has made a comeback in recent years, as scientists learn more about epigenetics.

Singer (2009)

[127]

This is further supported by the accumulating evidence for epigenetic or Lamarckian-type factors driving evolutionary processes across the board which are seriously beginning to throw a bit of a spanner in the works of our more modern gene-centred and selection-driven form of evolutionary explanations as in the book review *The Epigenetic Revolution* by Nessa Carey as published in the Guardian.

"A book that would have had Darwin swooning"

So far, this is instructive and highly promising for medical research, but epigenetics finally reaches that "everything you've been told is wrong" moment when it claims that some epigenetic changes are so long-lasting they cover several generations: they can be inherited. This flouts one of biology's most cherished dogmas – taught to all students – namely that changes acquired during life cannot be passed on – the heresy of Lamarckism. But the evidence that this can occur in some cases appears to be growing.

Forbes (2011 in the Guardian 19th August)

[128]

Lamarckian principles for the most part are revealed throughout a collection of excellent essays on Lamarck and his unrecognised contributions to evolutionary thought; his unfair dismissal, the ridicule and misrepresentation of his theory (or over-simplification of some of its fundamentals) and the confirmation of many of his ideas and principles (namely epigenetic in nature) are finding much support in the light of our most modern understanding of molecular processes as seen in: *Transformation of Larmarckism – from Subtle Fluids to Molecular Biology* (Gissis and Jablonka 2011) [129]. This book also contains a number of essays which are historically revealing and will give you a clear insight into why and how Lamarckian ideas became effectively written out of the history books and it wasn't due to the silliness of his ideas even if they were somewhat ahead of their time and it has taken us until more recent times to even begin getting them.

Below are a couple of very helpful video links which should help explain the misconceptions surrounding Lamarckian type evolution and the profound implications for evolution when we apply Lamarckian/epigenetic or non-gene-centred thinking to evolution.

‘Who was Lamarck? And what did he think?’ on Turner channel at YOU TUBE (a short and to the point myth-dispelling video presented by a scientist looking at what Lamarck actually proposed as opposed to what we think he actually proposed) [130] (Turner 2012); ‘Epigenetics in Evolution’ (short video interview with Dr Eva Jablonka on epigenetics and Lamarck and implications for our current model of evolution). [131] (EpiGenie 2011).

Also see *Lamarck and the Sad Tale of the Blind Cave-Fish.* where I have also dealt with the background relating to Lamarck and our modern synthesis and focus on the specific epigenetic effect of loss or gain of traits, features, even limbs and organs of species according to environmental triggers – a key concept within Lamarck’s evolutionary theory (O’Hare 2015a) [132]. And another epigenetic alternative to evolutionary processes and a historical perspective on Lamarck as seen in *The Epigenetic Caterpillar: An Alternative to the Neo-Darwinian view of the Peppered Moth Phenomenon* (O’Hare 2014) [133].

Indeed, this unnatural rejection of Lamarck (which never had any good scientific basis as the history books show) becomes all the more perplexing when we look at what Ernst Haeckel has to say regarding the fact that Lamarck’s evolutionary theory was the original theory of descent with modification and should be recognised as such as well as drawing attention to the fact that Charles Darwin came to hold Lamarck’s theory in high regard, with proofs:

The evolution of man

1897

> "*All the various species of animals and plants which we now see around us, or whichever existed, have developed in a natural manner from previously existing, different species; all are descendants of a single ancestral form, or at least of a few common forms. The most ancient ancestral forms must have been very simple organisms of the lowest grade, and must have originated from inorganic matter by means of spontaneous generation. Adaptation through practice and habit, to the changing external conditions of life, has ever been the cause of changes in the nature of organic species, and heredity caused the transmission of these modifications to their descendants.*
>
> *These are the principal outlines of the theory of Lamarck, now called the Theory of Descent or Transmutation, and to which, fifty years later, attention was again called by Darwin, who firmly supported it with new proofs. Lamarck, therefore, is the real founder of this Theory of Descent or Transmutation, and it is a mistake to attribute its origin to Darwin. Lamarck was the first to formulate the scientific theory of the natural origin of all organisms, including man...*

Haeckel (1897, 83-84)

[134]

I should perhaps clarify a few things regarding Haeckel's summary of Lamarck being the original founder of the natural theory of Descent, and this may be better explained in Lamarck's own words (they were in French, but the translation of 1914 Huge Elliot is the definitive version - apparently) what he actually meant by spontaneous generation and a few other things about his theory:

Philosophie Zoologique

1809

Nature, by means of heat, light, electricity and moisture, forms direct or spontaneous generations at that extremity of each kingdom of living bodies, where the simplest of these bodies are found. This proposition is so remote from the current notion on this matter, that for a long time to come it is likely to be rejected as an error, and even to regarded as a product of the imagination.

But, since men who are free even from the most ubiquitous prejudices, and who are observers of nature, will sooner or later perceive the truth contained in this proposition, I wish to contribute towards their perception of it.

Lamarck (1809, 244, Spontaneous Generation)

[135]

Yes, well, it did take a long, long time to get what Lamarck was saying, but I think we are finally getting it, especially in the light of all that was discussed in Chapter One and particularly Chapter Three of this book. Basically, Lamarck certainly had a less literal and more sophisticated view of the scales of evolutionary complexity embedded within living systems, than we adhere to presently. Below is a short excerpt about his thinking:

Philosophie Zoologique

1809

... I shall show that nature, by giving existence in the course of long periods of time to all the animals and plants, has really formed a true scale in each of these kingdoms as regards the increasing complexity of organisation; but that the gradations in this scale, which we are bound to recognise when we deal with objects according to their natural affinities, are only perceptible in the main groups of the general series, and not in the species or even in the genera.

Lamarck (1809, 58)

[136]

Essentially, throughout Lamarck's major thesis on evolution of more than 200 years ago, he describes the process of going from the simple to the complex within these main groupings of organisms. He appears to see a few or several fundamentally distinct organism types (Kingdoms or fundamental types) that had their own developmental process from very humble and primitive beginnings and transmutating (the old word for evolving) to many different scales of complexity, akin perhaps to Von Baer's epigenetic evolutionary scales of development from archetype forms or D'Arcy Thompson's distinct originations (or many little worms) with their diversification via natural laws of growth and form to ultimate species types concept?

Lamarck understood that the scales of complexity identified within the main groups could be described at one end of the spectrum as less perfected (less-complex) forms and at the other, what Lamarck described as more perfected forms. This he based on his deep anatomical observations where he placed a great deal of emphasis on the internal nervous fluids/system and the responsiveness of organisms to their environments, needs, and conditions of existence. He was also fully aware of the importance and some of the fundamentals of the functions of the cells that comprised the organisms.

To Lamarck, it seems, these scales of complexity observed within the different groups are explicable in terms of the less perfected forms being more limited in their ability to be independently interactive with their environments, thus restricting their limit of growth (or evolutionary potential), while other groups may have started out similarly simple, via their slightly more perfected system could according to their more interactive experience, ultimately reach a greater level of complexity.

Lamarck seems to follow Nature's pattern in this manner and explains increasing complexity arose when Nature further developed and elaborated upon the earlier and less perfected systems, perfecting it a little more and thus a new level of complexity would be reflected in the species and increasingly more dynamic species could be formed from this general (as yet un-programmed state to use the analogy of what we do know about the epigenetic programming of the stem or pluripotent cells) state.

Having more to play with if you like, a new level of complexity could be generated with the increasing ability to manipulate their environments, increase their mobility and via their more sophisticated and sensitive (nervous fluids/system), become more responsive and aware of their experiences, thus having the effect of increasing their complexity even further to the next level and all of this was explicable according to Lamarck in terms of acquired characters (epigenetic inheritance) which could be passed on to the next generation and so on and so forth.

Lamarck's deep observations into Nature's process led him to continually refer to the dangers of over-classification of species according to their affinities as being unwarranted and distracting as if animals and plants that we classify too rigidly based on small differences and these modification were brought about by environment, needs and interactions as well as the traits passed on from previous generations, how would we know if it was a really distinct species or simply a modified descendant of its former self?

Relating to all of the above, another key point to Lamarck's Evolutionary Theory that is distinct from the Neo-Darwinian model, and drawn from the concept that evolution is via environmentally-driven modification of organisms and ultimately, the species, is that extinctions may not be the full explanation for the distinct forms found in the fossil layers (which were fairly well known back in Lamarck's era), but represent instead essentially the same anatomical forms, yet modified versions of their unmodified kind as indicated in his writings below:

Philosophie Zoologique

1809

> *... among the fossil remains found of animals which existed in the past, there are a very large number belonging to animals of which no living and exactly similar analogue is known; and among these the majority belong to molluscs with shells, since it is only the shells of these animals which remain to us. Now, if a quantity of these fossil shells exhibit differences which prevent us, in accordance with prevailing opinion, from regarding them as the representatives of similar species that we know, does it not necessarily follow that these shells belong to species actually lost? Why, moreover, should they be lost, since man cannot have encompassed their destruction? May it not be possible on the other hand, that the fossils in question belonged to species still existing, but which have changed since that time and become converted into the similar species that we now actually find.*

Lamarck (1809, 45-46)

[137]

The above quote reflects, not only what we actually see in the fossil record which will become abundantly clear in Book Two and what the more recent studies are demonstrating in real-time as you will see below within this present chapter, but they also mirror proposals of increasing scales and graduations of complexity within broad groups and not necessarily from a single progressive origin of Von Baer and D'Arcy Thompson's concepts of generic forms being shaped by their experience and conditions of existence (environment) to form many variations of the same fundamental forms.

Moreover, as you will see below his entire principle of modification according to environmental conditions (epigenetics) is finding very strong support and beginning to give us a very real insight into the actual means of speciation itself that completely dovetails with fossil record. And as it turns out, his warnings regarding the over-classification of species were well justified as it would seem that we have been too specific about species and their classification as you will also see in Book Two, as an awful lot of our confusion and misinterpretations of the fossil record has been exactly to do with this very issue that Lamarck warned us about.

Epigenetic Evolution versus the Mutating Gene

Now as indicated above, regarding the support of Lamarckian type evolution according to environmental drivers (now known as epigenetics and is the main discipline that is confirming his central hypothesis of acquired characteristics during one's life time can indeed modify your epigenome and this can be inherited), essentially, Lamarck's concept of speciation via adaptation of the organism under natural laws to their specific environments and needs, is finding a tremendous amount of scientific support whereas, the Neo-Darwinian model is not.

One of the main problems, but certainly not the only issue, with the Neo-Darwinian view of evolutionary processes is that there is a fundamental assumption that genes run the evolutionary show. This effects directly the assumption and therefore the interpretation of the fossil record, in that the concept that the more genetically similar a species: the closer its relationship on the evolutionary tree.

Take for example, broccoli and cabbage. These are assumed to be more closely related based on their shared genes that code for proteins. We are told that as we share 75% of our genes with broccoli and a cabbage (of the 2% that code for proteins) according to our conventional wisdom, that this demonstrates our distance of relatedness on the branches of the Evolutionary (molecular) tree. These branches represent lineage splits from a common ancestor, and when these splits happened are supposed to be measurable using a molecular clock based upon genetic mutations.

Do recall from our discussion thus far, how the genetic code itself may have evolved from a more primary coding and environmentally sensitive epigenetic system, which is underlain not only by liquid crystal fluid dynamics and cells are seemingly quantum and then there is the crystalline nature of the code itself and those related proteins and not forgetting the bonding and chemically firing molecules and how all of this seems to be controlled and order in accordance with universal laws.

In other words, we don't require genetic mutations or natural selection to make the system work and it seems that the Darwinian version isn't quite producing the results one would expect from a molecular clock set according to the presumed timing and evolutionary presumed ancestral links and splits of these genetic mutations in the first place as you will see below:

The rate of DNA evolution: Effects of body size and temperature on the molecular clock

Observations that rates of molecular evolution vary widely within and among lineages have cast doubts on the existence of a single ''molecular clock.'' Differences in the timing of evolutionary events estimated from genetic and fossil evidence have raised further questions about the accuracy of molecular clocks...

Gillooly et al (2005, Abstract)

[138]

You know, the chimp/human split about 5/6 million years ago and out of Africa when Eve was our Mother and when, because of this clock ticking and her mitochondria DNA (which is only passed on along the female line). Then you might ask where does Adam come in? You find him some time later and then it gets really confusing as you probably imagine that Eve must have had virgin births and who begot EVE? The old chicken and egg problem arises. Well, it would appear that the molecular clock is running into some serious issues also as you will see below, with all its crazy fluctuations, it is leaving many more geneticists scratching their heads in puzzlement.

DNA mutation clock proves tough to set: Geneticists meet to work out why the rate of change in the genome is so hard to pin down.

In the past six years, more-direct measurements using 'next-generation' DNA sequencing have come up with quite different estimates. A number of studies have compared entire genomes of parents and their children — and calculated a mutation rate that consistently comes to about half that of the last-common-ancestor method.

A slower molecular clock worked well to harmonize genetic and archaeological estimates for dates of key events in human evolution, such as migrations out of Africa and around the rest of the world... But calculations using the slow clock gave nonsensical results when extended further back in time — positing, for example, that the most recent common ancestor of apes and monkeys could have encountered dinosaurs.

Reluctant to abandon the older numbers completely, many researchers have started hedging their bets in papers, presenting multiple dates for evolutionary events depending on whether mutation is assumed to be fast, slow or somewhere in between.

Callaway (2015, 'Nature' 10th March)

[139]

As we are beginning to realise it is increasingly difficult to show that the genetic similarity of different species can be accurately plotted and pinned onto the molecular tree according to the Neo-Darwinian assumption that evolution happened via genetic mutations – that could only be handed down linearly through direct ancestors, to grandparents and through parents to their offspring, where the fittest varieties survived to pass on the most successful genes.

Does evolutionary theory need a rethink?

We hold that organisms are constructed in development, not simply 'programmed' to develop by genes. Living things do not evolve to fit into pre-existing environments, but co-construct and coevolve with their environments, in the process changing the structure of ecosystems. The number of biologists calling for change in how evolution is conceptualized is growing rapidly. Strong support comes from allied disciplines, particularly developmental biology, but also genomics, epigenetics, ecology and social science...

Laland et al. (2014, 'Nature' 8th October)

[140]

You see, Darwin's species problem (how one species changes into another), remains unresolved as noted in *Resynthesizing Evolutionary and Developmental Biology: "The origin of species – Darwin's problem – remains unsolved"* (Gilbert et al 1996, 361) [141]. And this is in part due to the fact that genetic mutations don't actually account for adaptations as we are told by the modern Darwinists:

Margulis Says She's Not Controversial, She's Right

Neo-Darwinists say that new species emerge when mutations occur and modify an organism. I was taught over and over again that the accumulation of random mutations led to evolutionary change [which] led to new species. I believed it until I looked for evidence.

Teresi (2011, 60: 'Discover Magazine' April Edition)

[142]

Simply put, most scientists, and particularly embryologists at least since Von Baer's time, and prior to the hardening of the Modern Synthesis, knew that the organisms/species were not pre-programmed from the beginning in a preformed way and then simply grew into whatever they are to become, no more than cells containing the same genetics in their nucleus differentiate into completely different organs and systems within the body. Whereas, in modern terms, the Neo-Darwinian model adheres to pre-formation and is overtly anti-epigenetic (Lamarckian) and built upon the assumption that all an organism requires throughout its life and during development, is coded within the genes.

This brings us back to the topic of discussion in Chapter Two as seen in the article excerpt below outlining the direct epigenetic modification as cells divide and structures form.

Epigenetic Regulation of Pluripotency and Differentiation

The precise, temporal order of gene expression during development is critical to ensure proper lineage commitment, cell fate determination, and ultimately, organogenesis. Epigenetic regulation of chromatin structure is fundamental to the activation or repression of genes during embryonic development.

In recent years, there has been an explosion of research relating to various modes of epigenetic regulation, such as DNA methylation, post-translational histone tail modifications, noncoding RNA control of chromatin structure, and nucleosome remodeling.

Technological advances in genome-wide epigenetic profiling and pluripotent stem cell differentiation have been primary drivers for elucidating the epigenetic control of cellular identity during development and nuclear reprogramming. Not only do epigenetic mechanisms regulate transcriptional states in a cell-type–specific manner but also they establish higher order genomic topology and nuclear architecture.

Boland et al (2014, Abstract)

[143]

As I suggested in Chapter Two and Chapter Four, by applying the scaling laws as outlined in Chapter One and indeed, the scaling principle as the overarching pattern of evolution described by Lamarck himself, it would be expected that evidence should emerge to show that if epigenetic processes were involved in the individual programs of the genetically identical eukaryotic stem-cells to give them differentiated identifies, then it should follow that developing or evolving organisms as suggested in Von Baer's model of vertebrates and Lamarck's similar concept, epigenetics should operate on another scale to program, cellularly, the pluripotent-type generalist organisms to become increasingly specialised species and the excerpt above certainly implies that this might be the case.

To support this model, some of the rather radical effects of epigenetic modification according to environmental factors are given below. This should give you an insight into what was possible in the evolutionary past, particularly when organisms were just starting out (non-specialist species) and much more pliable and responsive to environmental conditions.

The excerpt below highlights some of the main characteristics of epigenetic expression of genes and helps explain the differential between the cells, cellular organisms such as mammals that have the same genes being expressed epigenetically according to environmental cues, timing of development etc. In essence, it is obviously not genetics that make different functioning cells and distinct cellular organisms; but rather it is epigenetics that bridges the gap between genotype and phenotype (the gap between genes and what an organism or group of cells looks).

Epigenetic Modifications Regulate Gene Expression

Introduction

Epigenetic research can help explain how cells carrying identical DNA differentiate into different cell types, and how they maintain differentiated cellular states ... Epigenetics is thus considered a bridge between genotype and phenotype ...

Interpretation of Epigenetic Modifications

The hope that completion of the Human Genome Project did reveal some secrets of the genome, but it did not fundamentally alter our perspective on how the expression of genes are regulated as much as initially hoped...

Gene regulation is under the control of multiple influences, ranging from those passed down from each generation, to those responsive to environmental stimuli, and has been recognized as important for genomic function ...

To understand the biological significance of epigenetic markers, it is necessary to identify the distribution of DNA methylation and histone modifications, where they occur (globally or regionally) among different tissue or cell types, and when they occur (normal development or disease processes).

The basic blueprint of epigenetic modification distributions among the genome and across a variety of mammalian cells indicates that genomic features underlie epigenetics.

SABiosciences (2008 'Pathways Magazine', Issue 8)

Recall that it isn't just a case of your genes being unpacked and read and the proteins built according to a fixed set of instructions according to the genetic code, but that it is how these genes are expressed, turned 'on' or 'off' or how the chromosomes are packaged in the cell etc that gives the instructions according to environmental cues, that makes the difference between what a cellular system or a multi-cellular organism look like in the end. This is called the phenotype.

We tend to say that the genotype is what instructs the genotype, but the epigenetic modification of those genes via environmental factors is seemingly implicated in the change and modification of the phenotype itself and it is looking increasingly likely that it is epigenetic modification that is the serious driver of evolutionary change and therefore implicated in the modification of the species as well as you will see as you read on.

I will briefly review some of the evidence below to give you an insight into how genetic mutations are not the drivers of evolutionary modification, but that epigenetic modification and how these factors (environmental drivers) can change how genes are expressed differently without changing the code itself.

