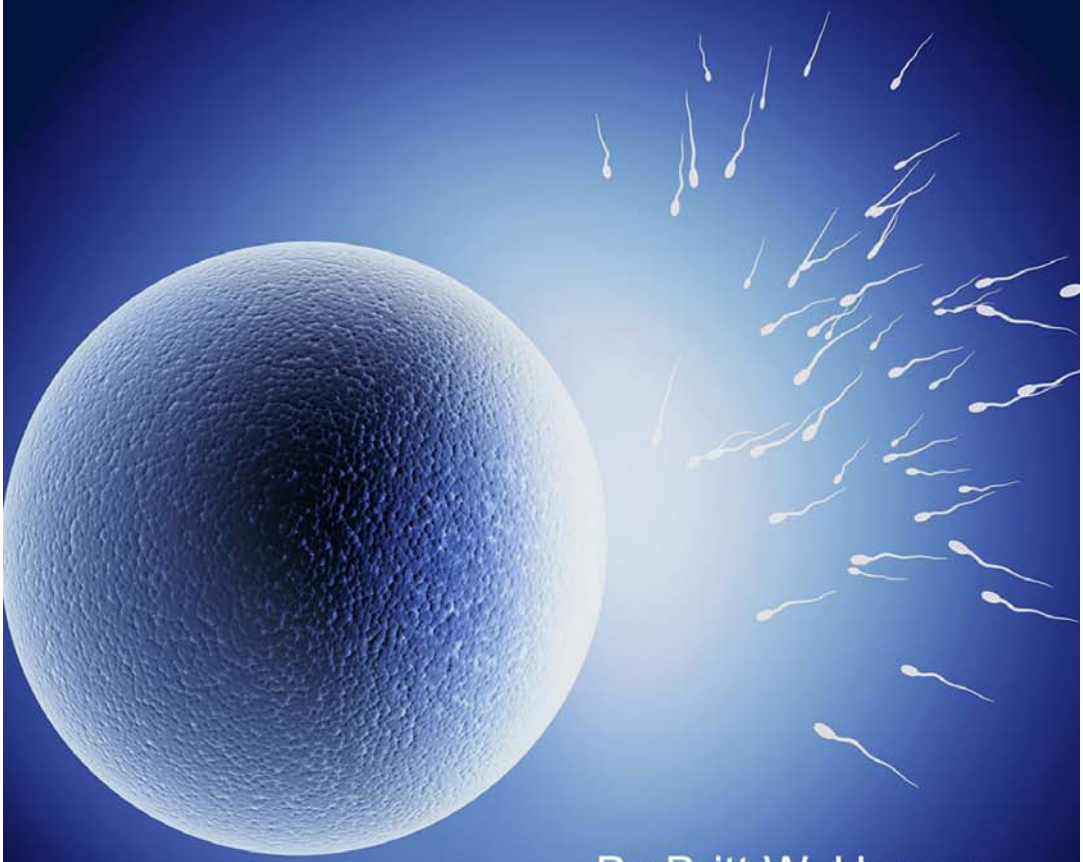
Genetic Experimentation:

The Adaptive Function of Sex and Conjugation



By Britt W. Hanson

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PREFACE

Although this book is intended to be read as the third in the sequence outlined below, it may be read independently, as well. So that each book can be read on its own, some of the material overlaps.

1. *Dynastic Theory: The Evolution of Altruism in Animal Societies (Replacing Kin Selection)*

2. *Epigenetic Evolution: A Theory of Cultural Evolution through Directed Creativity*

3. *Genetic Experimentation: The Adaptive Function of Sex and Conjugation*

—Britt Hanson

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INTRODUCTION

"Unless such [profitable genetic variations] occur, natural selection can do nothing."[1]

—Charles Darwin

Darwin knew that changes in heritable matter—which today we call genetics—were essential to evolution. The divergence of reptiles, birds, mammals, plants, and every other species must be underwritten by new, beneficial genetic changes. But Darwin didn't know what caused them: "I have hitherto sometimes spoken as if the variations—so common and multiform with organic beings under domestication, and in a lesser degree with those under nature—were due to chance. This, of course, is a wholly incorrect expression, but it serves to acknowledge plainly our ignorance of the cause of each particular variation." (Darwin 1952a, p. 65).

Since the neo-Darwinian synthesis in the middle of the twentieth century, evolutionary biology has suffered no similar doubt. Genetic variation is said to be caused by random mutations, with particular emphasis on point mutations—changes in individual alleles that code for specific traits.

One purpose of this book is to demonstrate that the doctrine of chance mutation is false. A second purpose is to demonstrate the falsity of related neo-Darwinian doctrines: the population genetics models that have been built upon Mendelian genetics. In short, the objective is to cast off neo-Darwinism altogether.

A third purpose is to demonstrate that significant genetic variation—the kind of variation necessary for evolution—occurs as rearrangements of DNA sequences through transpositions, translocations, insertions, inversions, splicing, deletions, additions, amplifications, and duplications. Much DNA, including that which is rearranged, does not code for specific traits or even specific proteins. Rather, it regulates the developmental sequences of organisms. Genetic rearrangements alter the developmental sequences. These can result in minor changes in specific traits, but they also can result in cascades that affect suites of traits or alter overall morphology.

The hypothesis that significant variations are due to genetic rearrangements is not new. It is fairly well-accepted among biologists, especially molecular geneticists and developmental biologists. What is new, or is at least more greatly amplified in this book, is that evolution through genetic rearrangement is utterly inconsistent with the neo-

[1] Darwin 1952a, p. 41.

Darwinian synthesis.

The fourth and ultimate purpose is to solve the puzzle of sex and conjugation. By "sex" I mean the effects of three genetic manipulations that occur during the process leading to reproduction: a) the event known as "crossing-over," which occurs during meiosis I, when homologous chromosomes transfer and reorganize DNA; b) the event that occurs during meiosis II, when chromosomes are recombined into new, unique haploid combinations in gametes (sperm and unfertilized eggs); and c) when gametes unite, which results in a new, unique combination of diploid chromosomes. By "conjugation" I mean the process that occurs in "lower" organisms when they donate or swap DNA, separate from the act of reproduction.

Sex has long been a difficult problem for neo-Darwinian theory: "The existence of sexual reproduction poses a big theoretical puzzle to Darwinians." (Dawkins 1986, p. 268). Although in some species, such as our own, sex is necessary for reproduction, that is not its adaptive function. Many lower organisms reproduce asexually (cloning). In many of these species, organisms switch to sexual reproduction at some stage in their life cycles. There are species, such as dandelions, that have even reverted from sexual reproduction to asexual. If reproduction were the function of sex, cloning would be far simpler, more efficient, and wouldn't require males. Moreover, even in species in which reproduction is tied to sex, reproduction itself doesn't explain the genetic manipulations that accompany sex, including the intricate molecular processes involved in meiosis and crossing-over. Furthermore, conjugation, which like sex involves genetic manipulations in the transfer of DNA, occurs separate from reproduction.

That sex is a puzzle should be embarrassing for evolutionary biology. Sex must be extremely important. Most organisms reproduce sexually at some point in their life cycles. Sexual reproduction is present in all taxa and most species. No known "higher" organisms have evolved through cloning. All either reproduce sexually (at least periodically) or have evolved from ancestors that did. (Bell 1982, p. 437; Maynard Smith and Szathmary 1995, pp. 164-66). As the study of microorganisms has progressed, it is no longer even clear that any lower organisms have evolved by cloning, since they engage in conjugation.

Not only should it be embarrassing, the fact that sex remains a puzzle should be a clue that something fundamental is wrong with the whole neo-Darwinian framework. A leading theorist on the subject, John Maynard Smith, once remarked that "[o]ne is left with feeling that some essential feature of the situation is being overlooked." (Ridley 1993, pp. 40-41, quoting Smith). The essential feature that has been overlooked, which Maynard Smith did not consider, is that the population genetics model and the concept of chance mutation are wrong. After describing sex as inconsistent with evolutionary theory, Williams stated that his "purpose is to propose minimal modifications of the theory to account for" sex. (Williams 1975, Preface, v). The argument that follows is

that sex can't be solved with minimal modifications to neo-Darwinism; neo-Darwinian theory needs radical surgery, including removal of the concepts at its core.

The hypothesis set forth in this book is that genetic rearrangements are not due to "mutations" in the sense of random errors. Rather, they are produced by experimental genetic tinkering. This is the adaptive function of sex in higher organisms. It is also the adaptive function of conjugation in lower organisms.

Mendel, Neo-Darwinism, and the Problem of Sex

When, at the beginning of the twentieth century, Mendel's laws of heredity were rediscovered, early proponents placed it on par with Darwin's theory of natural selection. (Carlson 1966, p. 12). William Bateson characterized Mendel's experiments as "worthy to rank with those which laid the foundation of the Atomic laws of chemistry." (*Id.*, p. 1). Later, in his 1942 book *Evolution: The Modern Synthesis*, which solidified the neo-Darwinian synthesis, Julian Huxley quoted an author as saying that "Mendelism is a theory of heredity: it is not a theory of evolution." (Huxley 1942, p. 26). Huxley responded: "[Y]et the assertion is purely formal. Mendelism is now seen as an essential part of the theory of evolution. Mendelian analysis does not merely explain the distributive hereditary mechanism; it also, together with selection, explains the progressive mechanism of evolution." (*Id.*).

Textbooks still speak of Mendel's laws in the most glowing terms. (*See, eg.*, Turnbaugh et. al. 1993, p. 35; Arms and Camp 1987, pp. 281-83). These laws are described as not only supplying the missing laws of heredity, but also as solving the problem of blending inheritance, causing the demise of Lamarckian inheritance of acquired characteristics, and leading to the concept of a unit of heredity—each unit corresponds with a discrete trait. Bateson called the bearers of Mendelian traits "unit characters." (Carlson 2011, p. 69). With *The Theory of the Gene*, published in 1917, Morgan, who was working with fruit flies, established the term "gene" as the unit of heredity: "The germ plasm [reproductive cell] must, therefore, be made up of independent elements of some kind. It is these elements that we call genetic factors or more briefly genes." (Carlson 1966, p. 76)(quoting Morgan)). The concept of the gene is thus the direct descendant of Mendel.

A corollary of the concept of the gene is the concept of the allele, a term coined by Bateson. (Carlson 1966, p. 12)(Bateson called it "allelomorph," later shortened to "allele"). Organisms with two sets of chromosomes (i.e., diploid) inherit one set from each parent. Most of the genes on both sets will be identical (homozygous). But for some genes, there are alternates—alleles—coding for different traits (heterozygous). In Mendel's peas, there were alternate alleles for white and red flowers at one slot (loci) on the chromosome and alleles for smooth and wrinkled peas at another.