Epigenetic Principles of evolution

EVOLUTION BY LOSS

> *The neoDarwinian paradigm sees no other source of that information except mutations affecting the function of genes involved in the development of eyes in the fish, or the increase of the frequency of a preexisting allele (in such a case no new information would be necessary). But there is no evidence for relevant mutations to have occurred in genes related with eye development and there is no evidence that any allele for "eyelessness" existed in epigean forms of Astyanax.*
>
> *On the contrary, experimental evidence shows that all of these genes are functionally normal in both the blind cave fish and its conspecific eyed form. A number of investigators have argued against genetic mechanisms of the loss of eyes in cave fish: …..The fact that the evolutionary change leading to eyelessness in A. mexicanus implies no changes in genes unequivocally tells us that the evolutionary change is transmitted to the offspring by nongenetic means.*

Evolution by Loss cont..,

> *What clearly have occurred in some experimentally determined cases of the loss of structures (loss of limbs in tetrapods, loss of eyes in A. mexicanus, loss of teeth in birds, etc.) are epigenetic changes in expression patterns of specific genes and gene regulatory networks...*
>
> *As an inherited character, the evolutionary loss of eyes … is not genetic, i.e. no changes in genes are involved .., the remaining alternative is that the information for this radical change in morphology is epigenetic. …*

Cabej (2008-2012)

[145]

The epigenetic study alluded to above (but there are many more throughout Cabej's book and we will look at specific studies further on) clearly show how the Neo-Darwinian genetic mutation form of evolutionary change cannot explain real-time changes in species such as loss or gain of limbs, teeth, organs etc, but epigenetic studies can and show categorically that these changes are non-genetic (i.e., the genes don't change to effect these radical trait differences, but epigenetics – the change of gene expression can).

And as also noted by Nelson R. Cabej, in the preface of: *Building the most Complex Structure on Earth: An Epigenetic Narrative of Development and Evolution of Animals*, the definition and implications of epigenetics are broad and far-reaching: "*I include in epigenetics the vast areas of the nongenetic mechanisms of reproduction, growth, cell differentiation, development, and evolution. It is in this broader context that epigenetics promises to be the genetics of the twenty-first century...*" (Cabej 2013, xiii preface) [146].

This section will present a few epigenetic studies that demonstrate quite radical and rapid changes in real-time and present day species that are not related to the change of the genes themselves, just its expression. Epigenetics can also explain the loss of limbs as in lizards becoming snakes, eggs coding for male or female depending upon the temperature. For instance, below are some recent epigenetic studies that demonstrate large and rapid changes within existing species that are affected without changing the genes themselves, just how they are expressed epigenetically.

Note that these experiments do not change one species into another, just their traits and the reason for this is presumably due to the fact that all life on earth has reached that metabolic equilibrium in tune with its environmental niche and therefore has become stabilised as a species – or as Von Baer predicted, they have reached their species maturity (adult) form. However, the epigenetic changes can still be profound and can activate or reactivate earlier ancestral features as you will see further on.

Honey, I shrunk the ants: How environment controls size

By increasing the degree of DNA methylation (a biochemical process that controls the expression of certain genes -- a bit like a dimmer can turn a light up or down) of a gene involved in controlling growth ... they were able to create a spectrum of worker ant sizes despite the lack of genetic difference between one ant and the next. Essentially, the researchers found that the more methylated the gene, the larger the size of the ants...

"We were working with ants, but it was a bit like discovering that we could create shorter or taller human beings."

Mc Gill University (2015 'Science Daily' 11th March)

[147]

There are lots of articles about experiments being carried out relating to developmental environmental temperature directly relating to the outcome of which sex an organism becomes. This is a well-known phenomena in some lizard species and below is an example recently found in certain fish species. The excerpt discusses molecular basis of this change and as you might have worked out: it is an epigenetic phenomenon as indicated in the methylation excretions, where this appears to be powerful enough to override the genetic instructions for (chromosomal-type) sexual determination.

Molecular mechanism links temperature with sex determination in some fish species

A study led by the CSIC's Institute of Marine Sciences, in collaboration with researchers from the Centre for Genomic Regulation (CRG), has found the epigenetic mechanism that links temperature and gonadal sex in fish. High temperature increases DNA methylation of the gonadal aromatase promoter in female.

The environmental temperature has effects on sex determination. There are species, such as the Atlantic silverside fish, whose sex determination depends mainly on temperature. And there are other species whose sex determination is written within its DNA but still temperature can override this genetic 'instruction'.

Centre for Genomic Regulation (2012 'Science Daily' 2nd January)

[148]

Well if epigenetic methylation has the ability to override chromosomes or their equivalent that make you male or female and temperature is the driving force, what else did epigenetic and environmentally-driven factors do to change the traits and characters of an evolving species? The mind boggles at the possibilities. Hopefully you are beginning to see Nature's powerful ability to adapt her species to whatever the weather; and cut her clothe to her measure. Adaptation depending upon which way the wind is blowing, especially when the species is developing in evolutionary time-scales.

Now can you see how a big fish in a small pond may not do very well, but if its eggs spawn a new generation of fish, nature just might shrink them so that they not only survive, but thrive in that same pond as it can do it really quickly. Nature has developed a fairly ingenious way of operating whole swathes of genes during development that works a bit like a master switch.

For instance, Nature has seemingly found an extraordinary way of short-cutting the whole system of genetic expression that are known from the isolated and small gene sets discussed above, by operating whole masses of genes in one fell-swoop during development, akin to master gene switches. This is highlighted in a science article from the University of Washington where the summary explains the role and discovery of millions of DNA switches for genes (these genes are generally referred to as Hox genes and are the master regulators and as you will see below as well as being operated according to epigenetic cues) and operate a bit like master switches for whole armies of genes to be activated during development and how they were, until recently, hidden within the genome as seen in the following:

Millions of DNA switches that power human genome's operating system are discovered

The locations of millions of DNA 'switches' that dictate how, when, and where in the body different genes turn on and off have been identified by a research team led by the University of Washington in Seattle. Genes make up only 2 percent of the human genome and were easy to spot, but the on/off switches controlling those genes were encrypted within the remaining 98 percent of the genome.

Without these switches, called regulatory DNA, genes are inert …

Seiler and Gray (September 5, 2012)

[149]

The above article does not explicitly state the central role of epigenetics in the initial start program for global genetic expression during development, but refer instead to gene regulatory networks, which are essentially epigenetic as discussed previously and it should become clear as you read on, as we know genes are inert without the biochemical switches known as epigenetics. Furthermore, the whole operating system by employing the epigenetic differential expression system akin to master switches, does the initial developmental patterning incredibly efficiently and fast and of course this has implications for evolutionary events of the past as you will see in the epigenetic study below:

Epigenetic control of Hox genes during neurogenesis, development, and disease

Epigenetics refer to changes in gene expression that are inherited through mechanisms other than the underlying DNA sequence, which control cellular morphology and identity. It is currently well accepted that epigenetics play central roles in regulating mammalian development and cellular differentiation by dictating cell fate decisions via regulation of specific genes.

Among these genes are the Hox family members, which are master regulators of embryonic development and stem cell differentiation ... Hox gene expression during development is tightly regulated in a spatiotemporal manner, partly by chromatin structure and epigenetic modifications. Here, we review the impact of different epigenetic mechanisms in development and stem cell differentiation with a clear focus on the regulation of Hox genes.

Barber and Rastegar (2010, Abstract)

[150]

Obviously, this short-cut and rather rapid method that Nature employs is not restricted to mammals; as seen in the role of the epigenetic regulation of Hox genes below, it is a mechanism used by all vertebrates as seen in the following title and excerpt:

Epigenetic regulation of vertebrate Hox genes: a dynamic equilibrium.

Temporal and spatial control of Hox gene expression is essential for correct patterning of many animals.

Soshnikova and Duboule (2009, Abstract)

[151]

The epigenetic differential expression of genes and particularly early on as they are being activated or not activated/expressed or not-expressed, when and to what degree, can have a big impact on what an organism ends up looking like in the end and indeed can shape its entire evolutionary trajectory. So no wonder why looking at the mere 2 to 3% of genes that code for proteins in the entire genome of humans made no sense (how 2 or 2 per cent of genes that code for proteins could account for such differences between species, and what was the other 98 per cent of the genome for?), because we didn't know that these genes were open to interpretation (epigenetic control) and could be expressed in a myriad of different ways.

It also explains how every cell containing the identical code could be different. However, to get the full picture of the other 98% of the proposed junk genes, now known to be functional for the most part and has a great deal to do with evolutionary processes of the past, you will to read to the end of this book to find the answers relating to the whole evolutionary mystery. At least epigenetics begins to fill-in one very critical piece.

For instance, it seems to be differential genetic expression operated according to environmental cues and orchestrated via epigenetic processes, particularly during development (and presumably during evolutionary development of pluripotent-type/generic species prior to becoming specialised) that begins to make much more sense of how so few genes seemingly produced so much variation.

The genes didn't have to change or get passed down specific lines of descent to survive if they just happened to fit in with a particular environment (selection) due to genetic mutations within interbreeding populations of recombined species after a long sojourn as the Neo-Darwinian model would propose. No, it seems that it is the differential expression of a novel exchange of genes (which you will see is the case in the following chapters) that is implicated in species modification.

All in all, it would appear that the epigenetically orchestrated Hox gene complex is not only implicated in the fast-track and highly accurate and orchestrated patterning of cells and organism during Morphogenesis, but on another scale, it is implicated in the rapid and highly orchestrated evolution of the species itself. The summary of Cabej's book describes the epigenetic role in this genetic toolkit as follows:

Building the most complex structures on Earth...

> *This is a novel theory that describes the epigenetic mechanisms of the development and evolution of animals and explains the colossal evolution and diversification of animals from a new post-genetic perspective. Modern biology has demonstrated the existence of a common genetic toolkit in the animal kingdom, but neither the number of genes nor the evolution of new genes is responsible for the development and evolution of animals. The failure to understand how the same genetic toolkit is used to produce millions of widely different animal forms remains a perplexing conundrum in modern biology. The novel theory shows that the development and evolution of the animal kingdom are functions of epigenetic mechanisms, which are the competent users of the genetic toolkit.*

Cabej (2013, Synopsis of book)

[152]

The answer of course, according to Cabej's research is that the hox complexes are genetic switches and are essential for the activation of the initial body patterns during development and that these are ultimately controlled and guided via epigenetic processes operating above the genes themselves, and act as controllers of the master genetic switches of these body plans (or differential cellular programs. Recall the discussion of Alan Turin's theory of the Chemical basis of Morphogenesis outlined in Chapter Two and the cellular sensitivity, cellular memory and the biochemical switching?

From these studies, it would appear that epigenetic expression of genes driven via environmental factors (context, particularly during development) is the controller of the operating system, once the initial stage of development begins to show the different expression or regulation of undifferentiated cells and their identical nuclear coding (DNA).

The following excerpt does not explicitly state the epigenetic control of these Hox genes. Although, I do hope it is now clear or will be after reading all the material on the matter, that this is an epigenetic-driven phenomenon, not a genetically-driven one. It is epigenetic processes that operate the genes, not the other way around. Anyway, bearing this in mind, below is a very solid example of just what these Hox complexes can end up expressing or not, in the following interesting example of the evolutionary history of how the snake lost its legs:

Hox Genes: Descent with Modification

Why snakes don't have legs

One of the most radical alterations of the vertebrate body plan is seen in the snakes. Snakes evolved from lizards, and they appear to have lost their legs in a two-step process. Both paleontological and embryological evidence supports the view that snakes first lost their forelimbs and later lost their hindlimbs ... Fossil snakes with hindlimbs, but no forelimbs, have been found.

Moreover, while the most derived snakes (such as vipers) are completely limbless, more primitive snakes (such as boas and pythons) have pelvic girdles and rudimentary femurs. The missing forelimbs can be explained by the Hox expression pattern in the anterior portion of the snake. In most vertebrates, the forelimb forms just anterior to the most anterior expression domain of Hoxc-6 ...

Gilbert (2000, Why Snakes don’t have legs)

[153]

An Alternative Evolutionary Model for the Evolution of the Species Begins to Emerge

Epigenetics processes acting upon the genomes of various organisms, not only begins to account for the dramatic and rapid formation of fundamental 'principal types', epigenetic evolution also appears to be responsible for the great variation of forms of these fundamental themes, as it acts via differential genetic expression of these fundamental forms throughout the life span of a species, albeit perhaps in a less dramatic way as the species become more mature, they presumably stabilise according to the Sigmoidal growth law – the universal pattern of 'lag', 'exponential' and 'stabilised' growth pattern that every living thing seems to abide by, so why should this same universal growth and development pattern – the Sigmoidal equation, not apply to the tempo and patterning of evolution of the species itself?

For instance, by applying the natural universal scaling laws of growth and form advocated by D'Arcy Thompson as the laws of Nature that drive the biological systems to complexity (observed by Lamarck) and indeed, via environmental and natural process ultimately would appear to inform the patterning expressed via epigenetic/genetic systems as indicated in Turing's chemical basis of cellular differentiation and pattern, form and function of the cells and organisms, which as we now know has an epigenetic explanation.

This system would appear to be underpinned by the processes offered in the model of the origin of the code of life within the cells proposed by Cairns-Smith in terms of patterned and self-organising crystalline systems emerging in the inorganic world (following a natural order from inorganic organising principles to organic and highly ordered life as proposed in Lamarck's model).

We can now begin to see the fundamental observations of both Von Baer and Lamarck with their different focuses of scale: embryological development within its epigenetic environment and the development of the species within its evolutionary environment emerge as self-similar scales of complexity, giving us an overarching model describable in terms of the Matryoshka (nested dolls) principle.

If as Von-Baer, proposed, the development of an organism follows the development (evolution) of the species on another scale, why not apply this scaling principle to the epigenetic-environmentally-driven form of evolutionary development of the species as proposed in Lamarck's model we now have the means for the species to evolve rather rapidly and profoundly that could account for an exponential phase as the application on an evolutionary scale of the Sigmoidal growth curve would accommodate.

The continuation and fine-tuning (at a micro-evolutionary level of development) of all this epigenetic variation in gene expression is clearly seen as ongoing, as exemplified within to-day's species as everything seems to have settled down and become relatively stable due to the fact that we don't typically see modern species becoming a different species these days.

This natural system of scale; driven and tending to increasing complexity and continual order, is certainly being well supported by the emerging evidence. This dovetails very well with Lamarck's overall epigenetically-driven evolutionary theory tending to increased perfection and driven by natural laws of development and form. It would seem that a fairly distinct evolutionary pattern is emerging when we assess these seemingly disparate and often historically obscured evolutionary concepts collectively.

The overarching pattern is one of scale and seemingly driven by efficiency requirements in the intimate interplay between an organism (particularly a developing one) and its environment. Everything is context dependent, where epigenetic factors operating above, over and upon the genetic code is the key to orchestrating in a meaningful way, the outcome of an organism's development and its final stabilised species form. However, as you will see in the chapters that follow, the genetic story is a much more fascinating one than we have previously understood. It has profound implications for how we now view the Neo-Darwinian genetic tree of life as well and it has given the epigenetic process something rather novel to work with in the process.

CHAPTER SIX

Hugo De Vries

(1848 – 1935)

LEAPS of EVOLUTIONARY NOVELTY – via HYBRIDATION?

Hugo De Vries a Dutch botanist and early pioneer of genetics, co-re-discoverer of Mendel's Laws of Inheritance proposed a very different form of mutation to the form of random mutation and gradual selection proposed in our current model of Darwinian evolution (De Vries 1914) [154]. He instead used the concept of mutation to mean that a whole species could be remodelled and as it turned out: via hybridisation in one fell-swoop, De Vries' observation and theory formulated from his research is turning out to be quite accurate.

For instance, an important means of speciation is emerging particularly in hybrid studies where the duplication of whole chromosomes and the rearrangement of genomes along with epigenetic processes that can silence/activate and expression of those genes is becoming a very powerful candidate for past evolutionary change as you will see shortly.

De Vries' research and Mutation model of evolution was based upon years of experimentation with hybrid plant species, and observations of: *"..., spontaneous alterations of genes that yield large modifications of the organism and give rise to new species. According to de Vries, a new species originates suddenly, produced by the existing one without any visible preparation and without transition"*. Ayala and Fitch (1997, 7692) [155].

In a nut shell: De Vries' theory and several other distinctly different theories, rejected gradualism and the idea of selection. For De Vries, gradualism was certainly not the way nature produced species, as borne out by his years of studies and experiments. Furthermore, he argued that natural selection did not have the power to produce new and novel variations and in some cases was actually detrimental to evolving a new species. This is clearly documented in the review of De Vries' Mutation Theory in the journal SCIENCE dating back to 1910:

Review of Hugo De Vries' Mutation Theory

1910

It has long been recognized that natural selection really explains, not the origin of species, nor even the origin of adaptations, but the elimination of the unfit, and the persistence of adaptations; the fact that characters, both adaptive and non-adaptive, specific or not specific, must exist before they can be selected was previously well nigh lost sight of.

The mutation-theory, then, seeks to account for "the origin of specific characters" (p. 211). In the second place, " Spontaneous variations are the facts on which this explanation is based" (p. 45), or, "We may express the essence of the mutation theory in the words: 'Species have arisen after the manner of so-called spontaneous variations'" (p. 165). This marks the fundamental distinction between Darwinism and de Vriesism. ... from the standpoint of the theory of mutation it is clear that the role played by natural selection in the origin of species is a destructive, and not a constructive one." ...

Mutations are characterized first, by being entirely new features, "In contradistinction to fluctuating variations which are merely of a plus or minus character (p. 213); second, by the abruptness with which they appear, and third, by being transmitted by inheritance' without selection. They arise suddenly and' without any obvious cause; they increase and multiply because the new characters are inherited"

Gager (1910, 741)

[156]

Our modern synthesis has consistently rejected leaps in complexity as a real fact of the fossil record, but they did manage somehow to assimilate mutation into their doctrine, even if it now meant gradualistic, random genetic mutation. Even after the well-founded rejections of gradualism and selection in relation to speciation by De Vries and other geneticists, botanists, embryologists and via experimental work in general around the turn of the 20th century, the modern synthesis eventually came to reject all things non-selection-based and certainly would not tolerate anything that suggested leaps of speciation, or anything that was environmentally determined (Lamarckian type acquired characteristics) as discussed in the previous two chapters in particular.

De Vries and many others before and after his time, had problems with the Darwinian concept of gradualism and selection, and indeed, even within the ranks of true Darwinians who adhered to Darwin's original concepts that are perceived as less rigid than the gene-centred model upheld by Darwinists such as Richard Dawkins, there has been some controversy regarding gradualism and even the strictest form of selection.

For instance, attempts to address the obvious gaps and lack of transitional forms and sudden eruption of new and novel forms of species within the fossil record, led to a theory based around stasis (meaning stability, presumably as an attempt to keep it broadly within the Darwinian tradition) with the occasionally leaps (punctuated parts) proposed in the 1970s Gould and Eldredge known as the punctuated equilibria model of evolution where environmental factors were considered important to these occasional punctuated parts. This was, and still is, a seriously tame version of De Vriesian evolution, but just to give you an insight into the manner in which this was considered as part of the Neo-Darwinian synthesis, which it was, but it was referred to by Richard Dawkins in the following from his book *The Blind Watchmaker:*

The Blind Watchmaker

The theory of punctuated equilibrium will come to be seen in proportion, as an interesting but minor wrinkle on the surface of neo-Darwinian theory.