A model of an organism emerges from Mendel's laws. Genes are lined up at slots (loci) on a chromosome, with each gene coding for a particular trait: a part of an eye, or wing, or leg, or leaf. Each trait is independent of other traits. An organism is the sum of these independent traits and, therefore, the sum of these independent genes. For individuals in any given species, the genes at most of the loci will be identical. But each individual will be unique, differing in alleles at some slots, and therefore differing in

some traits.

On this foundation, neo-Darwinism built a model of evolution. Some traits are more fit than their alternatives, which is to say that some alleles are more fit than their alternative alleles: "Genes are competing directly with their alleles for survival, since their alleles in the gene pool are rivals for their slot on the chromosomes of future generations." (Dawkins 1989, p. 36). Organisms with fitter alleles will be more likely to survive than those with less fit alleles. Thus, in each generation, alleles will shift in frequency as natural selection operates to cull the less fit and favor the fitter. A definition of evolution follows: "[E]volution is the change in frequencies of alleles in a gene pool from one generation to the next." (Arms and Camp 1987, p. 351).

Using these models, the adaptive role of sex seems to be evident, at least initially. Sex brings together half of the genes of the male and half of the female, creating a new, unique combination of genes and traits in each offspring. In addition, during meiosis, homologous chromosomes or sister chromatids swap alleles, resulting in new, unique combinations of genes and traits in each chromosome. Thus, each generation produces new combinations. Natural selection culls the inferior combinations. The superior combinations survive and reproduce. Some of these combinations might even be adaptively superior to any combinations in the parental generation. The effect of natural selection over time will be to improve the species through this ratcheting of better and better recombinations.

However, the framers of the neo-Darwinian synthesis saw limitations and flaws in this hypothesis. To begin with, this model does not explain how variation is generated in the first place. Mendelian (population) genetics speaks only to the rules that govern the way that *pre-existing* variation in parents is sorted in offspring (and, by statistical extension, over a population in general). (Huxley 1942, p. 51). It does not explain how variation in alleles came to exist. Mendelian genetics simply assumes the existence of variation. Hence, Mendelian genetics does not explain the *cause* of new alleles.

Moreover, while the shift in pre-existing variation in a population's gene pool might be a form of evolution, it is not a very significant form of evolution. Perhaps it is possible for birds in the wild to evolve a new subspecies by selective shifts in the frequencies of alleles in their gene pool. But it is another thing altogether to imagine evolving chickens, ants, and all other species merely by shifting frequencies of existing alleles. For this more significant evolution, new variation is required. As one of the architects of the neo-Darwinian synthesis, George Gaylord Simpson, put it, "New combinations of genes and chromosomes produce new variant sorts of organisms, but no basically new types of organisms can arise and evolutionary change cannot be long sustained...as long as the genes and chromosome sets remain of the same kind." (Simpson 1951, p. 90; *see also* Huxley 1942, p. 51).

Theorists have also spotted a defect in the hypothesis that the genetic reshuffling that occurs from sex can result in new, adaptively superior, genetic combinations. The defect is that any such adaptive recombination would be ephemeral; it would be broken apart by reshuffling in the next generation. (Futuyma 1986, p. 281; Butlin et. al. 1998, p.8). In fact, some theorists go further, positing that this effect of sex must be maladaptive: "In a stable environment, recombination is almost always selected against, because it breaks down favorable gene combinations, so that an allele for fostering recombination is associated with less fit combinations." (Futuyma 1986, p. 281). In a stable environment, cloning would be more adaptive because it would keep the successful genotypes and phenotypes intact.

The concept of the gene pool—all the alleles at all the loci of all the individuals in a population or species—is fundamental to population genetics; it leads to the definition of evolution as a change in the gene pool of a species. But the gene pool concept creates yet another problem for sex. Although sexual reshuffling makes for unique genetic combinations in individual organisms, from the standpoint of the gene pool, the net effect of sex is nil. (Butlin et. al. 1998, p. 9). All that sex accomplishes is to merely reshuffle existing alleles among the members of a population. No change in allele frequencies occurs. One way to see this is to imagine two populations that have the same allele frequencies, with one population reproducing sexually and the other asexually. When they reproduce, each population would wind up with the same frequencies of alleles in its gene pool. Allele shuffling thus has no effect on evolution of the gene pool. (Arms and Camp 1987, p. 354). This conclusion is codified in another neo-Darwinian doctrine built on Mendelian genetics: the Hardy-Weinberg Law, which sets forth the potential causes of changes in frequencies of alleles and genotypes. Sex is not a potential cause.

Because of these problems, many of the framers of the neo-Darwinian synthesis initially supposed that the adaptive advantage of sex must be that it maintains genetic diversity in a population. (*See, eg.*, Dobzhansky 1951, p.261). If environmental conditions change, genetic diversity would be beneficial to a species (or population) in allowing it to respond. The sexual recombination of alleles results in diverse, genetically unique organisms. In contrast, an otherwise comparable asexual species, with all organisms being nearly identical, could not adjust. Asexual species therefore would become extinct quicker than sexual ones.

However, this species selection rationale for sex has been virtually eliminated. Modern neo-Darwinians point out that natural selection operating at the level of an entire species cannot account for the evolution of sex:

> The machinery of sexuality, sex organs, sexual behavior, the cellular machinery of sexual cell division, all these must have been put together by standard, low-level Darwinian cumulative evolution, *not* by species selection.

(Dawkins 1986, p. 268 (emphasis in original); *see also* Bell 1982, p. 91). As a biology text puts it, "[g]enes that cause genetic recombination, but put their owners at a selective disadvantage, cannot increase in frequency now merely because they avert extinction later." (Arms and Camp 1987, p. 395).

The theory of kin selection, which has been neo-Darwinism's primary tool to account for the evolution of altruism, has compounded the problem of sex. To accommodate kin selection, neo-Darwinian theory has shifted from the traditional Darwinian maxim that organisms maximize their offspring to the concept that organisms maximize their genes: "[U]ltimately there is only one measure of [an organism's] evolutionary success: the proportion of its genes present in future generations." (Arms and Camp 1987, p. 392).

Gene-maximization compounds the problem for sex because organisms that maximize their own genes ought to clone themselves. Sex does precisely the opposite. "As recent theorists have insisted, the 'choice' of reproducing sexually carries a huge *immediate* cost: organisms send along only 50 percent of their genes in any one transaction (to say nothing of the effort in risk involved in securing a transaction in the first place)." (Dennett 1995, p. 76 (emphasis in original)). This has been interpreted as requiring two to one leaps of benefits to costs (compared to cloning) in order for sex to evolve: "Sex tears apart every genome in every generation…and in doing so it does not merely reduce fitness, but halves it." (Bell 1982, p. 78). A better alternative would be to reproduce by cloning: "Switching from sexual to asexual reproduction is the most obvious way of increasing genetic relationship with offspring in which resources are invested." (Williams 1980, p. 373).

Since theorists have been unable to agree on a hypothesis that posits even a slight advantage to sex,[2] the notion that benefits must double has made the problem seem even more intractable: "The primary task for anyone wishing to show favorable selection of sex is to find a previously unsuspected 50% advantage to balance the 50% cost of meiosis. Anyone familiar with accepted evolutionary thought will realize what an unlikely sort of quest this is." (Williams 1975, p. 11). Hence,

> The near universality of sexual reproduction remains a major unsolved mystery. It is explicitly a mystery in relation to kin selection, on which so much of sociobiological thought depends.

(Williams 1980, p. 382). Williams thus declared that the "prevalence of sexual reproduction in higher plants and animals is inconsistent with current evolutionary

[2] There have been a variety of hypotheses; none have achieved consensus. These will be discussed subsequently.

theory" and is "a kind of crisis in evolutionary biology…." (Williams 1975, Preface, p. v).

I have eliminated this two-for-one problem in a previous book, *Dynastic Theory: The Evolution of Altruism in Animal Societies*. In that book, I demonstrate that kin selection is wrong. Its predictions do not come close to matching the actual patterns of altruism in any species. Moreover, its mathematical formula requires implausible leaps of benefits to costs in order for altruism to evolve. Dynastic theory explains the evolution of altruism (and group adaptations) without the hypothesis that organisms maximize their genes. It thus jettisons the far-fetched idea that the benefits of sex must double the costs in order for sex to evolve. As with any other trait, sex can evolve if it is slightly advantageous.

But dynastic theory, by itself, does not address the other problems with the adaptive function of sex. Yet in order to have evolved, the intricate genetic manipulations that occur during sex and conjugation must serve some adaptive function. It would seem that these manipulations should somehow be implicated in generating genetic variation. But according to neo-Darwinian doctrine, sex just shuffles alleles and chromosomes. Another neo-Darwinian doctrine grants the role of generating genetic variation to another source: chance mutations.

Mendel, Neo-Darwinism, and Point Mutations

While sex has been a mystery, the source of genetic variation has been widely thought to have been found: they result from mutations. (Huxley 1942, p. 51). A genetics textbook sums it up: "Mutation is the ultimate source of all genetic variation; it provides the raw material for evolution.... Without mutation....organisms would not be able to evolve and adapt to environmental changes...." (Gardner et. al. 1991, p. 289).

Darwin was aware that offspring of plants and animals under domestication occasionally develop freakish, maladaptive traits, which he called "sports," that could not possibly have been inherited from their parents. (*Id.*, p. 13). Some biologists, including allies of Darwin, speculated that new species might spring into existence from similar kinds of instant leaps in traits—saltations. (Mayr 1982, pp. 542-44). Darwin, however, dismissed this possibility with the canon "natura non facit saltum": nature makes no leaps. (Darwin 1952a, p. 92). Darwin was so dismissive of saltations that he privately remarked that he "would give nothing for the theory of Natural selection, if it requires miraculous additions at any one stage of descent." (Dawkins 1986, p. 249, quoting a letter from Darwin to Lyell). Instead, "natural selection acts only by taking advantage of slight successive variations; she can never take a great and sudden leap, but must advance by short and sure, through slow steps." (Darwin 1952a, p. 92).

De Vries, who first rediscovered Mendel's work, nevertheless revived saltationism. He observed in a field of evening primroses two plants quite unlike any others, with multiple differences in traits. When self-fertilized, they remained true to type. De Vries concluded that the two plants were new species that had been caused by changes in heritable material, which he called "mutations."

Thus, the term "mutation" originally meant a change in heritable material that resulted in new, species-transforming traits, all in a single bound. (Carlson 2011, p. 33). Subsequently, however, other Mendelians observed small mutations in their laboratories, especially in experiments with fruit flies. (Carlson 2011, pp. 42-51). Geneticists were even able to induce them by bombarding the flies with x-rays and other kinds of stress.

With the development of the concepts of the individual gene and the allele, these small mutations were attributed to minor changes in alleles. These were dubbed "point mutations." This is how new alleles were supposed to come into existence.

The idea of mini-mutations in individual alleles affecting individual traits fit neatly with the Mendelian model that was then developing: "It was the gene that was the associated with the evolution of life… Hence, Muller equated the point mutation with 'the gene as the basis of life.'" (Carlson 2011, p. 51).

And the concept of point mutation, along with the Mendelian model, also fit nicely with Darwin's theory of gradual evolution through small steps. In contrast, De Vries' concept of saltation through mutation seemed to require major miracles. If species came into existence by chance in a single bound, natural selection would be immaterial. Saltationism thus fell out of favor. However, the concept of chance mutation took hold, but instead of referring to saltations, it referred to small point mutations.

Nearly all of the mini-mutations observed in labs were maladaptive or nonadaptive. In natural settings, mutations were supposed to be caused by random errors in copying genes during the reproductive process, and thus likewise would be mostly harmful to the organism. (Dawkins 1986, pp. 125-26). But it could be supposed that occasionally, even rarely, a point mutation might prove beneficial. When that occurred, natural selection would favor the individual organism that acquired the mutant allele, and eventually the allele would become fixed in the species. Bell sums it up:

> The classical view of genetic variation is that almost every locus in diploid organisms is occupied by two alleles which are identical in state or, at any rate, which have virtually indistinguishable effects on fitness. The major process of genetic change is the elimination of newly arisen deleterious recessive mutations; evolutionary progress results from the rare appearance of favourable alleles at mutation frequency and their subsequent fixation under natural selection.

(Bell 1982, p. 92).

This has skewed the role of natural selection in a different direction than Darwin had envisaged. Since mutations are mostly deleterious, the primary role of natural selection must be to eliminate variation. Thus, rather than natural selection being a mostly positive cause of evolution, it is mainly a negative force: "most of natural selection is concerned with preventing evolutionary change rather than driving it." (Dawkins 1986, p. 125).

There is also another way in which selection should prevent evolution. If point mutations result from random DNA copying errors, which are mostly harmful, selection ought to minimize harmful errors by reducing the causes of copying errors. But if selection cannot distinguish between harmful and beneficial errors, minimizing copying errors will diminish beneficial errors as well. According to Williams, organisms "strive" for a mutation rate of zero; evolution depends upon the fact that they fail. (Ridley 1993, p. 63 (citing Williams)).

Nonetheless, the concept of point mutation harmonized with the essential Darwinian idea of natural selection as the driving force of gradual evolution. These were the essential ingredients of the neo-Darwinian synthesis, Mayr's so-called "one-two punch": "The modern term 'evolutionary synthesis, was introduced by Julian Huxley in *Evolution: The Modern Synthesis* (1942) to designate the general acceptance of two conclusions: "gradual evolution can be explained in terms of small genetic changes ('mutations') and recombination, and the ordering of this variation by natural selection.…" (Mayr 1980, p. 1). Dawkins puts in more succinctly: "[M]utation is, ultimately, the only way in which new variation enters the species. All that natural selection can do is accept certain new variations, and reject others...." (Dawkins 1986, p. 125).

The Doctrine of Blind Variation

Another key element of the synthesis was ruling out Lamarckian inheritance of acquired characteristics. Mayr went so far as to define neo-Darwinism "as the Darwinian theory of evolution without recourse to any kind of soft [Lamarckian] inheritance." (Mayr 1982, p. 537). A corollary was acceptance of the Weismann doctrine, which holds that the germ plasm (reproductive cell) produces the somatic (body) cells, but that those somatic cells convey no information, and have no effect on, the germ plasm. (Mayr 1982, pp. 700-701). The germ plasm is segregated from the soma. Thus, effects of the environment on an organism, such as use and disuse of parts, could not alter inheritance. Weismann conducted an experiment in which he cut off the tails of lab rats. When offspring did not acquire shortened tails, he took that as evidence supporting his germ-line segregation theory—and thus as evidence against Lamarckian inheritance.

An inference necessarily drawn from the Weismann doctrine is that, lacking information from the environment, organisms' reproductive cells cannot produce variations that are biased in the direction of adaptation. In fact, for most biologists, the very idea of adaptively biased variations has become too unlikely to contemplate. According to Stephen Jay Gould:

> [W]e have found nothing in the workings of Mendelism or in the biochemistry of DNA to encourage a belief that environments or acquired adaptations can direct sex cells to mutate in specific directions. How could colder weather 'tell' the chromosome of a sperm or egg to produce mutations for longer hair? How could Pete Rose transfer hustle to his gametes? It would be nice. It would be simple. It would propel evolution at faster rates than Darwinian processes allow. But it is not nature's way, so far as we know.

(Gould 1982, p. 80). Other evolutionary biologists, however, have not been so cautious, instead heaping ridicule on the idea. Dobzhansky: "It may seem a deplorable imperfection of nature that mutability is not restricted to changes that enhance the adaptedness of their carriers. However, only a vitalist Pangloss could imagine that the genes know how and when it is good for them to mutate." (Futuyma 1986, p. 76, quoting Dobzhansky). Dawkins: "Mutation is not systematically biased in the direction of adaptive improvement, and no mechanism is known (to put the point mildly) that could guide mutation in directions that are non-random...." (Dawkins 1986, p. 312).

The doctrine that variation is not biased towards adaptation is consistent with the doctrine that mutations are random. These doctrines are philosophically significant.[3] They are viewed as eliminating vitalism and teleology from evolutionary theory—organisms have no "will" to evolve—and they are viewed as strictly adhering to Newtonian mechanics, which is to say determinism. (Lenski and Mittler 1993, pp. 188, 193). This, in turn, dovetails with the axiom of neo-Darwinian theory that natural selection has no foresight. (Dennett 1995, p. 76; Mayr 1982, p. 579). Evolution is "blind." Organisms do not "see ahead" and direct genetic variation in order to adapt and evolve.

These doctrines thus eliminate any hypothesis that organisms themselves participate in the evolutionary process such that they can generate new genetic variation. Organisms can have nothing to do with it. All causes of new variation are external to them, things over which they have no control. Errors happen. Mutations occur. Organisms thus do not really evolve; they get evolved. Biologist John H. Campbell

[3] A fuller exposition of the philosophical role of determinism in the biological and social sciences is set forth in Chapter 6 of *Epigenetic Evolution: A Theory of Cultural Evolution through Directed Creativity*.

summed it up:

> Newtonian dynamics relies on distinguishing a mechanical system from its surroundings.... Neodarwinism extends this framework of causality to evolution. Evolution is a process of change *in* a biological system, but *due* to forces from without.... The triumph of a complete, objective, reductionistic, and mathematically precise explanation for evolution is in finally banishing vitalism from the process. *Neodarwinism does so by denying the behavior of the biological system any causal role in its evolution.*

(Campbell, J. 1982, p. 191)(emphasis added in part).

This entrenched philosophy has enormous implications when hypothesizing about the possible function of sex and conjugation. It rules out any hypothesis that the adaptive function of sex has anything to do with facilitating evolution; that would mean that organisms *are* adapted to evolve, which would contradict Newtonian determinism. It would mean that organisms are not mechanical automata. They would be genetic engineers. To propose such a thing, however, one would have to suffer accusations of being a vitalist Pangloss.

Proof that Organisms Engage in Genetic Experimentation—Even within the Framework of Population Genetics

Neo-Darwinism latched onto the concept of random mutation as the source of variation because it seemed most consistent with determinism. The flip side of this concept, equally important, is that random variation wards off the specter of Lamarckian directed variation, which is not only teleological, but is supposed to be antithetical to Darwinian natural selection. (Dawkins 1986, pp. 288-306).

Darwin did not regard directed variation as inconsistent with natural selection. Although he objected to the vague notion that organisms have an "internal tendency to evolve," he accepted the Lamarckian notion of adaptation through the use and disuse of parts, as well as the idea that adaptation occurs by the direct action of the environment on organisms. (Darwin 1952a, pp. 65-69; see also Mayr 1982, pp. 689-93). Darwin's own later attempt at a theory of inheritance and variation, which he called "pangenesis," is strikingly Lamarckian. The direct action of the environment impacts "gemmules" in the organism, which are then transported through the body and eventually to the sex organs. (Mayr 1982, pp. 693-4). These adaptive new variations are then transported to offspring. Natural selection then sorts the fitter and less fit variations. Lamarckian directed variation is thus entirely consistent with Darwin's theory.

This book does not revive Lamarckism in the sense that use and disuse of parts are transmitted to offspring, nor Lamarckism in the sense that a rat with her tail cut off will bear offspring without tails. But the ultimate purpose of this book is to demonstrate that sex is an evolved device for directing genetic variation. To do this, it must be shown that organisms can produce genetic experiments—and that these are nonrandom. This is a kind of neo-Lamarckism.

I'll start by eradicating the taboo that organisms cannot direct variation. I will subsequently make the case that meiosis accomplishes more than mere allele swapping and chromosome reshuffling, as is supposed in population genetics. But first, even without disturbing the population genetics model, it can easily be seen that organisms do in fact produce nonrandom genetic experiments. This shouldn't even be controversial. The end results of crossing-over, meiosis, and uniting sperm and egg are genetically unique organisms. Each sexually-produced offspring differs from its parents. Each differs from every other member of the species. Each differs from every living thing and everything that has ever lived. Thus, sex produces organisms that are genetic experiments, never before tried and tested.

Crossing-over and meiosis involve intricate molecular devices. Sexual reproduction also involves intricate molecular devices for uniting sperm and egg, along with a great many physical and behavioral traits designed to make it happen. All of these devices and traits are highly evolved through natural selection. Being highly evolved, they must be adaptations.

It follows that these devices and traits are adaptations for producing genetic experiments—even using the models of the neo-Darwinian synthesis.

Furthermore, crossing-over, meiosis, and sex cannot in any sense be random. During crossing-over, chromosomes swap some alleles, but most alleles remain intact. During meiosis, the number of potential recombinations of chromosomes is enormous. In humans, the twenty-three chromosomes involved in the formation of gametes yield over eight million possibilities. (Brooker et. al. 2011, p. 316). But out of these possibilities, after any one meiotic phase, only four unique recombinants will result in haploid gametes. The sexual union of male and female gametes will involve only one of the four gametes from the male, and only one from the female, with the other six gametes disappearing.

In all of these processes, there are "determinations" to be made from a huge array of possibilities. These determinations must somehow be made. There must be a *cause* of why one thing results and not another—of which haploid nuclei will be chosen for the gamete, of where crossing-over takes place, etc. This cause must be a device internal to the organism. With random mutations, it is imaginable that these are induced randomly by external causes, such as x-rays, or just by plain copying errors in imperfect organisms.

But with allele swapping and chromosome shuffling, we're not talking about chance events. Unlike mutations, these features have been exquisitely "designed" by natural selection. Thus, for the determinations made during crossing-over, meiosis, and union of gametes to be random, we would have to imagine that DNA or some other part of reproductive cells contains an evolved device for randomly making these determinations, like rolling dice.