It certainly provides no basis for any 'lapse in neo-Darwinian morale', and no basis whatever for Gould to claim that the synthetic theory (another name for neo-Darwinism) 'is effectively dead'.

It is as if the discovery that the Earth is not a perfect sphere but a slightly flattened spheroid were given banner treatment under the headline: COPERNICUS WRONG. FLAT EARTH THEORY VINDICATED.

Dawkins (1986, 254-255)

This rejection of anything other than gradualism is somewhat irrational, I believe, in the light of the well established arguments for the leaping nature of the fossil record and from what could be observed via embryological studies; these giant leaps in whole complexity are certainly more than a wrinkle and these major monumental speciation events had been long understood by many evolutionary scientists, especially anyone working on hybridisation with plants and anyone working in embryology in particular, if they were paying attention.

Recall that in the previous chapter, I outlined a broad range of epigenetic studies, mainly within botany where, many scientists were experimenting with hybrids, but with the added dimension of studying environmentally-driven (non-direct genetic) effects. Furthermore, our present emerging understanding of the molecular mechanisms that can bring about profound leaps of complexity that have been identified via many recent studies can no longer be ignored for hybridisation as a means of speciation and epigenetic factors that seemingly guide the adaptive traits of those novel eruptions.

It is important, perhaps to point out, that De Vries was not particularly of a Lamarckian/epigenetic school of thought, as his focus was more on the emerging field of genetics. However, De Vries was fully aware from observational/experimental studies from his own research and that of a wide range of experimental horticulturalists and botanists from all over Europe at the time, that rapid and often, profound variations within species could occur and that these changes could be maintained via further breeding. These observations led to his Mutation theory.

The embryologists were not able to demonstrate such dramatic results as plants of course, but nevertheless, many understood from the non-genetically determined and rapid ordering of development and the precision of cellular differentiation to a fully-functioning and perfectly adapted organism, that environment did somehow drive evolutionary development and it was anything but gradual and many did not view, selection, as a creative force in bringing about new variations that could lead to a different species.

De Vries was therefore, not alone in his objections to gradualism and selection. He simply did not see how selection would produce novelty in the first place for it to act upon and he certainly rejected gradualism as noted above. However, he was not entirely sure what the ultimate cause of the experimental breeding, which on occasion - could produce such novel results. It is only in more recent years that the answer in part (as we now have to consider the role epigenetics and environment acting upon the genetic aspects of species variation as well), is beginning to emerge as seen in the following excerpt.

Roles of Mutation and Selection in Speciation: From Hugo de Vries to the Modern Genomic Era

In the history of evolutionary biology, Hugo de Vries is known as a proponent of the mutation theory of evolution, in which new species are believed to arise by single mutational events ... This theory is based on the breeding experiment he conducted for 13 years with the evening primrose Oenothera lamarckiana and its mutant descendants. In this experiment, he discovered a number of phenotypic variants, which bred true or segregated variant types in addition to the parental type...he unknowingly found the importance of polyploidy and chromosomal rearrangements in plant speciation.

Nei and Nozawa (2011)

[158]

Yes, isn't it interesting that the plant species he was working on was called after Lamarck. And of course, we can begin to see how the meaning of mutation has evolved to now mean gradually accumulating/random genetic copying mistakes, rather than its traditional meaning to: morph/transmutation from one form to another in a single generation. Below is a brief explanation of what is meant by polyploidy and genome rearrangement and how common it would appear to actually be amongst a diverse range of species (which of course has implications for how we should investigate and interpret evolutionary events of the past). This article excerpt should hopefully also help to explain what De Vries unknowingly discovered and place it within the context of the all-important epigenetic aspect of adaptive evolution:

Mechanisms of genomic rearrangements and gene expression changes in plant polyploids

Polyploidy is produced by multiplication of a single genome (autopolyploid) or combination of two or more divergent genomes (allopolyploid)...

Polyploidy and its forms

Polyploidy occurs throughout the evolutionary history of all eukaryotes, ... predominately in flowering plants ... including many important agricultural crops... Compared to plants, polyploidy occurs rarely in animals, but clearly exists in some invertebrates (e.g. insects) and vertebrates (e.g. fish, amphibians and reptiles)...

Allopolyploidy provides a unique system for study of the mechanisms for reestablishing functional biological pathways via genetic and epigenetic interactions between evolutionarily divergent genomes, orthologous genes and their products, and divergent regulatory networks. ...The underlying genetic and epigenetic mechanisms for these dynamic changes observed in the polyploids may be intricately related ... The genomic and gene expression data documented in the last decade have provided new insights into the many evolutionary and mechanistic questions that have been posed by polyploidy...

Chen and Ni (2006, Summary & Conclusion)

As intrinsically linked as seemingly genetics (polyploidy hybrids) and epigenetics are, the Neo-Darwinists rejected both. For instance, the main Neo-Darwinian of the Modern Synthesis who represented the botany aspect is quoted below regarding his views on the polyploidy in respect of genetic evolution:

Rapid and dynamic changes in genome structure in synthetic allopolyploids

Stebbins (1971) concluded "multiplication of chromosome sets either has little effect upon evolutionary progress at the gene level, or actually tends to retard it". However, molecular evidence suggests polyploid genomes display dynamic and pervasive changes in DNA sequence and gene expression...

Chen and Ni (2006)

[160]

And below is the traditional Neo-Darwinian rejection of hybridisation and multiplication of genomes/or rearrangements (producing polyploids) once again as highlighted in a recent science paper regarding the views of and influence of one of the leading Neo-Darwinists – Ernst Mayr:

A Century of Evolution: Ernst Mayr (1904–2005)

Mayr's view of Darwin: was Darwin wrong about speciation?

Mayr ... rejected any idea that hybridization might contribute to adaptive evolution, especially hybrid speciation. Furthermore, because in 1942 he was concerned only with animal speciation, and animal chromosomes were still poorly known, he was able to argue that speciation by any sort of polyploidy was in essence absent

Mallet (2008, 13)

[161]

Essentially, an increasing amount of evidence is emerging, due to our more sophisticated ways to probe such questions of past hybridisations and multiplying genomes, to strongly suggest that hybrid breeding across a diverse plethora of species means, that we can no longer ignore the possibility of some of the marvelous results that may have erupted from such matings in the evolutionary past as suggested in the excerpt below:

HYBRIDS MAY THRIVE WHERE PARENTS FEAR TO TREAD

DNA analysis is now allowing biologists to better decipher the histories of species and to detect past hybridisation events that have contributed new genes and capabilities to various kinds of organisms including, it now appears, ourselves...

The discovery of hybrid species and the detection of past hybridizations are forcing biologists to reshape their picture of species as independent units. The barriers between species are not necessarily vast, unbridgeable chasms; sometimes they get crossed with marvelous results.

Carroll (2010 'New York Times' 13th September Issue)

[162]

This increasing body of evidence for widespread hybridisation within all scales of animal life (both vertebrate and invertebrates – including ourselves) and their unexpected similarities (genetically-speaking) means that we should look again at hybridisation/polyploidy as an important contributor to speciation as indicated in the excerpt below:

ORIGIN & EVOLUTION of ANIMAL HYBRID SPECIES

The increasing number of hybrid species, discovered in both vertebrates and invertebrates ..., calls for a reevaluation of hybrid speciation and reticulate evolution in animals... Unexpected similarities are now apparent in hybrid evolution of animals as varied as insects, snails, fish, frogs and lizards.

Bullini (1994, Abstract)

[163]

Basically, if we are assuming that the more similar the gene sequence: the more related on the ancestral tree and the closer the ancestral split measured in molecular time (which doesn't work anyway), then, we may have to fundamentally re-think this assumption in the light of seemingly common polyploidy and hybridisation events crossing what were believed to be impassable species barriers. (Recall that even lizards can end up as snakes if, they don't epigenetically activate certain Hox sequence genes during development).

Essentially, what is proposed here, based upon the culminating evidence is that genetic and chromosome (genome rearrangements etc) exchanged between developing species (not specialised/developing species or species in making) created the genetic novelty from which epigenetics could act upon creatively (abiding by the universal laws of growth and form), to adapt the various species to their specific and specialised environments and conditions of existence. Even as far back as over 200 years ago the importance of hybridisation as a factor in shaping the species was discussed by Jean Baptiste Lamarck as a fairly rational explanation to account for much of the variations within the species, along with environmentally-driven adaption of these novel forms as indicated in the excerpt below:

1809

- Jean-Baptiste Lamarck -

'Zoological Philosophy...'

The idea of bringing together under the name of species a collection of like individuals, which perpetuate themselves unchanged by reproduction and are as old as nature, involved the assumption that the individuals of one species could not unite in reproductive acts with individuals of another species. Unfortunately, observation has proved and continues every day to prove that this assumption is unwarranted; for the hybrids so common among plants, and the copulations so often noticed between animals of very different species, disclose the fact that the boundaries between these alleged constant species are not so impassable as had been imagined.

Lamarck (1809, 39)

CHAPTER SEVEN

Carl Woese

(1928 –2012)

THE WORLD WIDE WEB (WWW.HGT) LITTLE HYBRIDS GET EVERYWHERE

The Man who rewrote the tree of life

Carl Woese may be the greatest scientist you've never heard of. "Woese is to biology what Einstein is to physics," says Norman Pace, a microbiologist at the University of Colorado, Boulder. A physicist-turned-microbiologist, Woese specialized in the fundamental molecules of life – nucleic acids – but his ambitions were hardly microscopic. He wanted to create a family tree of all life on Earth.

Arnolds (2014)

[165]

Carl Woese (American microbiologist and biophysicist) is perhaps best known for defining a new domain of life known as Archaea. In the 1970s, he pioneered a technique that revolutionised the field of microbiology. But most importantly, he redefined the tree of life as a web showing that genetically, domains of microbial life was teeming with little hybrids. Or what has been referred to as genetic material transferred across all domains of fungi, bacteria etc known as HGT (horizontal gene transfer).

But as it turns out, HGT is much more rampant within and between even the so-called higher domains of life as you will see further on and of course this has implications for the entire tree and as discussed in the previous chapter, hybridisation is rather common too and in principle, hybridisation is simply a less primitive and less direct means of genetic transfer. This is indicative of Nature operating on scales of self-similar replication patterns on every scale.

Indeed, perhaps Woese did more than he realised when he rewrote the tree of life, as if we apply the scaling principle (Matryoshka concept) to evolutionary development, as it life and evolutionary development does appear to work in self-similar and repeating patterns at every scale, then we may need to reassess this entire ancestral common descent model from the ground up, right to the outer branches and its very tips. The evidence would strongly suggest that the ancestral tree is more like a web (I would suggest a fractal tree/forest and its entire life-supporting eco-system) and it may have had many roots and that those roots are not actually entities, but more a commonly shared condition as you will see below.

PATTERN PLURALISM AND THE TREE OF LIFE HYPOTHESIS

...inclusively hierarchical pattern of relationships between all organisms based on their similarities and differences [the Tree of Life (TOL)] was a fact of nature, for which evolution, and in particular a branching process of descent with modification, was the explanation.

However, there is no independent evidence that the natural order is an inclusive hierarchy, and incorporation of prokaryotes into the TOL is especially problematic…

Doolittle and Bapteste (2007, Abstract)

[166]

As indicated in the above except and discussed in the previous chapter and alluded to in others, the whole genetic mutation assumption upon which we build our molecular trees and use to determine relatedness in genetic terms (the closer the genetic similarity: the closer the evolutionary relatedness), doesn't actually be appearing to work and there are much better answers emerging within science to show that there are other means by which evolutionary complexity may have erupted and/or unfolded.

And in particular, the emerging understanding of the prolific exchange of genes across, within and between the earlier microbial world have major implications for macro life along with the regular chromosomal rearrangements/polyploidy and the frequency of genetic exchange via hybridisation now emerging within the most complex organisms such as ourselves. These are just some of the factors, along with the quantum nature of Nature and the epigenetic adaptations according to universal scaling laws, which force us to fundamentally reassess the very foundations of the ancestral tree itself.

This leads naturally to the discoveries of Woese and others who have assessed the earlier tree of life and its actual roots. It would seem that life having emerged from a single or few origins as Darwin and the later Neo-Darwinists proposed and giving rise to all the species thereafter may be fundamentally flawed in the first place as an increasing body of evidence has emerged from the research of Woese and others strongly suggests. The following excerpts suggest this to be the case:

A FUNDAMENTALLY NEW PERSPECTIVE ON THE ORIGIN AND EVOLUTION

Darwin's hypothesis that all extant life forms are descendants of a last common ancestor cell and diversification of life forms results from gradual mutation plus natural selection represents a mainstream view that has influenced biology and even society for over a century. However, this Darwinian view on life is contradicted by many observations and lacks a plausible physico-chemical explanation. Strong evidence suggests that the common ancestor cell hypothesis is the most fundamental flaw of Darwinism…

Liu (2008, Abstract)

[167]

THE CONCEPT OF MONOPHYLY: A SPECULATIVE ESSAY

Recent research results make it seem improbable that there could have been single basal forms for many of the highest categories of evolutionary differentiation (kingdoms, phyla, classes). The universal tree of life probably had many roots.

Gordon (1999, Abstract, 331)

[168}

THE UNIVERSAL ANCESTOR

The universal ancestor is not an entity, not a thing.

It is a process characteristic of a particular evolutionary stage.

Woese (1998, Conclusion)

[169]

These statements begin to echo the idea of many origins proposed by D'Arcy Thompson discussed in Chapter One of this book and the ideas of Von Baer where the developing embryo reflects the stages of a species own evolutionary pattern, where some studies have shown independent origins of brain types for example (Butler's Brain study alluded to earlier) where it is strongly suggested that we should understand species evolution in terms of sharing a common ancestral condition rather than trying to trace our genetics and fixed traits back to a single or a few actual living common ancestors and also consider the growing body of evidence for independent evolutionary originations.

The Tiny World of Hybrids Scales Up to the Macro-World

As noted above, another integral part of Woese's research and his attempt to re-write the evolutionary tree of life, at least for microbial-type life and perhaps the beginning of the eukaryotes (the cellular basis of fungi, plants and animals for example) was the discovery of the ubiquitous transfer of the genetic material across these major domains of life known as horizontal gene transfer (HGT) which sets it apart from the more common form of hybridisation known as vertical gene transfer (VGT). However, these forms of genetic transfer are essentially the same, just on different scales. The means of transfer may be different (one more direct than the other), but the result is the same: Novel genetic transfer which creates a means for species change and adaptation.

Digging Down Below the Tree of Life

Evolving evolution

The late Carl Woese, ... was one of the first scientists to propose that early life leaned heavily on horizontal gene transfer...He is perhaps best-remembered for classifying life into the now-well-accepted domains of bacteria, eukaryotes (plants, animals, fungi and protists) and archaea. Nigel Goldenfeld of the University of Illinois at Urbana-Champaign is leading a new NASA Astrobiology Institute team that aims to understand how evolution works before there were species or even genes...

In 1987, Woese wrote about the consequences of rampant horizontal gene transfer. In such a scenario, "a bacterium would not actually have a history in its own right: it would be an evolutionary chimera."

A "chimera" is the name of a creature from Greek mythology that mixed together features of a lion, a goat and a snake....

Schirber (2013, 'Astrobiology Magazine' 28th March)

[170]

I left in the piece about NASA as it highlights the importance of trying to understand what an organism is before we classify it as a genetically-related species and by trying to understand their ancestral condition in terms of ancient chimera's (as suggested by Woese's research on HGT), we may begin to get past the 'Genes R Us' type of thinking. As E.V. Koonin points out in his paper in the following:

Carl Woese's vision of cellular evolution and the domains of life

Woese's key prediction that understanding evolution of microbes will be the core of the new evolutionary biology appears to be materializing.

Koonin (2014 Abstract)

[171]

For instance, when we go outside the microbial, bacterial and tiny world of amoebas, we come to the world of complex cellular life with DNA embedded within the nucleus of the cell and the multi-cellular world of incredibly complex animals and plants known as eukaryotes of the multi-cellular variety.

HORIZONTAL GENE ACQUISITIONS BY EUKARYOTES AS DRIVERS OF ADAPTIVE EVOLUTION

In contrast to vertical gene transfer from parent to offspring, horizontal (or lateral) gene transfer moves genetic information between different species. Bacteria and archaea often adapt through horizontal gene transfer.

Recent analyses indicate that eukaryotic genomes, too, have acquired numerous genes via horizontal transfer from prokaryotes and other lineages. Based on this we raise the hypothesis that horizontally acquired genes may have contributed more to adaptive evolution of eukaryotes than previously assumed.

Current candidate sets of horizontally acquired eukaryotic genes may just be the tip of an iceberg.

Schönknecht et al (2013, Abstract)

[172]

As suggested above, from the emerging evidence it would now appear that even eukaryotes have acquired numerous genes via horizontal gene transfer also and this of course requires a new understanding of the process of evolution and ancestral relatedness. This will be discussed in more detail in the following chapter and again in broader evolutionary terms in the final chapter of this book.

Digging Down Below the Tree of Life

The "tree of life," divided between major cell types, those with a nucleus (eukaryotes) and without a nucleus (prokaryotes: the bacteria and archaea).

...Some evidence suggests that early evolution may have been based on a collective sharing of genes...

...If every snippet of DNA was solely the product of descent with modification, then every organism could be placed on a tree of life stemming from a single ancestor. But as it turns out, "different genes go back to different ancestors," says Peter Gogarten of the University of Connecticut, who has done extensive work on comparative genetics. How is that possible? It can happen if organisms share genes. Imagine a gene belonging to members of a specific family tree. One day this gene becomes isolated and gets picked up by another organism with a different family tree. No reproduction between partners takes place – only an "adoption" of a specific gene.

This so-called "horizontal gene transfer" is quite common among bacteria and archaea, as exemplified by antibiotic resistance. When a specific bacterium develops a defense against some drug, the corresponding gene can pass horizontally to others in the same colony.

.Schirber (2013)

[173]

As noted above in the excerpt, bacteria seem to use horizontal gene transfer to adapt and become drug resistant, but, as they obviously adapt in a meaningful way, we should consider the important role of epigenetics in orchestrating this. This interplay between HGT, bacterial-like behaviour and epigenetics in response to environmental factors will be outlined in more detail in the final chapter of this book.

Once again we may be looking at shared strategies and ancestral conditions that were significant in helping everything evolve and adapt according to its conditions of existence and as the excerpt below suggests: even a portion of our own genes were donated courtesy of bacteria. So perhaps, these clever little rapid response teams are not that bad after all as it seems that we live in a symbiotic relationship to bacteria and without the little critters living in our guts or our atmosphere: live as we know it wouldn't even be here. Well, we might have lots of viruses and bacteria. But that would be all.

The Human Genome Race

A tale of the Tortoise and the Hare... and the fly and the worm and the mouse

Soon after the Human Genome Project published its preliminary results in 2001, a group of scientists announced that a handful of human genes – the consensus today is around 40 – appear to be bacterial in origin. The question that remains, however, is how exactly they got there. ….