This is implausible, first, because it makes no adaptive sense to evolve a random dice-roller.[4] Such a device would have to be fairly sophisticated; and if we can imagine the evolution of such a sophisticated device, it is just as easy to imagine the evolution of a device that can do better than random. A random dice-roller is implausible, second, because random determination would almost certainly result in disaster, especially during crossing-over. Splicing and swapping at random points on a chromosome would result in dysfunctional chromosomes. Of course, we could suppose that "random" doesn't mean that crossing-over will occur at any molecule on a chromosome; rather, that only segments that are discrete and functional (eg., a gene for a particular trait) will be crossed-over, thus averting dysfunctional chromosomes. But this means that our imaginary dice-roller, which can recognize functional segments of DNA, is at least semi-intelligent. And this device would still need to determine which segments to swap, how long the segments will be, how many will be swapped, etc.

It is not impossible to imagine that all this is somehow random, but it is not plausible. And even if it is random, in the end it still produces genetic experiments—genetically unique offspring—and thus would be an evolved device for producing genetic experiments. Yet this cannot be random, unless one adopts the notion that the fact that each sexually-reproduced organism is genetically unique is just a remarkable coincidence. This is not plausible.

We also know that sex is not random because, in species that switch between asexual and sexual reproduction, the timing of the switch is not random. In protists, it is common to "reproduce sexually when conditions favor feeding and growth, sexually when they do not." (Arms and Camp 1987, p. 488). Diatoms, a group of algae, do the same. (*Id.*, p. 491). So it is with greenflies (Ridley 1993, p. 29) as well as monogont rotifers. (*Id.*, p. 57). Grasses reproduce asexually until the end of summer, propagating vegetatively through new blades in existing clumps, then switch to sex and "go to seed." (*Id.*, p. 40). Asexual aphids are wingless, while sexual aphids have wings and will attempt to start new colonies after flying away to mate. (*Id.*, p. 56). The cause of the

[4] Moreover, rolling dice is not really random in the sense of chance mutation. Dice have six numbers, which limits the number of outcomes when they are rolled. Truly chance mutations, on the other hand, would be limited only by the number of nucleotides in a genome. Although this number is not infinite, it is so large that, for analytical purposes, it might as well be.

switch to sex is probably the result of overcrowding. (Arms and Camp 1987, p. 393). Volvox colonies will reproduce by cloning through the summer, then switch to sexual reproduction before the onset of winter. (Bonner 1971). They will lay dormant until the spring, when the sexually-reproduced offspring germinate.

This is typical of species that switch from asex to sex. So long as resources are locally abundant, an organism can take advantage of that by reproducing in the swiftest way possible, switching to sex when local resources become low. (Williams 1975, p. 32). This cycle is especially typical of the so-called "weed species," such as quaking aspens that vegetatively bud new trees in an area cleared by fire, then return to sexual reproduction. The system of asexual budding is adaptively designed for opportunistic, speedy, and monopolistic spread in temporarily abundant, patchily-distributed habitats; sexual reproduction is designed for dispersal into new habitats or changed environmental conditions.

Switching from asexual reproduction to sex in these circumstances makes sense—*if* the adaptive function of sex is genetic experimentation. Sex is slower and more inefficient than asexual reproduction, but the advantage of experimentation comes into play when organisms are provoked by necessity, overcrowding, or new environments. In these circumstances, reproducing identical genotypes holds no further promise, and the advantage of reproductive speed correspondingly diminishes.

Where it has been possible to compare otherwise similar sexual and asexual populations, sexual ones have demonstrated greater genetic variability. In a rust fungus, for example, "[t]here is no doubt that sexually reproducing populations are more variable," with the sexual population having many more virulent phenotypes. (Elliott 1993, p. 2). Moreover, the researchers considered the varying phenotypes in the asexual population to be "survivors from the time when the population reproduced sexually, prior to the eradication in the 1930's of barberry, the host on which the sexual stage occurs." (*Id.*).

That sex is not random is further evidenced by the fact that mating is not random: species prefer outbreeding, which results in greater genetic variation than inbreeding. The importance that organisms place on outbreeding is demonstrated by the many social species in which societies are matrilineal/matrilocal or, alternately, patrilineal/patrilocal, because when the offspring of one sex remain at home (are philopatric), the offspring of the other sex disperse to ensure outbreeding. They disperse even though the terrain through which they move is unknown and hostile.[5]

[5] The formation of animal societies through natal philopatry of one sex, accompanied by dispersal of the other sex, is documented in detail in *Dynastic Theory: The Evolution of Altruism in Animal Societies.*

The importance of outbreeding is also evidenced by the many physiological devices that have evolved to prevent or discourage inbreeding: "Outbreeding plants are those designed for cross-pollination. They form a very large proportion of flowering plants." (Bristow 1978, p. 114). Some of the evolved devices to facilitate outbreeding include stigmas that accept pollen only after the plant has shed its own pollen; flower design to prevent transfer of pollen to the same flower; separate male and female plants; or simply self-incompatibility. (*Id.;* Futuyma 1986, p. 126). Fungi, too, have various "mechanisms which favor or impose cross-mating and thus enhance outbreeding." (Raper 1966, p. 3).

Many species that outbreed nevertheless have fail-safe mechanisms that allow inbreeding when outcrossing cannot occur. The bee orchid, for example, depends for outbreeding primarily on bees who pick up pollen from one orchid and transfer it to another. But if there are no bees, the stalks containing male pollen droop down so that 'the slightest breeze which shakes the flower is enough to swing the limp stalks so that the male pollen is embedded in the sticky female recesses." (Bristow 1978, p. 34).

A phylum of fungi, *Ascomycetes*, has species that outbreed and those that inbreed. Outbreeders are self-incompatible, meaning that they cannot mate with themselves, which is similar to what is found in self-incompatible plants. Inbreeders can mate with themselves. Yet they can nevertheless produce recombinant offspring because they are heterokaryons, meaning that they possess multiple, genetically-distinct nuclei. Hence, inbreeders "can be selfed but which, by virtue of formation of sexual structures on heterokaryons, can escape the necessity of obligatory self-fertilization through hybridization of the components of the heterokaryon. This is analogous to self-compatible flowering plants, which though frequently selfed have a low frequency of cross-pollination and so produce a small proportion of recombinant progeny." (Elliott 1993, p. 15).

The ecology of some species forces them to preferentially inbreed. Naked mole rats maintain subterranean colonies averaging eighty members. (Bennett et. al. 1999, p. 78). Ecological constraints make it extremely difficult for the young to disperse. They feed on geophytes, which are sparsely distributed in the arid environment in which they live. The aridity also makes it difficult to dig. They disperse, if at all, after an infrequent rain. (*Id.*, p. 100). The difficulty in dispersing means that inbreeding is common. Significantly, however, if the opportunity arises, naked mole rats will outbreed. (*Id.*, pp. 103-04).

There are also some species that employ a switch between inbreeding and outbreeding for the same adaptive reason as species that switch between cloning and sexual reproduction. For example, there are species of ants in which the colony queen produces relatively few sons, who impregnate a relatively large number of virgin queen sisters. (Bourke and Franks, pp. 146, 192-93) (*E. kraussei* and *Technomyrmex alpibes).*

The functional explanation is that in these species, inbreeding is an adaptation to colony needs—swift reproduction in patchy habitat. Inbreeding within the colony allows it to expand rapidly. No time is wasted on daughters who would leave the colony to mate or in rearing large numbers of otherwise useless, nonworking males. The few males have enough sperm to impregnate many sisters. Supporting this explanation, the habitat of *Technomyrmex alpibes* consists of bamboo patches which are especially adaptive for a colony to rapidly occupy and monopolize. Significantly, when a patch is fully occupied, the colony then produces winged sexuals which disperse, outbreed, and attempt to colonize new bamboo patches. (*Id.*, p. 193).

I've stated that outbreeding has evolved in most species because it results in greater genetic variation. Thus, I should address a common explanation: that organisms outbreed in order to avoid inbreeding depression, in which inbreeding results in identical alleles—homozygotes—which express deleterious recessive mutations. (Williams 1980, p. 374).

As a reason for outbreeding, inbreeding depression is both overstated and misleading. It is overstated because the deleterious effects of inbreeding usually occur only in species that normally outbreed. As evidenced by the typically inbreeding ants and mole rats mentioned above, species that normally inbreed don't suffer inbreeding depression. The primary reason that a population that normally inbreeds does not suffer inbreeding depression is that continual inbreeding will cause it to lose most of its deleterious recessive alleles. (Templeton 1987, p. 259). Although wolves are typically outbreeders, both captive wolves and wild wolves with small populations have found themselves forced to inbreed, but with no sign of uncommon numbers of birth defects: "These conclusions tend to support Shields' (1982, 1983) theory of an inbreeding optimum and Templeton's (chap 17, this volume) contention that little inbreeding depression should occur in populations that are historically inbred." (Mech 1987, p. 70). Templeton also illustrates the point with captive buffalo, which had an effective population size of twelve animals: "After a few generations of inbreeding, this inbreeding depression vanished…." (Templeton 1987, p. 260). He even mentions human populations which, cutting against the human grain, customarily inbreed, yet suffer no inbreeding depression.

To say that the reason for outbreeding is to avoid inbreeding depression is misleading because it masks the function of sex. That argument assumes that sex is necessary for reproduction; given that, the only choice is whether to inbreed or outbreed. As demonstrated by the species that alternate between asexual and sexual reproduction, this assumption is false. Moreover, the inbreeding depression argument applies only to species in which organisms develop with two sets of chromosomes (diploid), and thus can possibly have duel recessive genes; yet many species develop entirely as haploid organisms, while nonetheless reproducing sexually through outbreeding.

Sex results in genetic experiments; outbreeding enhances genetic experimentation by increasing genetic variation in offspring. This is not random.

That the function of sex is genetic experimentation can be further illustrated by one additional pattern. In over one-half of all species of ants, queens mate with multiple males. (Bourke and Franks 1995, p. 380). This is also widespread in the social wasps. (Gamboa 1996). In honeybees, queens mate with up to seventeen males. (Moritz and Southwick 1992, p. 203). Multiple mating tends to occur in single queen (monogynous) colonies with long-lived queens, who produce very large colonies and are never replaced. (Bourke and Franks 1995, p. 279; Holldobler and Wilson 1990, p. 155). In these species, if the queen mated with only one male, genetic variation in the colony would be extremely low. Multiple mating increases genetic variation and colony diversity.