Karow (2000, 'Scientific America' April 24th Edition)

[174]

Again, we will return to these clever bacteria and bacterial-like behaviours in the next chapter and within the last one also. The answer to the question of how the bacteria got there and why we are seemingly so full of so-called junk genes in the first place is explicable if we understand that primitive bacteria or viral forms are symbiotically part of us from the ground-up, so-to-speak. However, in terms of their own individual evolutionary development, they are presently fully specialised species and presumable became as complex as they had the intrinsic metabolic means to become. In other words, bacteria remained essentially as bacteria (perhaps because they stabilised as fully efficient organisms and had reached their own particular plateaux of their development on the stabilisation phase of the Sigmoidal growth curve?)

Bacteria, we will assume, didn’t directly evolve into two-legged smart and upright creatures, but as we apply the self-similar and nested scales of complexity model, we can begin to see how at a cellular level, bacterial reproduction and their ability to cooperate as colonies of cells and adapt to changing environments is very similar to the highly orchestrated cellular differentiation phase prior to embryo development. In other words, early developmental stages may reflect on an evolutionary scale, early primordial cellular organisational strategies – a shared common ancestral strategy; this concept will be further explored in terms of the evidence in the next chapter, in the meantime, we’ll look at a few more examples of these novel genetic exchanges via Horizontal Gene Transfer and discover why we simply cannot continue to use our current simplistic and highly linear evolutionary model of common descent.

Space Invader DNA jumped across mammalian genomes

..."horizontal gene transfer" has been largely viewed as a trademark of single-celled organisms, with few examples among animals and plants. That is, until now.

A group of American researchers have discovered a group of genetic sequences that have clearly jumped around the genomes of several mammals, one reptile and one amphibian. It's the most dramatic example yet that horizontal genetic transfer outside of the bacterial realm is more common than we thought, and has helped to shape the evolution of animals. Meet the Space Invaders, genetic hitchhikers coming soon to a genome near you.

John Pace from the University of Texas originally discovered the sequences he named Space Invaders (or SPIN elements) by looking at the genome of a small primate called a bushbaby. He was searching for transposons, a group of parasitic DNA sequences that can cut themselves out of genomes and jump to new locations of their own accord. One sequence in particular stood out and Pace searched for it in all other vertebrates whose full genomes have been sequenced.

To his surprise, he found a large number of matches among the DNA of seven very distantly related species – the green anole (a lizard), African clawed frog, little brown bat, mouse, rat, opossum and tenrec , a small animal that looks like a hedgehog but is more closely related to elephants, manatees and aardvarks...

While these animals come from very diverse lineages, their SPIN sequences were incredibly similar; compare those of any two species and you'd get an average match of 96%. That is a remarkable resemblance; even genes for some of the most vital, unchanging proteins within the vertebrate repertoire aren't that similar between different species.

The widespread but patchy distribution of SPIN sequences means that it is extremely unlikely that the seven species inherited these sequences from the same common ancestor.

Yong (2008, November 3rd, 'Phenomena- Blog on National Geographic' forum)

As you can perhaps begin to appreciate also, hybridisation in any form, whether chimeras, or other experimental expressions of novel genetic transferences (hybridisation on a more microbial scale and seemingly across even larger scales of life, albeit via microbial type hitchhikers riding on the vertically transferred genomes), does muddy the waters regarding our entire evolutionary tree, never mind its root.

How a quarter of the cow genome came from snakes

> *Genomes are often described as recipe books for living things. If that's the case, many of them badly need an editor. For example, around half of the human genome is made up of bits of DNA that have copied themselves and jumped around, creating vast tracts of repetitive sequences. The same is true for the cow genome, where one particular piece of DNA, known as BovB, has run amok. It's there in its thousands. Around a quarter of a cow's DNA is made of BovB sequences or their descendants.*
>
> *BovB isn't restricted to cows. If you look for it in other animals, as Ali Morton Walsh from the University of Adelaide did, you'll find it in elephants, horses, and platypuses. It lurks among the DNA of skinks and geckos, pythons and seasnakes. It's there in purple sea urchin, the silkworm and the zebrafish.*
>
> *The obvious interpretation is that BovB was present in the ancestor of all of these animals, and stayed in their genomes as they diversified. If that's the case, then closely related species should have more similar versions of BovB. The cow version should be very similar to that in sheep, slightly less similar to those in elephants and platypuses, and much less similar to those in snakes and lizards.*
>
> *But not so. If you draw BovB's family tree, it looks like you've entered a bizarre parallel universe where cows are more closely related to snakes than to elephants, and where one gecko is more closely related to horses than to other lizards.*
>
> *This is because BovB isn't neatly passed down from parent to offspring, as most pieces of animal DNA are. This jumping gene not only hops around genomes, but between them.*
>
> *This type of "horizontal gene transfer" (HGT) is an everyday event for bacteria, which can quickly pick up important abilities from each other by swapping DNA. Such trades are supposedly much rarer among more complex living things, but every passing year brings new examples of HGT among animals. For example, in 2008, Cedric Feschotte (now at the University of Utah) discovered a group of sequences that have jumped between several mammals, an anole lizard, and a frog. He called them Space Invaders.*

Yong (2013, 1st January 'Phenomena- Blog on National Geographic' forum)

Below is an example that really illustrates the point regarding how distinct species can end up with sequences (genetic) that are common to both, yet could not possibly be anywhere near closely related and look nothing whatsoever like one another:

COWS ARE 25 PERCENT SNAKE

> *You vaguely know how DNA works, right? You get it from your parents. Well, hold onto your britches, because scientists from down under are about to turn your world upside down. A study by Australia's Adelaide and Flinders Universities and the South Australian Museum has found that in complex organisms, DNA is not only transferred from a parent to its offspring like your science book told you, but can also be "laterally" transferred between species. The research, published in the peer-reviewed Proceedings of the National Academy of Sciences in the US, involved comparing dozens of DNA sequences from different species. It found that cows inherited up to a quarter their genes from reptiles...*

Eichelberger (2013 'Mother Jones.com', 3rd January Edition)

[177]

The main point being: we cannot use genes directly to establish genetic relatedness on the assumed ancestral evolutionary tree and when we consider that whole genomes can be remodelled via jumping genes (HGT) or genes that jump around, not just between species but, within the genome that have bacterial/viral-like behaviours, which will be discussed in the final chapter of this book, then this really does render our current linear descent model from direct mature ancestral species somewhat useless.

CHAPTER EIGHT

Lynn Margulis

(1938-2011)

MICRO MERGERS AND SYMBIOSIS

Lynn Margulis - Biography

Throughout most of her career, Margulis was considered a radical by peers who pursued traditional Darwinian "survival of the fittest" approaches to biology. Her ideas, which focused on symbiosis – a living arrangement of two different organisms in an association that can be either beneficial or unfavourable – were frequently greeted with skepticism and even hostility.

Among her most important work was the development of the serial endosymbiotic theory (SET) of the origin of cells, which posits that eukaryotic cells (cells with nuclei) evolved from the symbiotic merger of nonnucleated bacteria that had previously existed independently. In this theory, mitochondria and chloroplasts, two major organelles of eukaryotic cells, are descendants of once free-living bacterial species.

...Margulis was elected to the National Academy of Sciences in 1983 and was one of three American members of the Russian Academy of Natural Sciences. She was awarded the William Procter Prize of Sigma Xi, an international research society, and the U.S. National Medal of Science in 1999. In 2008 she received the Darwin-Wallace Medal of the Linnean Society of London.

Tao (2015)

[178]

As indicated above, American evolutionary theorist, micro-biologist, geneticist and zoologist, Lynn Margulis did eventually become recognised for her significant contributions to evolutionary biology. Even Richard Dawkins said the following regarding her scientific contributions:

I greatly admire Lynn Margulis's sheer courage and stamina ... This is one of the great achievements of twentieth-century evolutionary biology...

Brockman (1995) Chapter Seven

[179]

The above is particularly important to bear in mind as you read some of Margulis' outspoken criticism of the rather rigid proclamations and assumptions of our rather restricted version of the Modern Synthesis.

Discover Interview: Lynn Margulis Says She's Not Controversial, She's Right

...When evolutionary biologists use computer modeling to find out how many mutations you need to get from one species to another, it's not mathematics – it's numerology.

Teresi (2011, 71, 'Discover Magazine' April Edition*)

[180]

**This is slightly different to the online version linked above - original online source link at discover.cloverleaf.com now defunct.*

Acquiring Genomes: A Theory of the Origins of the Species

Mutations, in summary, tend to induce sickness, death, or deficiencies. No evidence in the vast literature of heredity changes shows unambiguous evidence that random mutation itself, even with geographical isolation of populations, leads to speciation.

Margulis and Sagan (2008, 29)

[181]

The Phylogenetic Tree Topples

... Then how did one species evolve into another? This profound research question is assiduously undermined by the hegemony who flaunt their correct solution. Especially dogmatic are those molecular modelers of the tree of life who, ignorant of alternative topologies (such as webs), don't study ancestors.., they correlate computer code with names given by authorities to organisms they never see! Our zealous research, ever faithful to the god who dwells in the details, openly challenges such dogmatic certainty.

Margulis (2006, 1)

[182]

Discover Interview: Lynn Margulis Says She's Not Controversial, She's Right

Darwin's big mystery was why there was no record at all before a specific point [dated to 542 million years ago by modern researchers], and then all of a sudden in the fossil record you get nearly all the major types of animals. The paleontologists Niles Eldredge and Stephen Jay Gould studied lakes in East Africa and on Caribbean islands looking for Darwin's gradual change from one species of trilobite or snail to another. What they found was lots of back-and-forth variation in the population and then – whoop – a whole new species. There is no gradualism in the fossil record.

Teresi (2011, 68, 'Discover Magazine' April Edition*)

[183]

Modern scientists such as Margulis are one of the very few who have been able to voice a harsh and scientifically-grounded criticism of the fundamental flaws within our current Darwinian dogma without facing a serious detrimental professional impact. Although, for example, Woese, discussed in the previous chapter, seriously questioned the roots of the evolutionary tree and means of speciation at a micro-level; judging by his writings, he does not seem have had an issue with the fundamentals of Darwinism via selection etc being applicable after the microbial level of early life.

However, Margulis, went further as the above quotes reveal, and questioned the validity of the Darwinian theory at a macro-species level, questioning it all, from the bottom up and the means by which evolution occurred also. Margulis' frustration as indicated in the quotes above, and support from her scientific research, led to a very different solution to the species problem via our current mutationally-genetic-selection and population model version of evolutionary complexity and species change, and it also provides another important piece of the evolutionary puzzle giving us at least a partial alternative to the Darwinist doctrine as seen below.

However, when Margulis' theory is viewed and assessed in the light of all the other partial alternatives outlined in the previous chapters and particularly in the light of the final chapter of this book, an alternative and much more dynamic model of evolution naturally rises out of the ashes of the existing doctrine.

Endosymbiosis: Lynn Margulis

Evolutionist Lynn Margulis showed that a major organizational event in the history of life probably involved the merging of two or more lineages through symbiosis.

Symbiotic microbes = eukaryote cells?

In the late 1960s Margulis studied the structure of cells. Mitochondria, for example, are wriggly bodies that generate the energy required for metabolism. To Margulis, they looked remarkably like bacteria. She knew that scientists had been struck by the similarity ever since the discovery of mitochondria at the end of the 1800s. Some even suggested that mitochondria began from bacteria that lived in a permanent symbiosis within the cells of animals and plants.

There were parallel examples in all plant cells. Algae and plant cells have a second set of bodies that they use to carry out photosynthesis. Known as chloroplasts, they capture incoming sunlight energy. The energy drives biochemical reactions including the combination of water and carbon dioxide to make organic matter. Chloroplasts, like mitochondria, bear a striking resemblance to bacteria. Scientists became convinced that chloroplasts ...like mitochondria, evolved from symbiotic bacteria — specifically, that they descended from cyanobacteria ... the light-harnessing small organisms that abound in oceans and fresh water.

When one of her professors saw DNA inside chloroplasts, Margulis was not surprised. After all, that's just what you'd expect from a symbiotic partner. Margulis spent much of the rest of the 1960s honing her argument that symbiosis ... was an unrecognized but major force in the evolution of cells. In 1970 she published her argument in The Origin of Eukaryotic Cells.

Understanding Evolution (2016)

[184]

We can essentially interpret the research of Margulis in terms of the first and most direct (merging) dynamic hybridisation act that produced a whole new level of organisation and indeed a whole new type of organism and new domain of life that must have allowed for an almost exponential level of evolutionary development to arise. This model helps to explain how such a sophisticated level of life arose in the first place: cellular eukaryotic life (all plants and animals). Therefore, Margulis's theory really does begin to offer a very significant piece of the evolutionary puzzle and if we include her extended thesis that life and nature is intrinsically symbiotic, then the model becomes a very dynamic one indeed.

If some single-celled micro-organisms formed a strange alliance with other sophisticated cellular entities with a nucleus, via merging as Margulis has proposed, then it is important to bear in mind that these individual entities (prior to merging) would have had their own life histories and their own genome/epigenome. Both would have contributed to producing a completely novel (never before seen) cellular entity that had buried within its microscopic body the most sophisticated programming potential (as yet unexpressed as a multi-cellular and fully cohesive and coherent organism).

Therefore, as these proposed mergers are so far-reaching in their evolutionary potential, we can begin to see a fundamentally important piece of the evolutionary puzzle at this juncture. We can begin to understand just how these mergers could have morphed an entirely novel explosion of complexity on a quantum evolutionary scale, as it seems Nature has learned from its past experience, the most efficient and creative way to evolve via an interactive evolutionary feedback loop giving organisms a means to adapt to changing circumstances (rapidly and meaningfully) and to develop/grow and evolve symbiotically with each other and the environment.

This symbiosis is rather radically demonstrated in the early days (if, as Margulis suggests), dynamic and independent cellular entities joined forces literally, and became essentially greater than the combined sum of their parts. For instance, bacteria-like chloroplasts (found in the cells of plants) and its counterpart in animals: mitochondria that may have once been free-living cellular organisms or organ-like (organelles), as the excerpt above suggests: may have once been more like cyanobacteria (a very primitive and ancient life-form).

However, that is not to say that bacteria directly evolved from an actual cyanobacterial ancestor as such, but instead, we could say that all early life shared a primitive ancestral condition with cyanobacteria and some cellular entities further evolved into specialised species of bacteria (free-living and co-evolving with the environment) and other bacterial-like entities went on to merge with other cellular organisms forming a symbiotic relationship of co-evolution with them; perhaps reflecting the behaviour of the ancestral mergers described by Margulis..

For instance, bacteria live symbiotically within our own bodies (as in the bacteria that keep us alive and lives in our guts) and therefore appear to have co-evolved with us. Perhaps that is why humans have a significant number of bacterial genes as indicated earlier. Indeed, bacteria are essential to the all living things and for the atmospheric system that supports those living things.

Furthermore, I also noted in the previous chapter how some bacteria and perhaps other domains of life seem, according to more recent research, to be rapid responders to environmental stresses and may have simply adapted themselves by hybridising instantly (gene swapping etc) via horizontal gene transfer within bacterial colonies, well, it might therefore be interesting to look at this gene swapping again and perhaps some more sophisticated modes of genetic transfer that primitive type entities such as bacteria, algae and yeast and fungi life-forms appear to use to reproduce themselves in our modern era which may give us an insight into how the entire adaptive modification system according to scales of complexity seemingly self-evolved itself in the first place.

Binary Fission and other Forms of Reproduction in Bacteria

> *Binary Fission*
>
> *Most bacteria rely on binary fission for propagation. Conceptually this is a simple process; a cell just needs to grow to twice its starting size and then split in two. But, to remain viable and competitive, a bacterium must divide at the right time, in the right place, and must provide each offspring with a complete copy of its essential genetic material.*
>
> *... Some Unusual Forms of Reproduction in Bacteria:*
>
> *There are groups of bacteria that use unusual forms or patterns of cell division to reproduce. Some of these bacteria grow to more than twice their starting cell size and then use multiple divisions to produce multiple offspring cells. Some other bacterial lineages reproduce by budding. Still others form internal offspring that develop within the cytoplasm of a larger "mother cell". ..*

Cornell University (2016)

[185]

Essentially, it looks like bacteria may have experimented with many modes of reproduction. I see that they are even running the more direct merging mode of hybridisation in reverse is some instances by unmerging and splitting. Whichever way bacteria do it, the important thing is to make more of itself and it doesn't even need to be male or female at this point. Are male and female variations (two sides of the same coin so to speak) simply differentiated type cells and build upon this patterning thereafter?

Now, as the excerpt below reveals regarding yeast/fungal-types, we appear to have more budding and cloning going on which in terms of budding cellular differentiation, is almost a reverse of the primal mergers proposed in Margulis' model and is suggestive of a similar reproductive strategy used by some bacterial-types.

Mate and fuse: how yeast cells do it

Many cells are able to orient themselves in a non-uniform environment by responding to localized cues. This leads to a polarized cellular response, where the cell can either grow or move towards the cue source. Fungal haploid cells secrete pheromones to signal mating, and respond by growing a mating projection towards a potential mate. Upon contact of the two partner cells, these fuse to form a diploid zygote.

Merlini et al (2013, Abstract)

[186]

Yes, I suppose this really is an early form of sexual reproductive. Although, the acting out a primitive sex act under the right environmental conditions (perhaps an ambient mood and lighting) may have been important also as they seemingly give off signals to attract mates, but do not fully merge. They transfer their genetics via a little tail as seen in the article excerpt above. Again, this dynamic system appears to be employed by other forms of relatively primitive life such as Algae as seen below.

Building the Most Complex Structure on Earth: An Epigenetic Narrative of Development and Evolution of Animals...

In algae, sexual reproduction involves the conjugation or joining of two haploid individuals in which one individual provides genetic material to the other.

Cabej (2013, 95)

[187]

The algae are really interesting in this respect as they would also appear to be using the less dramatic genetic exchange mode rather than the actual merging reproductive system of some primal bacteria as proposed in Margulis' model. It also reveals the most rudimentary patterning of sexual reproduction.

We will look at a few more examples of modes of development of present-day species to try and get a window into the evolutionary modes of the past. For instance, the excerpt below outlines some of the modes of reproduction and development of some fungi forms that demonstrate rather experimental modes of both budding asexual reproduction and a rudimentary seeding system that is entirely about location (environment); symbiotic and weather dependent too.

Microbes Fungi Fungal Growth and Reproduction

Fungal Growth and Reproduction

Fungi usually reproduce without sex. Single-celled yeasts reproduce asexually by budding. A single yeast cell can produce up to 24 offspring.

Fungi that make hyphae can reproduce asexually as well. Bits of the hyphae can break off and continue to grow as separate entities, or can form stalks containing seed-like spores.

Although less common, fungi can produce spores sexually. Two mating cells from hyphae of different strains of fungi can mate by fusing together and forming a spore stalk....

...When the spore caps at the end of spore stalks fully mature, they burst. The spores may simply drop in the same area, or be carried by the wind or rain to new spots.

Where they land, spores will germinate like seeds. But if they don't land on a suitable food source or in ideal conditions, the spores can survive in a dormant state for extended periods, waiting for more favorable conditions or to be carried to a better spot.

....When you hear the word fungus, you probably think of mushrooms. Did you know bread mold is a kind of fungus, too? And that the itchy burning of athlete's foot is, yes, caused by another fungus? And that when you take penicillin, you're taking a medicine made by a fungus?

Fungi come in a variety of shapes and sizes and different types. They can range from individual cells to enormous chains of cells that can stretch for miles.

American Society for Microbiology (2014)

The interesting part of all of this is that in many ways we are seemingly getting a glimpse into the evolutionary past by observing the reproductive modes used by present-day organisms of the simpler variety. This might be seen as a kind of re-run/a mimicking of modes of production on another scale, where for example, we know that the first plants and trees didn't produce seeds until much later but used the methods above for fungi spawn akin to seeds instead. Does this suggest that the seeding mode used by some fungi organisms laid the groundwork for further development of even more complex plants that came later; plants that took their cue from the previous, but still existing system?

And as a matter of interest, flowering plants are significantly late in the record, when coincidently, or not, the first pollinating insects metamorphosis unto the scene. I will go into this further in Book Two. Truly, we might be looking at an entire interrelated symbiotic system on every conceivable scale of complexity, each built upon the previous one, while still requiring all the levels of the whole system to be operational.

The relationship between yeast and yeast-like fungi is quite telling in the following excerpts regarding these highly primitive, but symbiotic organelle types and points to a time in evolutionary history when the boundaries between species and even kingdoms of life were quite blurred.

The Microbial World:

Yeasts and yeast-like fungi

Saccharomyces, Cryptococcus and Candida albicans

Produced by Jim Deacon

Institute of Cell and Molecular Biology, The University of Edinburgh

> *Yeasts are fungi that grow as single cells, producing daughter cells either by budding (the budding yeasts) or by binary fission (the fission yeasts). They differ from most fungi, which grow as thread-like hyphae. But this distinction is not a fundamental one, because some fungi can alternate between a yeast phase and a hyphal phase, depending on environmental conditions. ...Yeasts grow typically in moist environments where there is a plentiful supply of simple, soluble nutrients such as sugars and amino acids...*
>
> *Saccharomyces cerevisiae ... is the budding yeast used for bread-making, where the carbon dioxide produced by growth in the dough causes the bread to rise. Essentially similar yeasts, but now given different species names, are used for production of beers, wines and other alcoholic drinks. This phase-contrast micrograph shows cells in various stages of budding. The buds are small at first, but enlarge progressively and eventually separate from the mother cell by formation of a septum (cross wall).*
>
> *Few of the cellular organelles can be seen by light microscopy, unless they are stained specifically. The only conspicuous organelle ... is the large central vacuole which contributes to cell expansion. S. cerevisiae is a member of the fungal group Ascomycota (the ascus-forming fungi).*

Deacon (*n.d.*)

[189]

In really simple terms, we can suggest that budding mimics the embryonic cellular differentiation stage of some fairly complex multi-cellular organisms, including ourselves. In fact, the description above indicates that these clones are organelles (basically miniature organs found inside a cell).

Just as mitochondria and chloroplasts are organelles that are significant hardware (organelles) and carry their own information requirements within their own cellular structure (software): these, by merging with distinct cellular (non nucleated) types (also with their own set of flexible instructions), we now have the nucleated and multi-cellular colony of cells that become highly coordinated – enough to build free-floating organs and ultimately to become fully coherent and self-contained organisms described as plants and animals which are themselves ultimately enveloped in a giant cellular organ we call skin.

From splitting into clones and then becoming differentiated cellular life according to environment and innate developmental complexity, reflects on another scale, the differentiation of the egg cells after fertilisation within a womb or egg-type environment. Even the courtship of yeast or the fission/fusion of some bacteria, and merging of the sperm itself is not unlike how modern sperm with tails seemingly attracted by hormones (akin to the signals given out by yeast-type organisms) and is quite literally (albeit on a self-similar pattern of scale) is in many ways a replay of how the sperm finds and merges into an egg prior to differentiation of otherwise genetically identical cloned cells.

The mode of genetic exchange, whether via HGT, or whole organelle mergers (combining different genomes), or even budding to produce clones with identical genomes that can become free-living organisms and the rudimentary sexual reproduction and rituals of some yeast, as Margulis indicates in her research, primitive forms of genetic exchange as suggested in the reproductive modes of some simpler present-day species such as yeast and bacteria etc., may account for the origin of the fertilisation of the egg by symbiotic sperms (Understanding Evolution. 2016) [190]. And this observation is also interesting in the light of what Lamarck's observations of the same as seen in the following:

I believe I have shown by a collection of comparative facts, that nature under certain circumstances imitates what occurs in sexual fertilisation and herself endows with life isolated portions of matter which are in a condition to receive it.

Lamarck (1809, 244 - Spontaneous Generation)

[191]

Lamarck is essentially correct, once again in his observations as Nature literally would appear to have mimicked herself at every scale of life where the modes of reproduction with modification is just one facet, but is amply illustrated by the few real-life examples of primitive type life and their courtship rituals given above and those to be reviewed below. First, we will revisit the underlying concept that this emerging alternative model of evolutionary development is built upon.

From fungi to forests: the same principles of growth and form would seem to apply as you will see as we develop this distinct view of descent with modification via fractal scaling. We are beginning to get an insight, particular by applying the Matryoshka principle and Von Baer's laws to present-day species development and observe that Nature does indeed seem to create via self-similar repeating patterns at every possible (space-filling) scale; each pattern being developed according to the previous scale; and seemingly, always improved upon.

Each free-living cellular organism is a whole system with its own genetic code (presumably with some biochemical means to imprint changes to that code and memorise it). Each individual cooperates at some level and on every scale there is an exchange of information: from direct genome mergers to create an entirely distinct and more dynamic cellular organisms containing cells – eukaryotes (plants and animals), or form free and independent, loosely associated (at times) cellular colonies, to some organelle type critters operating independently.

From the bacterial-like organelles to the quantum coherent organisms with organs created from specialised cells with different epigenetic programs (as after all the cells are simply identical clones with the same genetics, if we look at the earliest and simplest present-day species, we see clearly that Nature has mimicked herself at every scale. And just as D'Arcy Thompson suggested and supported by more recent evidence, this pattern of growth and development is the most efficient way

If we apply the principle of going from the undifferentiated to the differentiated species at every scale of life and see their modes of replication with modification as a shared common condition that allowed for further cellular complexity, then we can begin to answer the chicken and egg conundrum (which came first). We can begin to see that the chicken has not evolved yet; only its multi-cellular egg-cell form that has the potential to ultimately become an embryonic species and grow up one day to be a fully-fledged flying animal. But none of it might have happened if bacterial-like cells didn't replay in reverse via mergers with other cellular entities, the old cloning/budding routine of cellular differentiation with some novel gene swapping.

If we apply this concept of cellular life sharing common modes of replication (even a snowflake grows from a seed, forms according to laws of shape and form and crystalline matrices can reproduce themselves in self-similar forms using repeating pattern of scale via slightly modified clones according to their growing/developmental environment) as seen across all domains of life and even non-living systems, this means of reproduction/replication via environmentally-determined modification is discernible at every scale of Nature; each domain and sub-domain evolving to their ultimate specialised form.

By applying the Von Baerian principle and finding that from the most primitive and direct (if not rather radical) mergers of simple organisms to the most complex forms, the earliest stages of development of even ourselves could be traced as a repeating patterned evolutionary mode and stage retained (imprinted) during the earliest stages of our embryological development. Our development, prior to becoming embryo-like, along with all the eukaryotic life, (other multi-cellular organisms - animals and plants or primitive plants and animal forms) could be viewed on another scale as a type of evolutionary replay showing us the very means of how life got so complex in the first place.

Recall another way that Nature mimics herself at every scale as proposed by D'Arcy Thompson in terms of the self-similar patterning of growth and form according to proportion and scale and how a slight variation at the beginning (particularly when developing) can lead to a rather big change further down the line; but ultimately, follow overarching principles and laws.

For instance, a snowflake has to be a prism before it grows into a fully-fledged snowflake and also bear in mind that no two snowflakes are exactly the same (nor are two clones or identical twins because of the epigenetic factor). This slight variation can be amplified further down the line, but seems to be kept in relative order as even the unique variations and adaptations to life and circumstances must ultimately follow the path of least resistance and abide by the rules of scale, form and growth.

All in all, if we apply the Matryoshka principle, we begin to see the same fractal (self-similar patterning at predictable scales, each pattern being reflected in the whole and at each scale within the whole) operating at the cellular level on every scale. At one scale the strategies of even the most primitive emerging cellular colonies; such as bacteria, reflect the earliest stages of reproduction of much more complex organisms on another scale.

In other words, by understanding the present-day modes of differentiation, reproduction etc, we can begin to see the principle patterning proposed within Von Baer's laws of development: where, each major group of species reflect their own evolutionary development during their embryological development. And if we apply this principle, then the various modes and means of reproduction with modification of the primitives discussed above and others which we will review below, begin to give us clues to the earliest and most primitive evolutionary development modes of life itself.

Leaving aside, momentarily, the rich and varied means of genetic exchange across all domains of life, whether it is undifferentiated cells, or budding primitive organisms as identical clones with the same genetics or, at a more complex level: identical twins: the main cause of this genetic variation is seemingly the differential expression of identical genes according to environmental triggers via epigenetic processes.

Recall as discussed in Chapter Two in relation to what Alan Turing proposed, cellular differentiation and subsequent variations of patterning from initial biochemical triggers (depending upon the chemical/molecular interactions – epigenetics), can also make a profound difference in the end, as once these chemical 'on', 'off' switches are activated, they commit to that trajectory and the trajectory itself is predictable and explicable in mathematical terms. The epigenetic studies, particularly in Chapter Five, demonstrate the powerful modification of species according to epigenetic (differential genetic expression/programs).

I would also like to remind you of the example from earlier of how the temperature can determine the sex of some salamander/lizard embryos? Perhaps then we can begin to see how epigenetic and environmental factors may be also involved in evolving the sexual reproduction in the first place. Essentially, epigenetics would account for the differential adaptive diversification of the cellular organisms themselves with the added genetic novelty generated by symbiotic HGT within and between the cells and with the added dimension of less direct gene swapping via VGT (vertical gene transfer typically through various methods of hybridisation).

Thus, even when considering all the diverse means of gene transfer amongst and between the different domains of life, we have to also consider the ability for existing genes to be expressed in various ways epigenetically according to adaptive needs and the intelligence of the cells themselves.

Furthermore, the epigenetic dimension of differential gene expression is seemingly governed by laws of scale and form as seen in the repeating patterns at different scales. In other words, the adaptations would appear to be the most efficient responses to changing circumstances. Life appears to have learned to evolve based upon its past experiences and perhaps that is why Nature seems to mimic itself at every scale and we are able to retrace her steps by observing development and using this to replay the most significant phases of past evolutionary events.

Anyway, isn't it amazing what can happen when two distinct cellular entities come together and start to have families of their own? Or more to the point: when they become colonies of cooperative cells and then start reproducing themselves in more recognisable and coherent ways.

Digging Down Below the Tree of Life

"I like to think of early life as being more like an undifferentiated slime mold," Goldenfeld says. "Such a communal form of life would have no meaningful family tree, because it is the community that varies in descent, not individual organismal lineages."

Schirber (2013,'Astrobiology Magazine' 28th March)

[192]

Obviously, I would agree with the above statement in principle, but again, I don't think we are descended directly from undifferentiated slime mould, even if we can't trace our ancestral roots in a meaningful way, but perhaps we could say that this was an ancestral condition that led and was further utilised for the purposes of evolving into all that it could potentially be. For example, a recent study shows that some slime-moulds can complete a maze in record time, yet it has no brain, no mouth, or specific body form. I thought I would give a few more examples of present-day life that may give us a clue into the merging and replication properties of cellular life of the evolutionary past.

SLIME MOLD SMARTS

The slime mold Physarum polycephalum is a single cell without a brain, yet it can make surprisingly complicated decisions… slime mold navigates through a maze and solves a civil engineering problem.

Rothschild and Jabr (2012, Nova Science)

[193]

Slime Molds

Slime molds have traits like both fungi and animals. They have very complex life cycles involving multiple forms and stages. During good times, they live as independent, amoeba-like cells, dining on fungi and bacteria. But if conditions become uncomfortable – not enough food available, the temperature isn't right, etc. – individual cells begin gathering together to form a single structure. This happens when the cells give off a chemical signal that tells all of them to gather together. The new communal structure produces a slimy covering and is called a slug because it so closely resembles the animal you sometimes see gliding across sidewalks. The slug oozes toward light.

When the communal cells sense that they've come across more food or better conditions, the slug stops. It then slowly does a kind of headstand. Cells in the slug now begin to do different things. Some of the cells form an anchor for the upended slug. Others in the middle of the slug begin making a stalk and some at the tip turn into what's called a spore cap and others become spores in that cap. When a drop of rain or strong wind knocks the spore cap hard enough, the spores go flying out. These spores are like plant seeds. Each of them becomes a new amoeba-like cell when they land and each goes off on its merry way.

American Society for Microbiology (2006)

[194]

Perhaps, as you will see from the excerpt below and recall from our discussion in Chapter Three regarding the quantum-type cellular entities, you can begin to imagine the method of how these clever symbiots – the possible result of bacterial-type mergers, started hanging out together for the long haul.

Can Answers to Evolution Be Found in Slime?

Some experiments show complex choreography of signals in some species that allow 20,000 individuals to form a single slug-like body. Some species gather by the thousands to form multicellular bodies that can crawl. Others develop into gigantic, pulsating networks of protoplasm.

Zimmer (2011 'New York Times' 3rd October)

[195]

This also reminds me of Hebb's law, which would begin to account for the way in which cellular colonies communicate and don't forget the property of undifferentiated cells that act like memory foam when working and resonating together. The following excerpt points out for instance, how Hebb's law works and is finding support in more recent studies of the wiring of the brain:

Scientists control rapid re-wiring of brain circuits using patterned visual stimulation

"Hebbian Theory," named after the McGill University psychologist Donald Olding Hebb who first proposed it in 1949 has been confirmed in real-time experiments as reported in a science paper on neurology (2014) and confirmed the axiom: "Cells that fire together, wire together. Cells that fire out of sync, lose their link."

McGill University (2014,'Science Daily' 28th May)

[196]

In other words, there were potentially an awful lot of quiet eruptions of new and novel forms even before the eruption of more complex life is recognisable in the fossil record which is particularly obvious during the first major epoch known as the Cambrian explosion dating to almost half a billion years ago, which I will discuss and attempt to explain in the light of the above in Book Two.

The research of Margulis and others therefore helps us understand the ancestral conditions and means of speciation in the earlier stages of evolutionary complexity in combination with the symbiotic, epigenetic species adaptations according to environmental triggers, orchestrated according to universal growth laws guiding the growth and development of the organism. Even the least perfected forms (slug-like) seemingly have the all important means to coordinate and organise life even though they are brainless, eyeless, organ-less, they can still come together and resonate coherently to beget more complex life.

We will have a look now at sponge animals as these represent a significant leap of coordinated activity that may have shared a common ancestral condition and similar strategies originating in the behaviour of organelle-type entities from yeast/fungi or proto-bacterial life-forms that began to merge, exchanged genes via HGT and resonated together to form smart colonies or communicating and highly coordinated cellular entities that even got mixed up together to coordinate their efforts as clever slug-like creatures that only join forces when times are good and gobble up amino-acids and sugary substances.

To get an idea of their relationship (symbiotic) to algae and analogous slime-mould behaviour, as well as their very primitive reproductive modes which will give us a clue to later development/reproductive modes in other more complex animals, the excerpts below should give us an insight into an evolutionary phase when, again, the lines between what was an animal and what was a plant were quite blurred and demonstrate the all important context of environment during the species development process and cellular sensitivity/interactions and responsive adaptations that go beyond the direct or indirect exchange of genetics and most importantly, their seemingly independent origins.

SYNERGY AND THE EVOLUTION OF COMPLEX SYSTEMS

An illustration of the role of synergy in the evolution of complex systems can be found in sponges, one of the simplest multi - cellular organisms in the natural world... Although sponges come in many different sizes and shapes, the "model" sponge looks more like an urn or a vase than your typical kitchen sponge. Sponges are also the most rudimentary of all animals in terms of complexity.

Indeed, they are often confused with plants because they are immobile and have no internal organs, no mouth, no gut, no sensory apparatus nor even a nervous system. They are more like a colony of cooperating independent cells. Sponges even have their own separate classification (Porifera, or "pore - bearers"), and they may have evolved separately from other animals.

Corning (2012, 15)

[197]

I have quoted a large portion from the excerpt below about sponges as essentially, you will see in one amazing animal, an end eco-and co-evolutionary system that should give you many insights into the nature of Nature in its earliest and most primitive stages of developing a true animal in the way we define such an animal today. This present-day living organism living on the borderland between plant and animal can teach us a great deal about early complexity and the many modes of experimental developmental and reproductive modes explored. The sponge organism is perhaps a view of the evolutionary past as it bears all the hallmarks of what seems to have emerged later.

Sponge Animal, Encyclopædia Britannica

Written by: Michele Sar

Sponges are valuable from a scientific point of view because of their unusual cellular organization (the cells do not form tissues or organs such as those found in other animals), their ability to regenerate lost parts, and their biochemical features (they have many compounds not known in other animals). …… Most calcareous sponges are white. Some sponges (e.g., the Spongillidae) are often greenish because green algae live in a symbiotic relationship within them; others are violet or pinkish, because they harbour symbiotic blue-green algae. These symbionts endow the sponges with colour as long as light is available; the sponges become white in the dark when no photosynthesis occurs and the algal pigments utilized in photosynthesis are no longer produced….

Life cycle

Most sponges reproduce sexually, although asexual reproduction may also occur. Sponges are generally hermaphroditic (that is, having male and female germ cells in one animal); however, some sponge species are sequential hermaphrodites (that is, having male and female germ cells that develop at different times in the same animal).

Sexual reproduction

The fertilization of an egg by a spermatozoan is peculiar in sponges in that a spermatozoan, after its release from a sponge, is carried by the water current until it is captured by a specialized flagellated cell … Development of the embryo may occur in one of several ways characteristic of the different groups; as a result, more than one type of larva is found...

Regeneration

The extraordinary capacity of sponges to regenerate is manifested not only by restoration of damaged or lost parts but also by complete regeneration of an adult from fragments or even single cells. Sponge cells may be separated by mechanical methods (e.g., squeezing a piece of sponge through fine silk cloth) or by chemical methods (e.g., elimination of calcium and magnesium from seawater). ….During unfavourable conditions, sponges are reduced to small fragments ...A complete sponge forms from these fragments when favourable conditions return.The regenerative abilities of sponges, their lack of a central coordinating organ (brain), and the peculiar migratory ability of cells within the organisms combine to make it somewhat difficult to define sponge individuality. Zoologists involved in the study of sponges empirically define a sponge individual as a mass that is enveloped by a common ectoderm, i.e., by a common cellular layer…..

The most important symbiotic associations of sponges occur with single-celled and multicellular algae. The algae may live in the surface layers of the sponge, inside the cells, or among them. The sponge protects the algae from enemies, from unfavourable environmental conditions, and from their own metabolic waste products; the sponge uses the algae as a source of oxygen, as a mechanism for eliminating its products of metabolism, as a screen against sunlight, and as a food source (consuming both algal waste products and dying algae).

Sarà (2016)

[198]

Apart from the obvious symbiotic and environmentally-driven epigenetic type of development implied from much of the above, the other important information is how the animal (quite unclassifiable under normal circumstances) is so unique, it may have had its own origins, but still have ultimately been the result of some really interesting bacterial-type mergers as it lives on the edge of using algae to do the plant stuff that plants do and gets on with stuff that animals do and actually uses the algae for support and resembles in colour, the type of algae that it eats.