With the advent of kin selection theory, this became a problem, because kin selection predicts altruism among more closely related individuals. Multiple mating confounded predictions because it decreases the degree of relatedness within a colony. The hypothesis that individual males are simply incapable of supplying all the sperm to a queen was ruled out. There is no physiological reason that males would be unable to evolve greater sperm capacity. (Bourke and Franks 1995, pp. 380-82). Flight would not be impaired. Moreover, in many species, a single male does provide all of a queen's requirements. Nor is multiple mating due to an inability of queens to carry a full load of sperm. In most ant species, a queen acquires all the sperm she will ever possess in a single mating flight by mating with multiple males in succession. The same is generally true with wasps: "In Oxybelus, Trypolylon, and some other genera, the female mates several times over a period of days, but more commonly she mates one or more times soon after emergence and thereafter signals her unwillingness to mate by a characteristic flight or by moving the abdomen or legs in such a way that the male is unable to make contact." (Evans and West-Eberhard 1970, p. 41).

If we dispense with kin selection, we can see why multiple mating is adaptive, especially in colonies with single, long-lived queens: genetic variation might be evolutionary valuable to the queen's line of descent—*if* increasing genetic experimentation is adaptive.

In sum, even in the population genetics model of gene swapping and chromosome recombination, sex produces genetic experiments in the form of genetically unique offspring. The process cannot be random. Some device internal to the organism must make a nonrandom determination as to which genes are swapped and which chromosomes are recombined. It is nonrandom because organisms prefer to outbreed, a process that increases genetic variation. When organisms switch between sex and asex is not random. If the process is not random, it must be directed.

Thus, even under neo-Darwinian models, sex produces directed variation. There

is no reason for directed variation—neo-Lamarckism—to be taboo.

Opening the Black Box: The Immune System and Genetic Engineering

Organisms *do* participate in directing variation. Moreover, they are capable of directing variation in ways far more interesting than mere allele swapping and chromosome shuffling.

The neo-Darwinian synthesis coalesced before the discovery of DNA and the advent of molecular genetics in the 1950's. Until then, the source of inheritance in the interior of cells was mostly a black box; biologists could observe the traits that came out of the black box, but its contents could mostly just be guessed at.

In the last half century, molecular biologists have cracked open the black box and peered at its contents. They have found what biologists previously deemed to be too incredible to take seriously. One no longer needs to be a vitalist Pangloss to suppose that organisms can engineer their own genetics. It's not absurd. To the contrary, in the words of biologist James Shapiro, inside the black box is a "genetic engineer" with "an impressive toolbox full of sophisticated molecular devices for reorganizing DNA molecules." (Shapiro 1995, p. 374).

Organisms' immune systems are prime examples. Viruses and other parasites are constantly invading bodies. The immune system is designed to attack and destroy them. It does so with antibodies produced by specialized cells. Antibodies recognize the foreign viral antigens, bind with them, and remove them from the circulatory system.

There are a vast number of potential parasites. New ones swiftly evolve. How can organisms' immune systems accumulate and store an equivalent array of matching antibodies? How do they evolve new ones to keep pace with parasites?

Under classical neo-Darwinism, an organism is born with a set of genes and dies with the same set. An organism is thus either born with the genes coding for the right antibodies to attack parasites that happen to invade it, or it is not. This has been called the "germline hypothesis." (Steele 1979, p. 25). Organisms with the right genes would survive and reproduce, passing on these genes to future generations. The evolution of new antibodies would depend on chance mutations occurring in the organism's reproductive cells.

Chance mutation, however, is an unlikely way to keep pace with swiftly evolving parasites, especially given that most species reproduce (and therefore mutate) far more slowly than parasites. Meanwhile, it has been discovered that an organism is capable of producing millions of different antibodies. If each antibody depended on a separate gene,

the DNA required for antibodies alone would exceed the amount of DNA that is contained in an organism's entire genome. (Gardner et. al. 1991, p. 449).

Research has resolved these dilemmas. Antibodies are neither stored nor evolve as predicted by classical genetics. There is not a separate gene for each antibody. Nor are new antibodies evolved through a chance process. The immune system is far more sophisticated. It can create new antibodies in response to antigens that the organism has never before encountered. (Gardner et. al. 1991, p. 458).

The immune system does this through a system of trial-and-error experimentation. Instead of having specific genes for specific antibodies, the genome contains numerous small segments of DNA, or "domains." (Gardner et. al. 1991, pp. 449-63). These domains can then be spliced, transposed, joined, and rearranged in different combinations to produce a vast array of antibodies. Each antibody is an experiment. If it is a match for the antigen (i.e., it binds with it), the immune cells then produce a large number of clones to bind with and dispose of the antigens. If not, the immune cells continue to experiment by splicing, transposing, joining, and rearranging DNA segments until the right combination is found.

Cohn aptly sums up the trial-and-error system of antibody evolution this way: "a given antibody is a theory made by the animal about what is in its environment." (Steele 1979, p. 16, quoting Cohn). In effect, the organism's immune system anticipates the unanticipated. Through genetic experimentation and engineering, it expands the organism's repertoire of potential responses to parasites.

The trial-and-error genetic rearrangement of the immune system has been referred to as "hypermutation." (Gardner et. al. 1991, p. 458). This term, however, is a vestige. It retains the language of "mutation." But conceptually, it is poles apart from the classical concept of random mutation. The antibodies produced by the immune system are not point mutations. Instead, they are rearrangements of genetic segments. Moreover, the genetic rearrangements are not random. They are not errors. The process of evolving antibodies is an adaptive system of trial and error.

Trial and error does not mean random. It could not. Given what is now known about DNA, the number of nucleotides, the billions of potential combinations of DNA, and the sensitivity of proteins to precise DNA sequences, the odds of hitting upon the needed genetic recombination through a random process of splicing and joining would be tantamount to a mathematical miracle. This would be true no matter how many rolls of the dice and no matter how much time was allowed. For the trial-and-error process to work, the immune system must be able to narrow down the range of experimental rearrangements that might match the antigen. To reiterate Cohn's observation, each experimental antibody is a theory of what might match.

As with any system of experimentation, the process need not be perfect in order to be useful. It need only be better than doing nothing. Or, compared to chance mutation, it need only be better than waiting for a random copying error in a reproductive cell to supply the requisite variation in the next generation. Obtaining a chance variation would be an unlikely event in any case, since if the parasite kills the host organism, it would never get a chance to reproduce and err in copying its DNA.

The immune system is not a random process. It is a highly evolved system of designed genetic experimentation. It evolves antibodies faster than random mutation would allow.

The immune system, of course, is not sex or conjugation. Nor does it produce wings, arms, leaves, or whales. But it does demonstrate that genetic engineering is possible, that it can be accomplished by organisms, that it is nonrandom, and that it involves splicing and rearranging of segments of DNA in a process of genetic experimentation. And it functions to evolve one aspect of an organism: its protective immunity.

Opening the Black Box: Conjugation as Genetic Engineering

Bacteria engage in genetic experimentation in a process known as "conjugation." (Gardner et. al, 1991, pp. 213-219; Arms and Camp 1987, p. 461). In a well-known laboratory experiment, Lederberg and Tatum cultured two separate strains of *E.coli* bacteria so that each strain lacked the ability to synthesize certain amino acids needed for growth. Consequently, both strains were cultured to die. Some cells nevertheless managed to synthesize all the necessary amino acids. The important discovery was that they were able to do so because cells from each strain transferred DNA so that some cells happened to acquire all of the DNA needed to synthesize all the amino acids.

Much more has now been discovered about how bacteria manipulate their DNA during conjugation. (*See eg*., Shapiro 1995; Radicella et. al. 1995; Achtman 1975). It is a group activity, taking place among several or many bacteria: "A second conclusion from the lacI-Z33 results is that genetic change in bacteria is often multicellular. DNA rearrangements can occur in one cell and be transferred to another before a clone of a 'mutant' bacteria proliferates on selective medium." (Shapiro 1995, p. 373). It is a one-way transfer of genetic material, from a donor cell to a recipient cell, through a conjugation tube. Genetic segments are transferred using DNA that specializes in transposing other segments. These segments are spliced into the bacterial genome, and other segments spliced out, through a process generally known as "crossing-over" (which is similar to crossing-over during sexual meiosis).

Some bacteria contain plasmids, which are segments of DNA, usually circular, that

are separate from the bacteria's chromosomal DNA. A conjugate plasmid (F-plasmid) facilitates conjugation. An R-plasmid contains DNA that produces resistance to antibiotics. An R-plasmid can't initiate conjugation, but the R-plasmid DNA can be transmitted with the assistance of conjugate plasmid. (Maynard Smith 1989, p. 190).

Plasmids are one means of transferring DNA through conjugation. Another is through conjugative transposons. These segments of DNA are capable of excising themselves from the chromosomal DNA, then either reintegrating themselves into the chromosome or transferring to a recipient cell through cell-to-cell contact. They are common in bacteria: "Indeed, their broad host range…suggests that they are highly ubiquitous…. The degree to which they have been found in *Streptococcus* probably relates to the fact that plasmids, which in many other groups of bacteria commonly bear resistance determinants, are not particularly common in this genus. Indeed, in streptococci and perhaps some other groups, conjugative transposons are probably more responsible for the dissemination of antibiotic resistance than are plasmids." (Clewell and Flanagan 1993, p. 387).

Some bacteria have another evolved method of acquiring DNA, a process known as "transformation." *Anacystic nidulans* is a species of cyanobacteria, which is a class of bacteria that photosynthesize. When one strain of *Anacystic nidulans* that was resistant to one kind of antibiotic was grown together with another strain that was resistant to a different antibiotic, the result was a double-resistant strain. (South and Whittick 1987, p. 133). The means of evolving the double resistant strain was transformation. Unlike conjugation, in which the cells that exchange DNA are in direct contact, in transformation, the recipient cell uptakes "naked DNA," which is DNA freed by the donor cell into the environment or DNA taken from a dead cell. (Higgins 1992, pp. 209-10). The process for uptake and integration of naked DNA is extremely elaborate.

How regularly conjugation and transformation actually occur in natural environments is obviously difficult to witness and is therefore not known. (Arms and Camp 1987, p. 461). But they are a common phenomenon in the lab. (Willetts 1993, p. 12). And the fact that bacteria have elaborate devices to transfer and acquire DNA is ample evidence that these are evolved adaptations, not laboratory accidents—and not chance mutations: "A major conclusion from all these results [*E. coli* experiments] is that adaptive lacI-Z33 reversion represents more than malfunction of the basic replication machinery under stress. Additional specific molecules participate in selection-induced mutations that restore growth on lactose (namely, homologous recombination and plasmid transfer functions)." (Shapiro 1995, p. 373).

Like the functioning of the immune system, conjugation involves trial and error. In experiments like that of Lederberg and Tatum, where strains are cultured to die unless they genetically reconfigure themselves, organisms do not hit upon the solution immediately and sometimes not at all. But as with the immune system, the process

through which segments are spliced and joined, added and deleted, could not be random. Even bacterial genomes are sufficiently large and complex that if transposition and splicing of DNA were random, hitting upon the needed genetic rearrangement would require a mathematical miracle. Hence, to be functional, the conjugation process must be able to at least narrow down the range of "search options" —a "theory" of what might work and what will not. How good must a "theory" be? As with the immune system, to be adaptive it need be merely superior to doing nothing or waiting for the right random error to occur.

Other evidence demonstrates that conjugation does not produce random "mutations" but is instead biased towards adaptation. If the process were random, it would produce numerous maladaptive combinations, which would accumulate. This does not happen: "Adaptive mutagenesis implicates environmental stress factors as a cause of specific advantageous mutations and not just as a selective force that enriches for random beneficial mutations within the population…. In these systems beneficial mutations occur in the absence of significant cell growth and without the accumulation of non-advantageous mutations." (Peters and Benson 1994, p. 847).

Like sex, when conjugation occurs is also not random. In the laboratory, conjugation is commonly cued by starvation, crowding, seasonality, and other signs of resource stress. (Ricci 1982, p. 325; Shapiro 1997, p. 42). Genetic experimentation would be especially adaptive when organisms are stressed or, as in the case of the Lederberg and Tatum experiment, they will die if they do nothing. Hardly anyone doubts that these processes are responsible for the swiftness with which microorganisms have evolved resistance to antibiotics—an obvious source of stress for parasites. (Smith 1989, pp. 192-93). In experiments with *E. coli* in a particular environment, in order to grow the bacteria needed to fuse two operons, *lac* and *ara*. "*Ara-lac* fusions did not appear on plates with an abundant carbon source. However, after starvation on minimal plates containing both arabinose and lactose, *ara-lac* utilizing colonies were frequently detected. After several days, hundreds of independent colonies appeared on a single plate. Shapiro's results and careful analysis clearly showed that *ara-lac* fusion formation was caused by transposon-driven genetic rearrangements and that the carbon limitation history of the culture was also important." (Higgins 1992, p. 208).

Inducing conjugation in response to stress makes perfect sense if conjugation is an adaptation for evolving through genetic experimentation. For this reason, many biologists have called conjugation "adaptive mutation," in contrast with random mutation. (*See, eg.*, Shapiro 1997, p. 41; Peters and Benson 1994; Higgins 1992; Radicella et. al. 1995).

Opening the Black Box: Shifts in the Meanings of "Gene" and "Mutation"

Geneticist Barbara McClintock characterized the classical Mendelian view of the genome: "At the time our knowledge was limited. In retrospect we might call it primitive. Genes were 'beads' arranged in linear order on the chromosome 'string'." (McClintock 1987b, p. 627).

Genes aren't particles. They aren't beads. The genome is marvelously complex: the double helix, four nucleotides, nucleotide base pairs, nucleotide sequences, DNA replication, DNA proofreading and repair, DNA transcription to RNA, translation of RNA. The synthesis of a simple protein is anything but simple—from DNA to messenger RNA, with the help of transfer RNA, decoded in ribosomal RNA, where amino acids are specified, which join together to form polypeptides, which join together to form proteins. Proteins make organisms' "bodies."

But these "structural genes" that translate into proteins are just the beginning. There are also regulatory sequences, stop codons, promoters, other noncoding DNA, often repetitive and called "satellite DNA," which are located in the centromere, etc., etc.

While genetics shifted from Mendelian to molecular genetics, definitions shifted in order to link them. A "gene", rather than coding for a particular trait, could be thought of as coding for a protein, which combine with other proteins to make traits. A point mutation could be thought of as a change in a base-pair of nucleotides, thereby altering a protein. According to Carlson, "[s]ome of the terms were molecular replacements of classical genetic terms. One could speak of a nucleotide base-pairing change or 'base substitution' in the sequence of DNA instead of a point mutation in a specific gene." (Carlson 2011, p. 85). By ignoring all the other kinds of "genes," or by emphasizing the importance of genes for proteins, and by ignoring all the other kinds of "mutations" in DNA sequences, or by emphasizing the importance of changes in base-pairs, the Mendelian model could be salvaged—and, along with it, the synthesis that was built upon that foundation.

This is what has happened: "The basic idea of a mutation as being a small disturbance in a gene or point mutation was not challenged." (*Id.*, p. 81).

The thesis of the next several segments is that this is a colossal error. Significant evolution occurs through genetic rearrangements, not point mutations. To be clear, by "genetic rearrangement" I do not mean the concept of recombination in population genetics. "Recombination" refers to the shuffling of alleles for discrete traits and mixing chromosomes so that offspring consist of a new combination of existing traits. "Rearrangement" does not. It refers to the shuffling of genetic segments—which may or may not be alleles for discrete traits—to create novel sequences of DNA.

Not only does the evidence from molecular genetics lead to the conclusion that speciation is the result of genetic rearrangement, much DNA consists of devices for rearranging segments of DNA.

Opening the Black Box: The Evolution of Proteins through Genetic Rearrangement

The bodies of organisms consist of proteins. As scientists have opened the black box, they have discovered that proteins have evolved through rearrangement of genetic segments.

Proteins are known to typically consist of polypeptides joined together in convoluted chains: "A protein is fundamentally a long chain-like molecule built up out of twenty different kinds of amino acids. After its assembly the long amino acid chain automatically folds into a specific stable 3D configuration. Particular protein functions depend on highly specific 3D shapes and, in the case of proteins which possess catalytic functions, depend on the protein possessing a particular active site, again of highly specific 3D configuration." (Denton 1998, p. 57). Thus, to be functional, these convoluted shapes must be highly specific, not random. (Arms and Camp 1987, p. 46). They are so specific that the substitution of even a single amino acid can result in a dysfunctional protein. (*Id.*).

It has thus often been wondered how new functional proteins could evolve through point mutations. (*See, eg.*, Denton 1998, pp. 57-58). Nucleotide substitution or deletion is improbable because "the added regions would consist of an almost random array of amino acids." (Li 1997, p. 271). Thus, to evolve step by step through single substitutions in existing proteins would entail numerous nonfunctional proteins en route to a functional new one. Since the intermediate steps would be maladaptive, they could not be selectively favored:

> [I]t is now generally conceded by protein chemists that most functional proteins would be difficult to reach or to interconvert through a series of individual amino acid mutations…. To change…the shape and function of the active site (like changing the verb in a sentence or an important cogwheel in a watch) in isolation would be bound to disrupt all the complex intramolecular bonds throughout the molecule, destabilizing the whole system and rendering it useless.

(Denton 1998, p. 58).

Hence, the evolution of a new protein through chance point mutations would require a hypothesis of genetic drift, a drift that happens to result in a functional protein

configuration through an extraordinary sequence of point mutations without causing sufficient harm to be de-selected. It would be like evolving bird wings in which each incremental step is maladaptive.

The point mutation hypothesis is no longer necessary. Proteins have evolved by splicing together DNA sequences from other proteins. (Vogel and Motulsky 1997, p. 596). The entire DNA sequence for a particular protein consists of a number of "domains"—segments of DNA—that are joined together. These domains can then be recombined and rearranged in a multitude of ways to form a multitude of functional proteins. It has been estimated that perhaps "only about 200-500 domains may have been the basic units from which the great number of different proteins that occur in nature have been found." (*Id.*).

This is consistent with the fact that genes for many proteins are members of multi-gene "families." They may be identical (see the discussion of repetitive DNA below) or exhibit sequence homology—that is, they appear to have an ancestral gene in common, but have since diverged. (Raff and Kaufman 1983, p. 300). Some members of gene families have diverged through duplication followed by rearrangement. (Vogel and Motulsky 1997, p. 596). Others have evolved by increasing in size, or elongation, through internal duplication of sequences: "Many proteins of present-day organisms show internal repeats of amino acid sequences, and the repeats often correspond to the functional or structural domains of the proteins.... This observation suggests that the genes coding for these proteins were formed by internal gene duplication." (Li 1997, p. 269). According to Li, this "is one of the most important steps in the evolution of complex genes from simple ones." (*Id.*, p. 271).

One function of multiple identical genes is that certain gene products, such as ribosomal RNA, are needed in large quantities in a short amount of time. (Raff and Kaufman 1983, p. 304). A function of homologous but divergent genes may be to provide switching during development: "[R]elated but not identical genes produce similar products specifically required in distinct cell types or at different times during development. The best-understood example is provided by the small multigene families containing the genes for globins." (*Id.*).

Opening the Black Box: Transposons, Introns, and Exons

There are several ways to duplicate sequences of DNA. One means is duplicative transposition. The prevalence of transposons as a means of genetic rearrangement is one of the most fascinating discoveries of molecular biology. Discovered by Barbara McClintock in her research on maize, transposons are "genes" (DNA sequences) that can "jump" (transpose) from site to site within a genome. (McClintock 1987a). They sometimes jump independently. Sometimes they carry other sequences with them.

Sometimes they duplicate as they jump. (Li 1997, p. 336). There are numerous kinds of transposons. The fruit fly alone "contains multiple copies of 50-100 kinds of transposons." (*Id.*, p. 340).

Once regarded as curiosities, transposons have since been implicated in conjugation, in exon (domain) shuffling, the immune system, in the concerted evolution of gene families, in the tandem repeats of noncoding DNA, and other significant genetic events: "The fact that nearly every DNA sequence known to be critical for the regulated expression of eukaryotic genes can also be found in one or more TEs [transposable elements] suggests that an evolutionary relationship exists between TEs and eukaryotic control sequences." (McDonald 1995, p. 124). Where transposons occur in the genome is nonrandom. (Maguire 1987, p. 127). For example, different transposons have "preferred" sites. (Capy et. al. 1998, p. 5).

The discovery of introns also supports the hypothesis that proteins and other sequences have evolved through genetic arrangement. In eukaryotes (organisms with DNA enclosed in a membrane-bound nucleus), genes contain one or several noncoding regions that are translated into RNA, but are then spliced out before the RNA is translated into proteins. (Arms and Camp 1987, p. 204). These noncoding sequences which "intervene" between coding regions are called "introns." The coding regions are called "exons." Introns can be small or large, ranging from about fifty nucleotides to 10,000. Some (but not all) eukaryotic genes contain introns. As many as fifty introns have been found in a single structural gene (coding for collagen), and can account for up to 90% of the DNA in a gene. Introns have been placed into five categories: i) Group I, which are self-splicing; ii) Group II, which can also be self-splicing but via a different mechanism; iii) Group III, with no known splicing mechanism; iv) spliceosomal, which occur only in pre-mRNA; v) protein spliced introns, which occur only in certain tRNA and rRNA genes. (Maynard Smith and Szathmary 1995, pp. 133-34).