The sponge of today, show attributes that strongly suggest that if this was an ancestral condition for primitive life then life was very experimental and innovative and operated as a whole system of symbiosis with itself and its surroundings. Indeed, it is suggested above that these creatures in the making may have arose independently. Are we seeing a snapshot of the evolutionary past in these primitive animals that reveals how they could have come about from sharing an ancestral condition rather than having to descend directly from an ancestral adult species form?

The systems themselves are not ancestors, and do not appear to be entities, but processes as noted by Woese in the previous chapter or – a common ancestral condition as proposed throughout this book thus far. In terms of experimental modes of reproduction and development, it seems to have tried every possible form from budding, to larval metamorphosis and from cellular rearrangements and clumping to egg production and even using free-flowing sperm.

Recall Von Baer's Laws applied even beyond the vertebrate level of life, it is still the same principle and therefore, never at any time in evolutionary terms were we adult sponges. But that doesn't mean in your primitive form you didn't employ the same system to get past the sponge-system phase to become an embryo-like floating chordate (the most primitive condition of all vertebrates). And vertebrates are simply flipped invertebrates structurally-speaking. Again, Nature seems to find the most efficient means of never re-inventing the wheel, but using it in many varied ways.

Besides, even vertebrates and invertebrates start out as soft-cellular blobs prior to making their skeleton whether inside or out. Metamorphosis is a great example where a tadpole-like (with skeleton), munching aquatic creature that would die out of water, morphs rapidly into a four-legged land-dwelling full vertebrate that would drown in water if it couldn't get out. And fish cannot express their full Hox gene compliment for digits – so they never were able to walk anyhow. I will present the evidence for this in Book Two.

Furthermore, even when things settle down a bit in evolutionary terms and species may have become increasingly specialised recall that all that horizontal gene transfer and hybridisation at the micro and macro scale as well as the symbiotic organisms that reside inside your body, not to mention the differential epigenetic expression of the shared genetic code, it still doesn't get that much easier to track down specifically who you are related to, and to what degree.

We may not have even descended from apes, but instead shared a body-plan with some generic species which we might describe as a primitive hominid form and again, hybridisation is seemingly rather common in the early days between broadly generic and as yet, unspecialised species. These generic and most sophisticated forms (that had nothing whatsoever to do with metabolically simpler cold-blooded lizard/reptilian SPECIALIST and FULLY ADULT SPECIES forms, except perhaps a shared ancestral (primordial) condition as chordate and generalist four-legged land-walkers and a great deal of genetic exchange) had a flipped spinal architecture to walk upright (properly) and it would have been really difficult to stay on all fours and this evidence dates back to some 21 million years (Filler 2007) [199].

All of this will of course be supported with scientific evidence and the fossil record in Book Two as it really does throw a serious monkey-wrench in our current model of common literal descent. It is simply that some with this body-plan didn't use it as much as others and there is strong evidence to suggest that as we were uniquely aquatic, our generic ancestral condition/fundamental hominid form may have gotten quite smart from eating all that rich marine/fresh water food. In this scenario, what you eat and how you interact with your environment (particularly as a developing species) has seemingly a profound impact on a species-in-the-making ultimate evolutionary trajectory and final form. Again, this thesis is supported by a wealth of evidence in the next book.

Perhaps, our generic and more cohesive form started out in a richer environment and had a longer gestation period making our evolutionary trajectory somewhat more complex in the end.

CHAPTER NINE

Donald Irving Williamson

(1922- 2016)

HYBRID-METAMORPHOSIS?

As you may be beginning to appreciate, the amount of well-respected scientists who have questioned the Neo-Darwinian model at its most fundamental level are not that rare, but to actually question the foundational principles of direct linear descent aspect of the model is still relatively rare, although, Donald Williamson did as seen in his forthright statement below:

> Caterpillars evolved from onychophorans by hybridogenesis
>
> *I reject the Darwinian assumption that larvae and their adults evolved from a single common ancestor. Rather I posit that, in animals that metamorphose, the basic types of larvae originated as adults of different lineages, i.e., larvae were transferred when, through hybridization, their genomes were acquired by distantly related animals.*
>
> Williamson (2009, 19901)
>
> [200]

Yes, well considering all of the many and varied means and mergers described above for introducing genetic novelty between and within whole domains and lineages of life, it does seem more than likely that Williamson was at least looking in the right direction as seen from his more general assessment of hybridisation as a very probably means of evolutionary change in more primitive animals.

I find Williamson's proposal of speciation due to novel larval genetic transfer - hybridisation and expressed via metamorphosis, particularly interesting in the light of the discussion in the previous chapter regarding the strange behaviour of some sponge animals and their loose affiliation with floating spermatozoa and larval morphs. Below is another excerpt from Williamson which should give you an idea of his broader application of his theory to explain certain novel eruptions in the early fossil record.

.Hybridization in the evolution of animal form and life-cycle

... there were no true larvae until after the establishment of classes in the respective phyla, early animals hybridised to produce chimeras of parts of dissimilar species, the Cambrian explosion resulted from many such hybridisations, modern animal phyla and classes were produced by such early hybridisations, rather than by the gradual accumulation of specific differences.

Williamson (2006, Abstract)

[201]

You can perhaps imagine that this type of radical thinking didn't go down to well in many quarters. However, not all scientists dismissed it simply on the grounds of being outside the norm of evolutionary thinking as scientists such as Lynn Margulis, who had been there herself, understood. Margulis states the following regarding Williamson's rather controversial paper:

Butterfly paper bust-up

In August, the Proceedings of the National Academy of Sciences (PNAS) published a paper online by Donald Williamson, a retired zoologist at the University of Liverpool, UK, reporting that ancient butterflies accidentally mated with worm-like animals to give rise to caterpillars. The study – which was 'communicated' by Lynn Margulis, of the University of Massachusetts, Amhers

.... Margulis maintains that Williamson's and the other papers are scientifically sound and are only being censured because they don't adhere to Darwinian orthodoxy. "We don't ask anyone to accept Williamson's ideas – only to evaluate them on the basis of science and scholarship, not knee-jerk prejudice," says Margulis, who is threatening to bring the PNAS editorial board before the Academy's advocacy committee if the final paper is rejected.

Abbott et al (2009 'Nature' 24th December)

[202]

According to Williamson, these successful hybridisations would most likely occur in organisms with external fertilisation (recall the many wonderful and experimental ways that a sponge animal has found to replicate itself with modification). So this form of loose fertilisation from all sorts of diverse critters (creating the conditions for natural hybridising) is certainly not a stretch of imagination for a marine biologist. However, when it came down to the specific testing of Williamson's theory, this is when the proposal was finally put to rest and everyone breathed a sigh of relief and the Neo-Darwinian model was seemingly safe once more as indicated in the following excerpt:

Caterpillars did not evolve from onychophorans by hybridogenesis

> *The evolution and loss of distinctive larval forms in animal life cycles have produced complex patterns of similarity and difference among life-history stages and major animal lineages.*
>
> *One example of this similarity is the morphological forms of Onychophora (velvet worms) and the caterpillar-like larvae of some insects. Williamson [(2009) Proc Natl Acad Sci USA 106:15786–15790] has made the astonishing and unfounded claim that the ancestors of the velvet worms directly gave rise to insect caterpillars via hybridization and that evidence of this ancient "larval transfer" could be found in comparisons among the genomes of extant onychophorans, insects with larvae, and insects without larvae.*
>
> *Williamson has made a series of predictions arising from his hypothesis and urged genomicists to test them. Here, we use data already in the literature to show these predictions to be false. Hybridogenesis between distantly related animals does not explain patterns of morphological and life-history evolution in general, and the genes and genomes of animals provide strong evidence against hybridization or larval transfer between a velvet worm and an insect in particular.*
>
> Hart and Grosberg (2009, Abstract)
>
> [203]

However, if we view the evidence on all scales of life, where there has seemingly, been extensive hybridisation events: as the record clearly indicates (from early actual mergers, to chimera's produced in the microbial world and whole chromosomal exchanges/polyploidy, and HGT across distinctly different species to the frequent hybridisation events amongst and between diverse species during evolutionary development), perhaps Williamson's urging of geneticists to test his theory was not the way to go as the scientists exemplified in the above paper: *Caterpillars did not evolve from onychophorans by hybridogenesis,* assumed the gene sequence matching or non-matching as indicative of ancestral relatedness model in their study and genetically established (in their minds) a null hypothesis for Williamson's theory; thus, relegating the theory into the dustbin of great ideas that never went anywhere as they didn't fit the current orthodoxy.

It is a great pity, as essentially, I believe Williamson's theory is unto something, but we are unable to see the wood for the great all-encompassing molecular tree. Perhaps you can see where Williamson and others have gone wrong. It is not possible to assess the genes alone, perhaps even if we could assess the entire genome and even then, if, as strongly suggested, we need to look deeper into the so-called junk genes (where much of the evolutionary genetic mergers/HGT events and genome remodelling evidence resides) and this is not to mention the epigenome, which has continually rewritten the adaptive programs for existing genes.

These factors will be the topic of discussion in the following chapter, and from this, we would begin to understand why we cannot test Williamson's hypothesis directly by using the Darwinian molecular measurement. In other words, by only assessing the genes (from already published material: not actual specimens), this would, as you might imagine, produce meaningless results as even identical genomes or genes that code for proteins (coded) epigenetically express wildly different morphologies (how a creature looks) depending upon which developmental stage they are in.

Therefore, even if larval organisms are genetically examined and compared to the adult form of an entirely different species, their distinctive forms are not going to relate to which genes they possess as epigenetic studies clearly show. As discussed previously, epigenetic processes are the different programs running for cellular forms at different times during development. So how are we to know if they were not the modified descendent of their former species within the scales of evolutionary seasons?

Recall how undifferentiated cells (Pluripotent or un-programmed cells) can be environmentally triggered into running widely different programs to become specialised cellular colonies linked and communicating via their biochemical signalling networks expressing the identical genes in many different ways resulting in neurons, skin, and bone cells etc.

For instance, a case in point of the dramatically different epigenetic expression of the same genome would be best illustrated by the classic metamorphosis known to us all in terms of the caterpillar to flying insect (butterfly or moth). The same creature in its undeveloped form is radically different to what it will morph into when it becomes an adult, yet it has the exact same genes; just expressed, radically differently depending upon its maturity. This concept is no better exemplified in metamorphosing animals such as: a butterfly/moth (a flying insect) and its primitive or developmentally immature form – a caterpillar (O'Hare 2014) [204].

Therefore, as radical as Williamson's general evolution via novel genetic transfer (hybridisation) and the mechanism of metamorphosis in insects, it actually has some support when understood in the context of epigenetic program switching. Take for example, the critical and amazingly dexterous role of epigenetic processes in metamorphic transformations as described by Cabej in his book (*note that blauplans refers to body-plans*):

Building the most Complex Structure on Earth: An Epigenetic Narrative of Development and Evolution of Animals

> *Metamorphosis is an amazing example of the dexterity of animals to switch to different development programs. This certainly contradicts the prevailing opinion that an egg or a zygote provided with a program that determines development up to the adult stage.*
>
> *This gains more significance when one remembers the ease with which some metamorphosizing amphibians can switch to a direct mode of development, or even skip metamorphosis altogether. It is possible that the same egg/zygote contains the programs for two different Bauplans, and sometimes even a program for skipping its species-specific Bauplan? Metamorphosizing species, besides their own developmental program, have incorporated and executed ancestral developmental programs.*
>
> *Amazingly, like biological Houdinis, they shift the gears of development both forward (insects and amphibians) and backward (ascidians).*

Cabej (2013, 179)

[205]

Indeed, if we run this developmental program back in time from present-day species to evolutionary development, there is no reason why we could not suggest: on another scales, that species in-the-making (undifferentiated) worm-like/caterpillar-types/larval and embryonic-types, may have grown up to be radically different to their former more primitive selves and that some particularly novel hybrid (chimera events) allowed for equally novel epigenetic expression, triggered by environmental events, from these ancestral encounters (differential and nested scales of complexity programs).

I would therefore, still adhere to the more general principle of hybridisation (including HGT) as a means of metamorphosis as suggested by Williamson and seek to explore this proposition using the nested scales of complexity model, rather than be specific about who is related to who – which seems to be a futile pursuit in the genetic game of life. However, in order to fully apply this thinking to the fossil evidence, there is a final pieces of the puzzle that needs to be assessed which will be discussed in the next chapter in the light of epigenetic mechanisms, which will make more sense of the rapid and profound changes that metamorphosis can bring about; triggered via stressful conditions – a type of SOS rescue system.

Returning for example to Von Baer's concept of scales of complexity, where evolutionary epigenetic development of the species directly reflects on another scale the development of modern organisms and vice versa and D'Arcy Thompson's view of several distinct little worms that diverge rapidly into their whole form according to their starting and developmental conditions, or Lamarck's concept of going from the unperfected (less defined) to the perfected (specialised) within its fundamental form via epigenetic means, can be extrapolated beyond insect metamorphosis to amphibian metamorphosis, a type of leap-frog evolution, where it is easier to explain how a tad-pole-like basal chordate (the fundamental form of all vertebrates including fish and ourselves), might go from a soft-bodied, limbless, algae-munching, water breathing swimmer dependent upon water to a plant-eating, land-breathing, full vertebrate, limbed, land-walker that would drown if they didn't find a way unto land.

I will present the evidence via the fossil record in Book Two to support such a radical application of different scales of metamorphosis as a means to produce rapid, whole and profound species adaptations under the guidance of epigenetic control of the genetic novel material generated as a result of hybridisation/mergers/genetic transfers at every scale of life and the opportune utilisation of naturally occurring minerals and new resources (carbonate in the seas to help build skeletal structures both inside and out for example), which became critical to the further development of as yet undifferentiated/non-specialised organisms. I will argue that it is these dynamic epigenetic cellular differentiation programs that has adapted life during its species development and written in accordance with natural laws of scale and form and essentially in response to environmental shifts, upheavals and stability.

Who knows, Williamson may have been unto something with his evolution of the species from primitive hybridisation and novel exchanges expressing rather dramatically distinctive adult forms as exemplified in obvious forms of metamorphosis. At least, he may have stumbled onto the principle of something very important in the whole evolutionary puzzle. Again, Williamson was a scientist working from actual observation of living species in the context of their real living environments (he was a marine biologist) and therefore felt a great need to offer an alternative to the mainstream model dogmatically adhered to within his own field of research.

Therefore, I believe Williamson's theory should be reassessed in more general terms and in the light of epigenetic evidence for the meaningful modification of developing species (reflected in the meaningful patterning on scales of complexity of present-day species development routines – employing Von Baer's laws to all the fundamental groups) and understood in terms of hybridisation on every scale (to include mergers, HGT and hybrids between more mature species) and in terms of the different scales of metamorphosis to include, not just the obvious insect or amphibian type, but all the nested grades thereafter such as: the metamorphosis, albeit more controlled, that takes place within an amniotic egg and the nested scales represented in marsupial-type amniotic development and finally to the most controlled metamorphosis of them all: the mammalian amniotic internal carriers.

CHAPTER TEN

Barbara McClintock

(1902 - 1992)

SOS - SPECIES REMODELLING VIA JUMPING GENES

The term jumping genes has been used to describe how genetic material can jump between species (HGT – horizontal gene transfer as discussed above), creating genetic novelty. It is however, more often used to describe the genetic material that jumps around within genomes of a single species and is responsible for a great deal of its modification according to environmental triggers. This discovery is mainly due to the research of Barbara Mc Clintock. The following biography reveals the historical context of her discovery: by Sandeep Ravindran, Science Writer.

Muted Reaction

> *For much of the 20th century, genes were considered to be stable entities arranged in an orderly linear pattern on chromosomes, like beads on a string...In the late 1940s, Barbara McClintock challenged existing concepts of what genes were capable of when she discovered that some genes could be mobile...By the 1970s the great strides made in molecular biology led to the discovery of transposons in other organisms, starting with viruses and bacteria. We now know that transposons constitute more than 65% of our genomes and approximately 85% of the maize genome....*
>
> *Confirmation that transposons were widespread among eukaryotes eventually led to the wider appreciation of her original discovery. McClintock received a number of prestigious awards, including the 1970 National Medal of Science and culminating in an unshared Nobel Prize in Physiology or Medicine in 1983...McClintock described the initial reaction to her discovery as "puzzlement, even hostility" ... Speaking of the scientific community at large she said "I was startled when I found they didn't understand it; didn't take it seriously" ... The concept of transposition did not fit easily within the framework of genetics at the time... These pioneering studies foreshadowed later work showing the importance of epigenetics, heritable changes not caused by changes to the DNA sequence, in development.*

Ravindran (2012, 20199)

Recall that the foundational pillar of the Neo-Darwinian synthesis, where all the genetic novelty was supposed to be derived from isolated species mating after a long period apart to spice up the gene pool (not technically hybridising) with their accumulated genetic mutations under the naturally controlling environmental selection factors, such as predators eating the less well adapted (weaker) variants, and therefore, we can begin to see how and why perhaps, McClintock's genetic experimental observations in real populations, rapidly and radically adapting to harsh environmental conditions in one generation and passing on this adaptation didn't go down too well. This is an epigenetic phenomenon as it operates beyond the directly inherited information encoded in the genes.

What McClintock essentially observed was acquired characteristics via environmental triggers (epigenetic evolution as Lamarck had proposed it) in action. The genes themselves could not explain such phenomena as there was no means of passing on genetic mutations or for selection to operate in such a short time within her highly controlled experiments. These species of plants and later confirmed in other organisms including animals, had exactly the same genes, but their genomes (the rest of the genetic system was radically rearranged.

This of course had tremendous implications not only for one of the major tenets of the Neo-Darwinian model, but for how we viewed evolution and the formation of the species itself. In McClintock's paper presented during her long overdue Nobel award in 1983 she writes:

THE SIGNIFICANCE OF RESPONSES OF THE GENOME TO CHALLENGE

It is the purpose of this discussion to consider some observations from my early studies that revealed programmed responses to threats that are initiated within the genome itself, as well as others similarly initiated, that lead to new and irreversible genomic modifications. These latter responses, now known to occur in many organisms, are significant for appreciating how a genome may reorganize itself when faced with a difficulty for which it is unprepared. Conditions known to provoke such responses are many. A few of these will be considered, along with several examples from nature implying that rapid reorganizations of genomes may underlie some species formations...In the future attention undoubtedly will be centered on the genome, and with greater appreciation of its significance as a highly sensitive organ of the cell, monitoring genomic activities and correcting common errors, sensing the unusual and unexpected events, and responding to them, often by restructuring the genome.

McClintock (1983)

[207]

One clue as to how the epigenetic mechanism may have acted upon the natural propensity for bacterial/viral-like elements to remodel, rearrange and generally rapidly replicate their new innovative programs is indicated in the excerpt below. It discusses how the relaxation of the epigenetic control of gene expression may trigger mobile genetic elements (TEs) or jumping genes into action below:

Jumping genes and epigenetics: Towards new species

Transposable elements (TEs) are responsible for rapid genome remodeling by the creation of new regulatory gene networks and chromosome restructuring. TEs are often regulated by the host through epigenetic systems, but environmental changes can lead to physiological and, therefore, epigenetic stress, which disrupt the tight control of TEs. The resulting TE mobilization drives genome restructuring that may sometimes provide the host with an innovative genetic escape route. We suggest that macroevolution and speciation might therefore originate when the host relaxes its epigenetic control of TEs.