Although the exact function of introns has not been determined, it has been proposed that they assist in "exon shuffling," connecting genes that once existed separately. A similar hypothesis is that they aid in shuffling domains, which correspond to sequences for polypeptides rather than whole genes, and which thus aid in evolving new genes. The correspondence of exons with domains is most apparent in the antibodies of immune systems. (Gardner et. al. 1991, p. 359). Smith and Szathmary believe that the most plausible hypothesis is that introns are "fossil transposable elements"; some retain their self-splicing mobility, while others lose it. (Smith and Szathmary 1995, p. 133). It seems to be well-documented that transposable elements generally exist in introns, that "fossil" transposable elements exist in introns, or that transposable elements can be inserted into introns. (Capy et. al. 1998, p. 83; Li 1997, pp. 357, 418). Although introns are rare in prokaryotes (organisms with a single strand of DNA, not enclosed in a nucleus), prokaryotes do have the same ability to splice and rearrange through transposable elements. In other words, as with transposable

elements—or, in association with transposable elements—introns assist the evolutionary function of genetic rearrangement.

In short, introns are not functional in the sense that they are transcribed into proteins. Rather, they are part of larger DNA sequences, but are spliced out before transcription, with the remaining segments (exons) being rejoined. (Gardner et. al. 1991, p. 248). In some cases, the rejoined exons are from different regions the genome. The picture that emerges is that the introns either represent a device that in the past facilitated protein evolution through “exon shuffling” (or domain shuffling) or are a vestige of it. (Li 1997, p. 297).

Whatever the exact function of introns turns out to be, like transposons, their existence is further evidence that the evolution of complex DNA sequences, including proteins, has occurred through the rearrangement of segments of DNA, not point mutations or the re-shuffling of alleles.

Opening the Black Box: Noncoding DNA

The evolution of proteins has traditionally been thought to be the ultimate evolutionary event. Proteins, after all, are what bodies are made of. The idea that specific genes correspond to specific proteins (or polypeptides) also loosely corresponds to the Mendelian notion that the genome consists of genes for specific traits. However, the growing body of data suggests that protein evolution does not account for the most significant evolution, which is due instead to noncoding DNA and the overall arrangement of DNA sequences, including the "context" in which they occur in the genome.

This body of data derives in part from comparisons of genomes between species. If protein evolution accounted for the primary differences between species, these differences should be reflected in differences in proteins and the sequences of DNA that code for them. This is not the case. For example, in a comparison of humans, gorillas, and chimpanzees, “[f]or practical purposes our proteins can be regarded as identical.” (Vogel and Motulsky 1987, p. 602). Yet there are tremendous differences in morphology and behavior among these three species. Genetic variations of some sort must account for them, but it must be something other than variations in genes that code for proteins.

The genetic differences that have been identified fall into two general categories. The first relates to another surprise in the contents of the black box. In eukaryotes, especially the higher plants and animals, the amount of DNA that codes for proteins comprises a relatively small amount of the genome. There is far more noncoding DNA, much of which is in the satellite and heterochromatin regions of the genome. It is estimated to constitute 20% to 50% of DNA in eukaryotes. (Gardner et. al. 1991, p. 143).

The genomes of humans, chimpanzees, and gorillas differ in these noncoding sequences. (Vogel and Motulsky, p. 594).

Much of this noncoding DNA is repetitive. Classifications of DNA by repetition are as follows:

- Single copy DNA. These are usually structural genes (i.e., coding for proteins). (Gardner et. al. 1991, p. 147). They are typically located in euchromatin, regions of DNA that are loosely-packed and usually actively transcribed.
- Middle-repetitive DNA. Ten to 100,000 copies. Some middle-repetitive DNA codes for proteins (but not tissues), as histones, rRNA molecules, and ribosomal proteins that are redundant. Other middle-repetitive DNA is interspersed with single-copy DNA and is postulated to serve an as-yet-unknown regulatory function. (Gardner et. al. 1991, pp. 147-48). Much of repetitive DNA is mobile, nomadic, and associated with transposable elements. (Futuyma 1986, p. 50; Gardner et. al. 1991, p. 148). Transposition of these sequences is "known to be responsible for a surprisingly large number of mutations of yeast and drosophila." (Gardner et. al. 1991, p. 148). However, the sequences themselves are fairly "conservative," i.e., are not prone to "mutation."
- Highly repetitive DNA. 100,000+ copies. These are typically located in heterochromatin, tightly-packed DNA that is genetically inactive in the sense that it is not transcribed. (Gardner et. al. 1991, p. 143). It is often located in centromeres and telomeres. These sequences undergo frequent "mutation." (Arms and Camp 1987, p. 185). Highly repetitive DNA are believed to serve regulatory functions. They can bind proteins, preventing transcription, or release them. That is, they can activate or deactivate structural (coding) genes. (Nicolas 1987, p. 69; Hilliker and Sharp 1987, p. 91; Arms and Camp 1987, p. 224).

An organism's DNA also contains other sequences that do not code for specific proteins or traits. These include promoter sites, at which DNA transcription is initiated; enhancers; tails; stop codons; gene spacers; and many others. All of these affect the ultimate polypeptide (and hence protein) products; changes in these can thus affect the products and therefore an organism's traits.

The second general difference among the genomes of humans, chimpanzees, and gorillas is in the way that DNA is structurally arranged, not just in proteins, but in noncoding sequences. This does not entail differences in the content of the DNA, but rather differences in the overall sequences and arrangements. These appear to have come about through inversions, insertions, transpositions, translocations, amplifications, and other structural rearrangements in the genome. (King and Wilson 1975, p. 114). This generally holds true in cross-species comparisons with genomes of other species. (Campbell 1982; Muller and Wagner 1996).

Thus, alterations in developmental pathways, rather than occurring through changes in DNA that code for proteins (or through genes for specific traits), can occur through noncoding "regulatory" DNA. It is known that “[d]ifferentiation occurs by the regulation of gene expression, rather than by changes in genome composition. This has been demonstrated by various techniques in many different organisms.” (Gardner et. al. 1991, p. 412).

In fact, it is not even necessary that a genetic variation involve a change in the composition of DNA, but rather a change in where a coding sequence occurs in the genome and in what "context." For example, a gene “for” a leg of a fruit fly may instead become a gene "for” an antennae, depending on when and where it is expressed during development. In general, the morphological development of organisms is controlled by a cascade of regulatory genes, each acting at the proper time and place to trigger the expression of the next set of genes in the cascade. (Gardner et. al. 1991, p. 445). “[T]he coordinated regulation of sequential pathways of gene expression is primarily responsible for the diversity of cell phenotypes that unfold during the development of a higher plant or animal.” (Gardner et. al. 1991, p. 411).

Opening the Black Box: Homeotic Genes

One class of regulatory genes that control the process of organism development is called "homeotic” genes. Small changes in the sequence or location of homeotic genes can alter the expression of coding genes and thereby significantly alter development. A consistent feature of many homeotic genes is that each contains a highly conserved DNA segment consisting of 180 base pairs, called the “homeobox”: “The homeobox lies within the coding region of the gene and specifies a 60-amino acid segment, called the homeodomain, of the polypeptide product. These polypeptide products regulate transcription by binding to specific DNA sequences.” (Gardner et. al. 1991, p. 422-23).

Across species and families of species, homeobox sequences are highly conserved. (*Id.*). Changes in homeobox genes can transform a whole or part of a body segment into the corresponding part of another segment. For example, the body epidermis of one species has the potential to differentiate into mouth organs in another. (Muller and Wagner 1996, p. 9).

“Hox genes” are groups of related genes that contain homeobox sequences, and exist in clusters. Transposition and duplication of these clusters are hypothesized to be significant events that cause species divergence. (Holland and Garcia-Fernandez 1996, pp. 382-383). For example, “[t]he most intriguing genetic difference between invertebrates and the vertebrates is the number of *Hox* gene clusters...." (Id.). “A relatively small number of homeobox-containing genes (eg., Hox gene clusters) are now known to control many aspects of development in metazoans [multi-celled animals], the

genetic sequence, position, and function of such genes are highly conserved, with more advanced phyla having a greater number of homeotic genes and gene clusters.... Developmental novelty within a group can arise through gene duplications within Hox gene clusters, changes in the function of individual homeobox genes, and altered interactions among such genes...." (Givnish 1997, p. 29). It has been hypothesized that the genetic evolution of "cassette-like" kits of homeotic genes in the pre-Cambrian era accounts for the subsequent Cambrian explosion:

> The first great flowering of morphological body-plans in the Precambrian...may have been just then that metazoans began to assemble cassettelike kits of homeotic genes that governed fundamental aspects of the development of multi-celled organisms.... Once such cassettes evolved, they could rapidly be duplicated, arranged, activated, and interrelated in different combinations in the genome, with very different consequences for morphology and for the development linkages among morphological and physiological traits.

(Givnish 1997, p. 11). "This and other evidence suggests that the origin of vertebrates is associated with the duplication or quadruplication of developmental control genes...." (Muller and Wagner 1996, p. 8). It is possible that all homeobox genes arose "by duplication and divergence from a single progenitor gene in early eukaryotes." (Holland and Garcia-Fernandez 1996, p. 382).

Exactly how changes in homeotic genes—either in numbers, position, or sequence—influence specific developmental changes is still not well known. But enough is known to say that genetic identity in sequences—that is, genome composition—does not necessarily correspond to morphological identity. Rather, *where and in what context coding sequences are located in the genome, along with the regulatory sequences that control them—and thus when and where they are expressed during the developmental cascade—significantly alter morphology and behaviors.* Hox genes are important parts of this regulatory cascade.

Evolution through Changes in Developmental Sequences

How do these differences in noncoding DNA and structural arrangements translate into the evolution of morphology and behavior? It would be an understatement to say that much is yet to be discovered. However, the discovery of noncoding DNA has to some extent re-focused attention towards developmental biology, which is neglected in the classical Mendelian string-of-genes model. (Raff and Kauffman 1983, pp. 21-22). In the hypotheses of developmental biology, significant evolution can occur through relatively small alterations in the developmental sequences (ontogeny) of organisms. These alterations can be caused by relatively minor changes in the genome, manifesting

(for example) during the development of the embryo. These changes need not involve specific protein sequences, but rather changes that regulate development—and, hence, morphologies and behaviors.

The development of an organism is epigenetic. An organism begins as a single "germ" cell with a set of DNA. As the organism develops, cells multiply. As they multiply, the cells become differentiated, ultimately developing into the distinct "parts" of the organism—liver, legs, leaves, and the rest—which unfold during morphogenesis.

How organisms are capable of epigenetically differentiating from an original undifferentiated germ cell is partially understood. A multi-celled organism such as a chicken contains billions of cells, all of which descend from a single "parent" (germ) cell. This single cell necessarily carries the "instructions" in its DNA to develop the multitude of specialized somatic (body) cells, as well as the reproductive cells that will lead to the next generation of chickens. Generally speaking, cell specialization does not occur by parceling out different portions of DNA to the various cells. With some exceptions, each cell of the organism is identical in its DNA. (Futuyma 1986, p. 56). Cell specialization is thus caused not by genetic differences between cells, but rather by epigenetic differentiation in the environments of the cells. These environmental influences trigger expression of different regions (or configurations) of DNA, resulting in differentiation in the phenotypes of individual cells and thus to cell specialization. The means of epigenetically activating and deactivating various segments of DNA include hormones, methylation, chromatic marking, and other epigenetic devices.