Rebolloa et al (2010, Abstract)

[208]

In other words, if we understand how epigenetic processes release their normal control and hold over jumping genes (transposable elements or horizontal gene swapping and remodelling), or all those viral-like micro-hybrid innovations and their environmental triggers (activating ancestral programs perhaps?), we may actually be able to: not just find out some very interesting things about past evolutionary events and how Nature has learned to creatively sculpt meaningful adaptations according to environmental needs to ultimately form and shape the species from all the available genetic novelty (expressing these genes differentially and remodelling the genome itself when needs are great), but, to understand how these deeper insights into biological processes have the potential for enormous implications for our health and well-being in general.

If we understand that we are not fixed genetically, selfishly-driven lumbering robots (but highly sensitive organelles and adaptable creatures in response to whatever life may throw at us). Essentially, it would appear that as much as epigenetics (cellular responsiveness and biochemical memory) is the guiding hand in the orchestration of events, seemingly, most of the time and constricting things from morphing into all sorts of strange critters, and it could be suggested that Nature holds a genetic wild-card which is forced into play occasionally, and perhaps when the species were young and more pliable, this hand was forced in rather dramatic ways on occasion.

Metamorphosis comes to mind as one possible solution that may be a remnant of the evolutionary past. After all, the article above suggests that when this tight epigenetic control of TEs is released, this could be enough to cause large macro evolutionary changes and even speciation itself. Take for example one scale of life that we can assess over millions of generations within just a few of ours, bacteria.

Now we know that bacteria never become anything other than bacteria, as presumably evolutionary development of the species has settled upon considerably since the early days of morphing and now knows what it is going to be when it grows up (each time that a new generation is spawned). However, that doesn't mean that bacteria cannot adapt and change quite rapidly and somewhat dramatically even in modern populations. See excerpt below:

Scientists develop new technique for analyzing epigenetics of bacteria

There is a potential new tool to combat pathogens and overcome antibiotic resistance. Scientists have developed a new technique to more precisely analyze bacterial populations, to reveal epigenetic mechanisms that can drive virulence. The new methods hold the promise of a potent new tool to offset the growing challenge of antibiotic resistance by bacterial pathogens.

The Mount Sinai Hospital / Mount Sinai School of Medicine (2015, Summary)

[209]

In many ways, the flexibility of bacteria to rapidly respond to something trying to kill them, such as an antibiotic, has seemingly been the very adaptive (epigenetically-triggered or letting those jumping genes run wild for a bit) which can entail gene swapping instantly via Horizontal Gene Transfer between actual individual bacteria – but remember, they operate in colonies and remember via chemical signalling. So, essentially, bacteria exhibit all the behaviour of jumping genes on another scale, where these mobile or transposable elements similarly do direct gene swapping and remodelling according to environmental threats.

In light of this, I thought the excerpt below stating that bacterial drug resistance cannot be explained by genetic mutations and selection (two of the main tenets of the Neo-Darwinian model for species change and adaptation) was of interest, even though its authors do not subscribe to this being evidence against mutation or selection being applicable to more complex scales of life such as animals or plants.

EVOLUTION OF DRUG-RESISTANT BACTERIA

Bacteria in nature do evolve resistance to antibiotics faster than mutation and selection allow...

Campbell and Schopf (1994, 95)

The statement above is particularly of interest in light of the earlier quotes from Margulis regarding the inadequacy of mutant genetics to bring about such creative and adaptive change. But by now, you should have worked out that if we are applying the Matryoshka principle (which is seemingly: universal to them all at every scale), then it only makes sense to see cellular life at any scale, as governed by the same laws of growth, form and principles of life.

So how smart are bacteria really? As discussed in the previous chapter, if as the evidence strongly suggests: slime-mould is intelligent enough (and it doesn't even have a brain) to complete a maze, then you know my answer: Very smart indeed! And James A. Shapiro presents the evidence to fully support this premise.

Bacteria are small but not stupid: cognition, natural genetic engineering and socio-bacteriology.

> *Forty years' experience as a bacterial geneticist has taught me that bacteria possess many cognitive, computational and evolutionary capabilities unimaginable in the first six decades of the twentieth century. Analysis of cellular processes such as metabolism, regulation of protein synthesis, and DNA repair established that bacteria continually monitor their external and internal environments and compute functional outputs based on information provided by their sensory apparatus.*
>
> *Studies of genetic recombination, lysogeny, antibiotic resistance and my own work on transposable elements revealed multiple widespread bacterial systems for mobilizing and engineering DNA molecules. Examination of colony development and organization led me to appreciate how extensive multicellular collaboration is among the majority of bacterial species.*
>
> *Contemporary research in many laboratories on cell-cell signaling, symbiosis and pathogenesis show that bacteria utilise sophisticated mechanisms for intercellular communication and even have the ability to commandeer the basic cell biology of 'higher' plants and animals to meet their own needs. This remarkable series of observations requires us to revise basic ideas about biological information processing and recognise that even the smallest cells are sentient beings.*

Shapiro (2007, Abstract)

[211]

In the model applied here, we are trying to identify self-similar patterns for evolving all scales of life – a shared common ancestral strategy. Essentially, as indicated previously, we know that genetic mutations is not the source of creative adaptation; nor is Natural Selection an adequate explanation either according to an ever-increasing body of evidence against it. The alternative scenario (beyond mutating genes and survival or non-survival via selection process) is to look to the adaptability and ability of the genome itself to respond to the conditions surrounding a developing and living organism. Essentially, Nature appears to be self-adaptive and self-sustaining and this is summarised succinctly in Shapiro's term for this whole adaptive system as seen in the title and short excerpt below.

Natural genetic engineering in evolution

> *In other words, it can be argued that much of genome change in evolution results from a genetic engineering process utilizing the biochemical systems for mobilizing and reorganizing DNA structures present in living cells.*

Shapiro (1992, 101)

[212]

Genetic engineering by Natural means begins to give us a more realistic insight into the evolutionary processes of the past; a more sophisticated understanding of biological adaptation over the concept of Natural Selection, as genome remodelling (which raises the profound possibility of species remodelling according to adaptive needs during earlier evolutionary development as one of the main drivers of evolutionary change) and the role of jumping genes in particular, and their response to environmentally-driven factors, are an essential player in evolution itself. See some more of Shapiro's research relating to Natural Genetic Engineering: Does Natural Selection Really Explain What Makes Evolution Succeed? (Shapiro, 2012) [213].and How Life changes itself: The Read-Write (RW) Genome (Shapiro, 2013) [214].

Essentially, via the decades of research carried out by Shapiro and others and pioneered by McClintock, we are beginning to grasp the more sophisticated means by which Nature had evolved the great diversity of species, even if the underlying method is surprisingly simple and predictable once we clear back the dead wood. Certainly, Shapiro's term: Natural Genetic Engineering does begin to encapsulate the essence of a very distinct evolutionary scenario where, epigenetic processes seemingly write the meaningful programs according to environmental cues. Genome remodelling means that organisms can outwardly look and act dramatically different, particularly when this remodelling occurs within a developing species (prior to becoming stabilised metabolically efficient).

Ultimately, when we review all of the evidence on aggregate, we would appear to have a whole finely-tuned and highly coordinated genetic/epigenetic and cellular system within the context of the larger eco-system that orchestrates the successful production and output patterning conforming to predictable scales of complexity.

Can you imagine, what could be constructed by the complete remodelling of a genome in the evolutionary past, perhaps prior to the full development of the epigenetic controlling system itself was primitive, and the more direct exchange and gene swapping and modifications according to adaptive needs and dramatically changing environments were the order of the day? Examples of these sorts of rapid remodelling events of the evolutionary past and their implication in the evolution of even the most complex organisms are indicated below.

JUMPING GENES DRIVE EVOLUTION

Orthodox evolutionary theory does not tally with the fossil record, but a new school of thought points towards 'jumping genes' as essential agents of periodic changes in the rate of evolution … Punctuated equilibrium is rapid evolution followed by slow evolution, or a stoppage in evolution, as is observed in the fossil record.

This can be explained by the fact that jumping gene activity does not occur at a low and uniform rate over time. Instead, it sporadically occurs in sudden bursts resulting in rapid evolution, followed by decreasing activity and slowing evolution. These rapid bursts of evolution can happen when a new type of jumping gene is suddenly transferred into a lineage from some other lineage, or when a new type of jumping gene naturally emerges from within a genome.

Oliver & Greene (2009 'Australasian Science' September Edition)

[215]

For instance, in another science paper, the importance of TEs (Jumping genes) is stressed in terms of past evolutionary implications as these mobile elements make up a very large part of our genome and appear to have played a major role in evolution (complex cellular life making up plants and animals are Eukaryotes):

Transposable Elements and Eukaryotic Complexity

Eukaryotic transposable elements are ubiquitous and widespread mobile genetic entities. These elements often make up a substantial fraction of the host genomes in which they reside. For example, approximately 1/2 of the human genome was recently shown to consist of transposable element sequences.

There is a growing body of evidence that demonstrates that transposable elements have been major players in genome evolution. A sample of this evidence is reviewed here with an emphasis on the role that transposable elements may have played in driving the evolution of eukaryotic complexity.

A number of specific scenarios are presented that implicate transposable elements in the evolution of the complex molecular and cellular machinery that are characteristic of the eukaryotic domain of life.

Bowen and Jordan (2002 Abstract, *p*. 65)

[216]

Below is another example of how important transposable elements and their implications for larger evolutionary adaptations and how jumping genes are not confined to the so-called lower organisms, but apply to the higher organisms, including ourselves.

Transposable Elements May Have Had A Major Role In The Evolution Of Higher Organisms

It now appears that at least some transposable elements may be essential to the organisms in which they reside. Even more interesting is the growing likelihood that transposable elements have played an essential role in the evolution of higher organisms, including humans.

University of Georgia (1998)

[217]

Furthermore, we are beginning to understand how jumping genes even drove specialist sophistication within primate evolution as indicated in the excerpt below.

How Jumping Genes Drove Primate Evolution

Jumping genes have been important in the evolution of higher primates, leading to faster brain function, improved foetal nourishment, useful red-green colour discrimination and greater resistance to disease-causing microbes – and even the loss of fat storage genes in gibbons.

Oliver & Greene (2012 'Australasian Science' Jan / Feb Edition)

[218]

All in all, it seems that environmentally-triggered and epigenetically controlled, jumping genes and Natural Genetic Engineering explanation, rather than Natural Selection and Genetic Mutations, along with population models, is a much more dynamic explanation of speciation as it would seem as studies show which I will outline further on, the ability for transposable elements (TEs} to remodel whole genomes according to environmental stresses, has been implicated in much of the evolutionary diversity we now witness in present-day species.

Evolution: A View from the 21st Century

Among the most striking features of the fossil record are the periods of accelerated mass extinctions followed by periods of accelerated mass "originations" (appearances of morphologically novel organisms).

Shapiro (2011, 139-142)

[219]

Take for example, a rather dramatic example such as the radical makeovers within some less metabolically complex species of insects and amphibians in present-day species – evolution by metamorphosis and as discussed in the previous chapter, how this concept can be extrapolated back into evolutionary timescales to help explain such rapid leaps of speciation and of course scaled up and applied to different levels of genetic expression of even the most complex mammalian forms of amniotic metamorphosis or embryonic development and its controlled and ready-made environment.

As discussed, particularly in Chapter Two of this present book regarding the most basic principles of the chemical basis of Morphogenesis according to Turing's model as being one and the same as epigenetic environmentally orchestrated processes – using the chemical switching methods which are initially triggered by environmental conditions and the concept of cellular and molecular memory, begins to give us an insight into the fundamentals of the whole species adaptation system that is responsive to environmental cues.

Shapiro's observations that even the smallest cells are responsive sentient beings brings to mind another view of the scaling principle, as the coordinated colony of cells that make up plant and animal life (the eukaryotes) into whole and independent organisms are themselves contained within a giant cellular membrane that is sensitive to its environment (external conditions) just as much as the trillions of cells within the outer skin (membrane) are sensitive to their inner and outer environments and interactions between each other.

Whether we are talking about an organelle within a cell or a scaled up organ within a multi-cellular organism, or the crystalline proteins within the cell or the chemical 'on', or ‘off’ switches operating above the coded sequence of molecules, these systems are all highly sensitive, adaptive organelles, organs, and organisms that have the inherent properties to adapt and modify and change according to the challenges of their respective development environments.

It would seem by implication, extrapolation and the application of scaling laws, that the triggering of jumping genes into action that can cause the rapid remodelling of the genome itself via environmental stresses may be a re-run of an ancestral program that was employed in the evolutionary past and brought into play if things get rather challenging even when a species is fully specialised and otherwise genomically and epigenomically much more stable.

In other words, when the species were relatively undeveloped (undifferentiated and un-specialised), this may have been the very means of making the greatest changes to the species and it may have been due to some of its greatest environmental challenges. It begins to resolve the so-called gaps and serious lack of transitional fossils as well as explaining the relative rapidity of certain seeming explosions of life (exponential perhaps after a lag phase?) with no apparent predecessors.

This idea is not unfounded, as it seems to be the case for most species today reflect in their developmental stages (on a faster and shorter timescales); their evolutionary species development stages and timescales as postulated in Von Baer’s model. If we apply the nested scales of complexity, each according to their own little independent origin worm-type as proposed in D’Arcy Thompson, non-linear descent model (discrete and discontinuous forms) and diverging increasingly as more specialised species forms according to laws of growth and form, then we naturally begin to gain an insight into the true processes and cohesive pattern underlying all of Nature and how it might have gotten so complex in the first place.

Summary

THE MATRYOSHKA PRINCIPLE REVIEWED

We now have the main principles and means and processes of an alternative evolutionary proposal, to our current direct linear descent via genetic inheritance model to the exclusion of all other environmental factors and selection: the elimination of the unfit and the preservation of the fittest species being replaced by a much more sophisticated system of adaptive evolution according to an the organism's conditions of development.

Employing the over-arching universal laws of scale, the principle of repeated scales of increasing detail and complexity, nested within discrete sets, of self-similar patterns of growth and form reflect: D'Arcy Thompson's understanding and insights into Nature's method. His concepts are finding good support by a growing body of research particularly within the world of chemistry and physics (and describable mathematically), and we now have enough information to directly put the fossil record to the test in Book Two.

We can begin to apply the overriding principles of going from the shared ancestral condition from a diverse range of organisms akin to the pluripotent state of the cells during the early stages of development with a convergence (a bottleneck) following Von-Baer' principles represented by the hourglass model where an organism's cellular/embryological development should reflect on one scale the larger scale of its evolutionary development towards an adult species, and see if these concepts hold.

Similarly, by employing Turing's chemical basis of Morphogenesis, we can apply the scale of cell differentiation and the individual programs of cellular colonies and networks taking their cue from the environment and activating these biochemical programs (epigenetic processes) on another scale to suggest that the multi-cellular organisms in which these cells reside, developed differentiated programs in direct relation to their interactions and environmental responses.

Recall the pluripotent (un-programmed cells) that knew what to be when they grew up, they just needed a reminder to trigger the chemical cascades and it was all seemingly to do with what Petrie environment and surface they developed in. They essentially became programmed by their environment even though their genes were identical regardless of what pluripotent (stem-cells) they resided in.

Another application of the repeating patterns of self-similar fundamental whole systems at every scale can be seen within the world of genetic/epigenetic transfer in terms of the vast genetic exchange across all domains of life, whether via HGT, mergers, mating microbial life, or hybridisation as seen in the eukaryote forms of life (plants and animals) are in a sense, hybridisation at all scales of life.

The result is the same: rapid and profound speciation in one fell swoop, just as De Vries had inadvertently observed; a scenario that is gaining increasing support as another important means of rapid and profound speciation events within the evolutionary past when species were relatively unformed and still developing, as further and deeper exploration of the genomes and epigenomes reveals.

This is not to mention all the HGT, mergers, hybridisation events in general which presumably provided organisms with a fantastic diversity of novel genetics that could then be used to entirely remodel genomes via jumping genes (using the same strategy as bacterial types) via splicing, dicing, rearranging and generally remodelling developing organisms in the process. Rapid and dramatic remodelling according to environmental triggers (probably quite profound ones), may have resulted in the metamorphic strategy which later settled down to less dramatic means of producing developing organisms/species, in amniotic eggs and ultimately within some species as internal eggs with their amniotic sacks; yet another scales and self-similar pattern of development.

On an earlier scale of life, we can take this scaling principle and apply it to another related aspect of evolution, seemingly to the evolution of the genetic code and epigenetic code (the genome and the epigenome). On another, we can see the formation of the multi-cellular organisms (pluripotent to specialised species) reflecting the unformed (undifferentiated) archetypes body-plan forms that later differentiate/diversify and become increasingly specialised, evolving presumably according to another scale that applies to all living things: the universal Sigmoidal growth pattern of going from a lag phase, exponential when the time is right and then stabilisation.

This scaling model of the formation of the species in essence begins to support the evolutionary views of Lamarck, Von Baer and D'Arcy Thompson and is supported by the emerging scientific literature.

As with all scales of Nature's innovations, it has to be viewed as a whole system and in the case of the genetic/epigenetic system, it seemingly took the fundamental properties of crystalline growth in solution as its cue as seen in the fundamental properties of self-organising according to growth laws of chemical bonding and self-assembly, pattern imprinting and memory, replication and modification and in accordance with environmental and resource availability and concerns.

This fundamental system can be scaled up (if conditions allow) to the chemical bonding of meaningful sequences of information (amino-acids) protected by a crystalline protein structure with similar self-organising, memory, and responsiveness/modification according to environmental conditions. These chemical cascade of 'on' or 'off' switches and molecular positive or negative memory bonding is not only the fundamental basis of epigenetic processes within the context of perhaps a highly evolved protein structure, the cell, but it may explain the origin of our modern coding system (the DNA and the genes), which itself may have evolved from the simpler molecules of RNA and TNA.

Even the crystalline properties embedded within all of the above, appears to have evolved into a much more sophisticated crystalline system by using the very special properties of phase transition (causing coherence as suggested by Mae-Wan Ho and certainly supported by other evidence) to a liquid crystalline state, from our own optic systems in the lens of our eyes, to the amazing process of photosynthesis in plants (the energy exchange with the environment and a plant organism), to the evidence of a liquid crystalline phase, as occasionally observed in real-time experiments during development of a larvae/embryo formation, from the properties of the DNA double helix, to the folding properties of proteins and the just about everything else we have observed in Nature, it is crystalline in some form or other.

This really does bring Cairns-Smith's crystalline origins hypothesis into sharp focus indeed. It also begins to give us an insight into the incredible means that Nature has employed to evolve the great diversity of life we see on the planet to-day, by building upon the earlier system and according to overarching universal laws of growth and form at every scale and builds each level as a fully efficient whole system before moving on to the next level up.

However, as also addressed in Chapter Three, seemingly at some stage, or perhaps from the get-go, in the tiny quantum atomic world, Nature made the most spectacular progress, but it was so hidden in its smallness, we never noticed until more recent times, but do remember the next time you munch on your salad lunch, that these are made up of trillions of liquid crystalline-nano-quantum computers. But they do taste awful juicy.

This principle whereby the more primitive an organism is the more pliable and direct the influence of the environment is important here. Applying the Matryoshka principle, of self-similar forms of complexity formed as whole systems (dolls) on every possible scale, it would take longer to carve and finish the larger and later dolls than it would the earlier dolls. Furthermore, the basic pattern and template of the earlier is the same as the later, just that the later form is usually larger and more elaborate, but all fit in predictable scales as one single set or can be observed individually, but within one, the whole is reflected.

Similarly, in Nature, it would seem that each leap of complexity (represented by the individual dolls within the set or the whole set) whether talking about the earlier crystalline origins in solution or the development of TNA, RNA, and finally DNA and its related protein/cellular and epigenetic system, or talking about the shape and form of the bodies or the metabolic systems, it is seemingly the same fundamental system on increasing scales of complexity, by measurable factors of scale. By following present-day developmental phases from the first merger of the sperm and egg to fully formed adult, we may be seeing the replay of the evolutionary phases of the formation of the species itself.

If a simple bacteria which is only relatively simple compared to a human being, is studied to see how it develops and reproduces, then we might be looking at the replay of its evolutionary development. If we work our way up the scale of life, we could keep replaying all the stages of an organism's development to gain an insight into its evolutionary development. The transference of the coding system across and between seemingly, all domains of life creating a vast web of symbiotic connectedness (a fractal network), could be described as hybridisation on every scale.

The self-similar and repeating patterns at every scale are evident again, when we review the means of replication/reproduction (copying with modification) according to environmental conditions, in the diverse modes used from actual mergers of organisms run in reverse as splitting into two or more individuals and on another scale: the coordinated cooperation of many cellular entities that can coherently resonate (quantum-like) to form a whole multi-cellular organism. From asexual budding (a chip of the old block) to cellular differentiation during Morphogenesis, the same pattern applies at another scale.

The ancestral epigenetic programs are all a means of remodelling the genome and seems to be a form of metamorphic development on different scales of expression; ranging from the almost miraculous transmutation of a chrysalis to a flying insect to the mode of remodelling a swimming sperm-like tadpole into a four legged, land-breathing vertebrate land--walker, and from a very special land-based sophisticated egg to one that is retained internally – the amniotic species (non-amphibian), these modes of development may seem radically distinct on the surface, but they are self-similar patterns of increasing complexity with a correspondingly less punctuated and dramatic timing.

This principle is applied to the fossil record in Book Two and assessed in terms of more recent data relating to ancestral modes of metamorphosis, and is looking rather likely that species really did use a commonly shared ancestral tool-kit as described above, to develop as embryo/larval/tadpole-like organisms into increasingly specialised and mature forms as proposed by Von Baer and others.

By applying Von Baer’s laws to all domains of life, not just vertebrates, a fascinating view of evolution begins to emerge which is fundamentally different to our current linear descent model, as it seems that we may not be looking at literal ancestors such as bacterial forms giving rise to yeast and this domain of life then spawned fungi. Or that sponge plants became so complex that they were able to produce animal-life. But a self-similar system that allows all expression of complexity, modification and adaptation according to its environment and interactions with each other within that environment at every scale of life that was the means to shape and form the species itself.

Life may be a complex web of symbiotic processes that has allowed for fundamentally distinct domains of life to emerge independently (but develop dynamically interactively and symbiotically) and all appears to be driven to its own ultimate expression of its intrinsic complexity according to the conditions of its development as proposed by

Lamarck. Many convergences and divergences and independent developments are all possible under this model and all it ultimately coordinated and driven by universal laws of growth and development, shape and form as proposed by D'Arcy Thompson.

The nested dolls principle becomes apparent as we review the possible evolutionary development of organisms by observing their present-day modes of development and reproduction methods. Just as the merging or fusion of bacteria as suggested by Margulis, is the means by which a leap in complexity and novel diversity could have arisen creating a whole new domain of eukaryotic life (plants and animals), this appears to be replayed in even the most sophisticated organisms such as ourselves on another scale.

The sperm merges with the egg, the egg now with the novel donation splits itself into many un-programmed clones (stem-cells), environmentally, these are triggered via the chemical basis of Morphogenesis (according to Turning) and supported by the epigenetic nature of cellular differentiation, is seemingly a rerun of evolutionary complexity, as these colonies of programmed/differentiated cells then start signalling and resonating together to build even more complexity on self-similar patterns and scales and eventually, an entire and highly organised and coordinated multi-cellular organism – a whole embryo that can further develop and diversify as it learns to know what it is going to be when it grows up – the differentiation of the pluripotent species perhaps?

This model certainly seems well supported when I attempted (not knowing what the result would be) to apply the present-day modes used by living bacteria and those used by living eukaryotes and their modes of development and reproduction, all the way up to vertebrates and the many scales of reproduction/developmental modes used presently with the aim of gaining an insight into the evolutionary processes that led to the formation of the species itself. Essentially, this was inspired by Von Baer's principle as applied to vertebrates, but taken right down to the most primitive scale of the coding system and the cellular world itself.

For instance, when applied to the eukaryotic world, we can begin to see how the old bacteria mergers of two distinct coding systems and cellular systems produced many modified copies of itself by splitting apart again, which could operate as individual entities and grow and develop and become modified until they learned to transfer their modified coding system in less drastic ways using their little tails as seen in yeast courtships.

The product of these novel transfers could produce whole colonies of individuals and so on and so forth until the next level of scaled complexity: the eukaryotic colonies coordinating their activities and becoming a whole multi-cellular organism. From the organelle to the organs and finally the whole organisms which itself is an environmentally sensitive and responsive organ. It's seemingly, nested dolls all the way up to largest scale, and nested dolls all the way down to the smallest scale.

What we essentially have then, is nested scales within nested scales of increasing complexity and sophistication, but still abiding by the self-similar patterns repeating on every scale which characterises fractal systems. Hence, we have the Matryoshka principle seemingly underpinning all of the evolutionary process.

It seems that when we look deeply into even the smallest and seemingly, earliest cellular or coding system, that it is self-similar and repeating patterns of complexity all the way back to the atomic and molecular level. Returning to our Matryoshka analogy, the starter doll, as we can recognise this at a macro level as a whole doll and we might perhaps begin classifying them into categories (based upon shared features) as "smallest and earliest and most primitive types" or classify others as the "most advanced and later types". And keep doing this, or we could simply say that each set was created using similar materials, similar methods and each successive doll in the set is formed spatially in direct proportion to the former version and if we were lucky enough to stumble on a whole set, then we could deduce the principle of how nested dolls were made and not worry about all the distracting detail and many shapes and sizes found in the isolated dolls.

In other words, instead of looking for the genetic code that was passed down directly according to a belief that they had a literal last common ancestor, would this not be like trying to find out the particular lineage of the wood (which forest it came from and perhaps the actual tree now fossilised) that the wooden dolls were carved from. It is a source of wood: and a fairly good material to carve wooden nested dolls from. Presumably some wood types are more amenable to carving than others depending upon its grain etc. Similarly, if certain patterns of code or molecular bonds work best for instructing proteins to do an initial rough carving, then that seems like a fairly good way to start and refine and sculpt as you go along thereafter.

The original nested doll would also inform the ultimate shape and form of the more complex scales of nested dolls from the same type of set. However, we could describe the seemingly original doll as a whole self-contained system that has an in-built natural system that has also evolved in scales of complexity that formed the original doll in the first place. Many other dolls could be scaled up from this doll in proportion to the former and according to environmental resources and conditions, by simply employing the same system for growth and development and so on and so forth.

On a very simple level of simple patterns of form and features (topography), we could suppose that an original organic and pliable (and environmentally responsive) Matryoshka-type doll has a more undulating shape than our normal commoner garden type Matryoshka set. The growing field (morphogenetic) has been established fundamentally at the tiny scale and therefore, every doll at every scale would have to be sculpted similarly to the more undulating originator doll. This mirrors D'Arcy Thompson's model.

For instance, we could imagine then that the initial rough carving (modular formation during development before the detail is filled in) of the organism (a blob with no symmetry, a star or flower-shape or crystal prism to become an extended six-sided snow crystal, or a bilateral – type of mirror image pattern like vertebrates within an inside skeleton including ourselves or invertebrates with an external skeletal coat) fundamentally informs the outcome further down the line.

And presumably, by applying the laws of growth (the universal development curve or the Sigmoidal growth curve) and the metabolic scales and intrinsic rate of growth etc to the equation, it would seem that once the whole set and the self-contained, but self-similar individuals within the set have become stabilised as a whole system (within its environmental niche as in the case with organisms), then as a self sustaining system, these can grow, shrink and generally adapt on a micro-scale (it is fundamentally a particular species type) according to available resources and general environmental conditions thereafter. This we see within a number of epigenetic studies outlined in Chapter Five.

This naturally driven system of a tendency to order and complexity observable at every scale of life and level of complexity within the main fundamental groups that appear to diverge increasingly as evolution unfolded as suggested by both Von Baer and D'Arcy Thompson, also begins to reflect the type of evolutionary development proposed by Lamarck over 200 years ago. Furthermore, all three offered perfectly natural means by which this tendency to complexity within the main groups could be achieved, where D'Arcy's universal patterns of life seem to inform at another scale, the form of evolution elaborated on by Lamarck and underpinned Von Baer's laws, namely: speciation via epigenetic modification.

All in all, the ancestor may not have been an actual tangible entity, but rather a process, a shared ancestral condition and the means of remodelling and further refinement were literally shared across all domains of life. This self-sustaining system appears to have coordinated itself into meaningful cellular life as seen in the colony of synchronised cells (oozing blobs of protoplasm – liquid crystalline sluggy creatures that weren't always wired together as perhaps they didn't always fire well together and kept losing their link).

The crystalline mobile viral critter may have sort of become an entity, but I don't think it is a literal ancestor to us either, it is a whole nested set of complex systems, each built from the previous principles simply because the system itself is self-replicating and self-similar on every conceivable scale. In other words, it is a fractal evolutionary system, just as Russian or Matryoshka dolls are made according to a fractal principle that are predictable at every scale, even if you haven't got the full set.

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Then her research began to take a different direction a few years ago as it came to encompass a fairly distinctive field of science, namely: the historical and critical scientific examination of the Darwinian version of evolution and its scientific alternatives, which is the main subject matter within the books listed in the next section.

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- Prof. Noble (2013, Rocking the Foundations of Physiology)

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But Old Mr. Darwin wasn't to Blame: The Little Book of Evolutionary Quotes

As the title suggests, Old Mr. Darwin wasn't actually to blame for all that ensued in his name. This was perhaps the most surprising aspect of what I discovered when I stumbled upon the more obscure archives of evolutionary history. Well, almost as surprising as finding out that our current evolutionary theory is beyond repair, apparently and its replacement by a quantum-like synthesis has been looming around the corner for some time now, at least, that is according to the peer-reviewed literature as you will see as you read on.

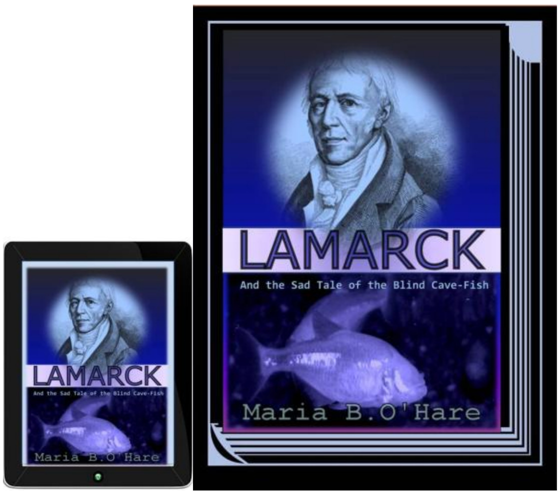
Collectively these quotes form an outline of a narrative that I hope you will find illuminating and get as much from reading them as I did from discovering them. You may even be a little shocked, stunned and occasionally let out a little gasp when you hear what some top scientists have actually said about our modern synthesis.

Sample Quote:

LIFE IS PHYSICS: EVOLUTION AS A COLLECTIVE PHENOMENON FAR FROM EQUILIBRIUM

"*Evolution is the fundamental physical process that gives rise to biological phenomena. Yet it is widely treated as a subset of population genetics, and thus its scope is artificially limited….*
The lack of widespread appreciation for, and understanding of, the evolutionary process has arguably retarded the development of biology as a science, with disastrous consequences for its applications to medicine, ecology and the global environment".

Goldenfeld & Woese (2011, 375)



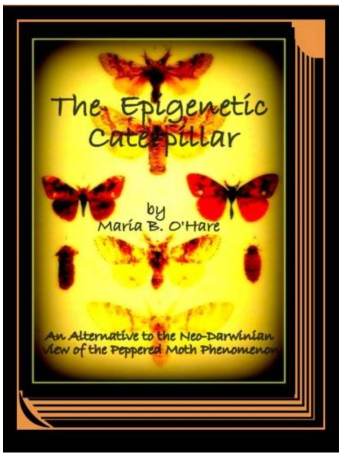
ISBN: 978-1-78280-465-9 -

Lamarck & the Sad Tale of the Blind Cave-Fish

This book assesses the unjust suppression & more recent scientific vindication of the 'Original Founder of Evolution' Jean Baptiste Lamarck. Not many know that Darwin himself was a Lamarckian as he believed that blindness in cave-fish was due to the disuse of their eyes brought about by finding themselves in dark environments. It turns out that he may have been right....

Review on Smashwords dedicated e-book platform
by: Bud Stark on March 17th, 2015 :

This book is a must read for those interested in evolution, especially if you consider yourself a Darwinist or a NeoDarwinist or are not sure of the difference between the two. I remember reading Richard Dawkins' name only once in this book, but his name kept cropping up in back of my mind. For those many followers of his, you need to see what he is struggling to hide, the discoveries in epigenetics that will undermine evolution by natural selection and Dawkins' campaign to make the entire progress of nature random and directionless.
(reviewed within a week of purchase)



ISBN: 9781782803881

The Epigenetic Caterpillar: An Alternative to the Neo-Darwinian View of the Peppered Moth Phenomenon

I was delighted to get a very early and most supportive *Five Star* review of the paperback version of this book on Amazon UK, before it was even in full circulation (first series). I believe it expresses exactly what I hope you will get from reading this little book:

Review of Epigenetic Caterpillar 14th Jan 2015

"…I bought this book for my father, and want to share his comments on the book. "I have recently read a wanted and received present, 'The Epigenetic Caterpillar' by Maria Brigit O'Hare. I was so delighted to have had my 60 year old understanding of the subject, which was belittled by my teachers at the time, reinforced by this great little book. It was informative and explanatory, but not too technical, and will cause many who read it to question their indoctrinated simplistic Darwinism thoughts on the subject of Evolution. A great read, and a must have for anyone who has an interest in this topic".

The Epigenetic Caterpillar refers to the fact that a sluggy creature (a caterpillar) has exactly the same genes as its adult form (a butterfly/moth), yet it looks nothing like a flying insect.

The epigenetic caterpillar is used to illustrate the fact that genes themselves don't change during metamorphosis causing such radical alternations to the caterpillar, but rather, it is how its genes are EXPRESSED (epigenetically) according to environmental adaptive needs, which makes the big difference in the end.

Therefore, the epigenetic caterpillar concept should help us assess the true validity of the Neo-Darwinian version of the case of the text-book example of Industrial Melanism in moths, which has often been described as: evolution in action via natural selection. At the same time, the epigenetic explanation begins to offer a much overdue evolutionary alternative.

The Epigenetic Caterpillar refers to the fact that a sluggy creature (a caterpillar) has exactly the same genes as its adult form (a butterfly/moth), yet it looks nothing like a flying insect. The epigenetic aspect of the caterpillar is used as an analogy, as we now know that genes themselves don't change via metamorphosis in order to make such radical alternations to the caterpillar, but it is how these genes are EXPRESSED (epigenetically) according to environmental adaptive needs, that makes the big difference in the end.

Therefore, the epigenetic caterpillar will be used to assess the validity of the Neo-Darwinian, text-book example of Industrial Melanism in moths, (often described as evolution in action via natural selection). And as it turns out, Darwin may not have disagreed.

E-Book version also available at all major outlets

Origins of this Book

I should explain how I ended up writing an alternative to the whole of evolution from a non-Darwinian perspective and as you already may have worked out, although, I am: far from qualified to do so, at least that is according to our conventional system of doing *science,* that this book does present the facts from others who are deemed to be qualified by our current system, to do so.

I didn't set out to tackle such a controversial and massive topic; nor did I even realise, initially, that it was such a controversial topic, other than the fact that I personally never quite felt comfortable with the slavishly-driven/selfish-gene concept promoted by the likes of Richard Dawkins (the British biologists who is most famous for his book *The Selfish Gene* amongst other publications of that type). I just put that down to me not facing up to the reality of the so-called *dog eat dog* world that we seemly find ourselves in. I should however, point out or remind you that it wasn't Charles Darwin who dogmatically promoted, at the expense of all other valid theories, this particular version of life evolved and all its complexity, upon the rest of us (O'Hare 2015).

It all began when I started to research a book – a novel idea – yes a work of fiction, but as all fiction should be (this one was futuristic, but the same goes for historical fiction), it works best when it is well-grounded in facts, or at least believable scenarios that are rooted to some in reality.

In the case of the particular novel I found myself working on (only as a labour of love, fulfilling my passion for writing and a light distraction from archaeological research), the main protagonist: Michael Mc Namara, a young and rather naïve geneticist who had taken his first gulps of life some 25 years earlier, as the world shuddered and looked on in dismay at the fateful events of 9/11 in New York City, because of his particular career path, inadvertently found himself embroiled in a highly classified scientific subterranean world. In other words, the in-depth research required to give this story believability, led to me stumbling down a rather large rabbit hole myself.

The novel was put on hold, I believed that this was temporary, but several years later and still no published novel about Michael's adventures, I ended up finding out instead: a great deal about our current evolutionary theory. Essentially, I discovered to my amazement that according to the science: Darwinism has never satisfactorily explained evolution, and according to the historical record, it never did (See Free Flip book version: *But Old Mr. Darwin wasn't to Blame: The Little Book of Evolutionary "Quotes"*). Fortunately, I also began to unravel some tantalising insights from these same sources, as to how it might have happened and to cut a long story short, I finally have an evolutionary scenario that would not be out of place in a futuristic genetics lab in the bowels of the earth. Hence, this book is the result of that thought experiment.

Book Two, if you are interested in following the actual application of these theories, runs chronologically rather than thematically and commences with the first formation of animal organisms (the microscopic level), then zooms out to the larger evolutionary picture as we proceed through time. By the time you have hopefully read both of these books, you will be fully versed in the alternative time-line given at the end and be able to make up your own mind regarding which timeline makes more scientific sense: it, or our conventional one.

In combination, both books should begin to answer the rather big question posed in the main title: *If it wasn't by Darwinian means, how did it happen*? And hopefully, after reading Book Two and other related books by Dig-Press on the topic of alternative evolutionary theory, you might come to understand fully the need to replace our modern synthesis with something a whole lot better.

IF YOU GAINED ANYTHING FROM READING THIS SCIENTIFICALLY-GUIDED THOUGHT EXPERIMENT, PLEASE SHARE/REVIEW/DISCUSS with others and do not hesitate to get in touch for any specific comments, constructive criticism and general feedback and/or signup for occasional updates on research by contacting Me at: EMAIL: diggingupthefuture@gmail.com

Cheers

MariaBrigit