The result is epigenetic differentiation of cell "phenotypes" without genetic differentiation. Thus, DNA does not prescribe a particular "form" of a cell. Rather, DNA prescribes a repertoire of developmental possibilities. Which of the developmental possibilities is realized is determined epigenetically. The end result is a whole organism consisting of many different types of cell lineages and many different body parts.

Even in lower organisms, development is epigenetic. Through genetic rearrangement, cells in *E. coli* bacterial colonies phenotypically differentiate in order to perform specialized functions. (Shapiro and Higgins 1989, p. 5985). In *P. Mirabilis*, a colony develops specialized, elongated swarmer cells which, instead of having a single chromosome, are polyploidy with about twenty chromosomes. (Belas 1997, p. 184).

The development of paramecia following conjugation illustrates another method of epigenetic development in lower organisms. Unlike bacterial conjugation, in paramecia, the transfer of DNA is not one-sided. Instead, the participants equally exchange DNA. (Barnes 1980, p. 66). Each paramecium has a macronucleus, which performs protein synthesis and which is copied and divided during asexual reproduction (binary synthesis). Each paramecium also has a micronucleus, which does not synthesize proteins, but is involved in conjugation. When undergoing conjugation, the

macronucleus of each paramecium disappears. The micronucleus, which is diploid, undergoes meiosis, including dividing and crossing-over, just as in meiosis in sexual reproduction. (Ricci 1982). This results in four unique micronuclei. All but one of them degenerates. The remaining micronucleus "then divides, giving two gametic micronuclei that are genetically identical." (Barnes 1980, p. 66). One paramecium stays put (the "female"), and a second paramecium (the "male") wanders over to it. They exchange nuclei, which then fuse to form a zygote. The conjugants then separate, divide, restore the macronucleus, and return to their "normal" state. The net effect for each conjugant is that it keeps one-half of its original DNA, jettisons the other half, and acquires one-half of its DNA from its conjugant partner.

After conjugating, in the paramecium's developmental stage, the macronucleus is restored through cloning of the micronucleus. However, during this process, some DNA sequences are amplified, rearranged, and deleted. (Miyake 1996, p. 294). In addition, as the macronuclei develop, the spacer DNA, which represents 95% of the genome, is removed and destroyed. The micronuclei contain transposons, whereas the macronuclei do not, suggesting that transposons are probably responsible for the rearrangement during production of the macronuclei: "These processes are under the control of both genes and extra-genic factors (reviewed by Yao 1989). The formation of the mature macronucleus can be termed the development stage of the organism. The final result determines the phenotype, which in certain instances may be more a consequence of these processes [rearrangement] than solely a direct expression of the information in the micronuclei genotype." (*Id.*).

In higher organisms, the study of development (ontogeny) through embryology provided one of Darwin's most important proofs of his theory of evolution from common ancestry. (Darwin 1952a, pp. 219-225). Stages of embryonic development in diverse animals are often strikingly similar, suggesting common ancestry: "No other explanation has ever been given of the marvellous fact that the embryos of a man, dog, seal, bat, reptile, &c., can at first hardly be distinguished from one another." (Darwin 1952b, p. 265). Moreover, the fact that various stages of embryonic development in "higher" animals suggest more primitive ancestry—such as gill slits and tails in human embryos—also supports the general Darwinian theory of gradual, step-by-step evolution over long periods of time.

This evidence became enshrined in Haeckel's doctrine that "ontogeny (development) recapitulates phylogeny (evolutionary ancestry)." (Futuyma 1986, p. 303). This doctrine has been discredited for a number of reasons. For example, embryo development does not reflect all ancestral stages. During evolution, organisms may jettison developmental stages as well as gain them. Also, embryo development may reflect ancestral juvenile developmental stages, not adult stages. But still, the fact that higher, derived organisms retain primitive features in embryonic development after millions of years is instructive not only about common ancestry, but also about the way in

which evolution builds on ancestral features.

More recently, developmental biology has emphasized heterochrony—changes in the rate and/or timing in an organism's development—as a common means of evolving. Changes in heterochrony can significantly alter the features of an organism. Categories of heterochronic change are as follows:

> a) Acceleration: acceleration of somatic features, while the organism matures at the same rate.
>
> b) Paedomorphosis: timing of the somatic feature remains the same, but maturation is accelerated.
>
> c) Neoteny: timing of the somatic feature is retarded, while maturation stays the same.
>
> d) Hypermorphosis: timing of the somatic feature stays the same, while maturation is slowed.

(Gould 1977a).

Heterochronic change can affect speciation: "Klingenberg and Ekav (1996), for example, show that repeated evolutionary shifts from benthic [bottom dwelling] to pelagic [open water] habitat in Antarctic nototheniod fish involve simple shifts of a shared growth trajectory during the larval stage; such shifts mainly affect fins and other swimming structures, and are manifested in bursts of morphological change associated with invasion of open water." (Givnish 1997, p. 31). As another example, "The late development of the keel bone and associated muscles in rails and allied birds may help explain why they have frequently lost the power of flight on islands and become the avian equivalent of small mammals...." (*Id.*).

One particularly intriguing hypothesis for the evolution of some human features is neoteny, where development of a feature becomes retarded or ceases altogether. A relatively large brain/head size in embryos and in juveniles is a common feature in mammals. However, the difference in humans is that we retain these relatively large features into adulthood, which suggests retardation of the development of adult features compared to other mammals. The relative hairlessness of humans, compared to other mammals, suggests the same. (Gould 1980, pp. 106-07; 132-33; Gould 1977b, pp. 63-67).

There are many physiological mechanisms for altering the timing/rate of heterochrony, such as altering the amounts, kinds, and timing of hormone release to developing tissues during morphological development. (Raff and Kaufman 1983, p. 189). These alterations can be induced by relatively small changes in DNA, resulting

from amplifying or reducing the genes that produce the hormones, for instance.

Of course, the development of organisms is highly integrated. This places obvious constraints on evolutionary change in a lineage because the development of one "part" must integrate with that of others. (For example, reflecting these constraints, during embryo development, the more primitive stages precede the higher, derived stages). However, developmental biologists have documented an evolutionary "technique" that facilitates developmental change—*dissociability*:

> In 1933 Joseph Needham pointed out that although developmental processes are closely and elegantly integrated with one another, they are in fact dissociable; that is, it is possible to experimentally separate differentiation from growth or cells division.... The importance of this observation is enormous. Dissociability provides a key to the description of the evolutionary consequences of changes in relative timing in development on morphological evolution.

(Raff and Kaufman 1983, p. 141).

The segmented development of insects is a well known, fairly obvious use of dissociability. The famous, extinct first flying "bird," Archaeopteryx, is not halfway between a bird and a reptile; suggesting dissociability, it is a mosaic of bird-like features, such as feathers, and reptile features, such as its tail and teeth. (Eldredge 1999). Dissociation in microbes has long been known. In bacterial colonies, different cell lineages give rise to differentiated, dissociated traits: "Microbic dissociation referred to pleiotropic hereditary changes that were observed to occur regularly in older bacterial colonies, giving rise to papillae and sectors in which multiple phenotypes diagnostic for the parent strain (morphology, fermentation, antigenicity, etc.) had 'dissociated' into a new set of characters." (Shapiro and Higgins 1989, p. 5985).

In sum, changes in regulatory sequences of DNA cause significant evolutionary events by altering the developmental sequences of organisms. These are not point mutations. They are rearrangements of DNA. They cause significant evolution not by altering genes for specific traits, or by altering alleles, but by altering development.

Speciation through Polyploidization

In higher species, diploidy—one set of chromosomes from each parent—has been considered the norm. However, it has been discovered that species with three, four, six, and eight sets of chromosomes is common, especially in plants.

New species can be created by multiplying chromosomes. One way is through the

fusion of two sets of chromosomes from two different species—hybridization—which is known as “allopolyploidy." For example, a new species of a flowering plant, *Mimulus peregrinus*, was recently determined to be a likely hybrid cross of *Mimulus guttatus* and *Mimulus luteus*, based on its intermediate physical characteristics and number of chromosomes. (Vallejo-Marin 2012). Hybrids are often more vigorous or occupy new niches. (Otto 2007, p. 452). A second way of creating a new species is through autoploidy, which is the simple doubling (or tripling) of chromosomes of an existing species. (Otto 2007). This might occur when gametes do not reduce their chromosomes, leading to fusion of unreduced gametes. Speciation is aided by the fact that polyploidization leads to immediate reproductive isolation from the “parent” species.

Given that a high percentage of plants are polyploid, speciation through polyploidization is probably a major cause of diversification of flowering plants. (Vallejo-Marin 2012, pp. 2-3). In many plant species and lineages, polyploidy appears to be an ancient evolutionary event. (Rieseberg and Willis 2007). Many crops cultivated by humans have evolved through polyploidization. Polyploidization is also widespread in ferns and fungi. It also occurs in lizards and lower animals. In mammals it is rare (Otto 2007, p. 453), although some kinds of cells, such as muscle and liver tissues, are polyploidy.

Hybrid crosses are typically sexually sterile, but they reproduce and spread vegetatively. However, they often “recover” fertility, as did *Mimulus perigrinus.*

The genomes of newly formed polyploids are often unstable and undergo genomic rearrangements: “[T]here are many reasons to expect that hybridization may be causally responsible. Transposable elements that are repressed within each parent lineage but activated in hybrids can facilitate the movement of genes and promote unequal crossing over.” (Otto 2007, p. 455). Expression of particular genes is also greatly altered due to methylation, heterochromatin disruption, genomic imprinting, etc.

The Connection between Sex and Genetic Rearrangements

The genetic rearrangements that have been described are changes to reproductive cells. When, and during what process, do these changes take place?

In polyploidization,[6] chromosome numbers double. This happens during meiosis. (Brooker et. al. 2011, p. 323). During the formation of gametes, each gamete is reduced from a diploid set of chromosomes to haploid. Polyploidization will occur when the

[6] Biologists don’t usually classify polyploidization as genome rearrangement, but rather as genome duplication. I have included it as a rearrangement because it contrasts with the supposed evolution through point mutations in neo-Darwinism.

chromosomes do not separate normally, resulting in diploid gametes.

Although this is abnormal, it is not necessarily an error. Species formation through hybridization is typically accompanied by sterility. Polyploidization that follows hybridization has a role in restoring fertility: "[S]terile plant hybrids often recover fertility after genome duplication (Stebbins 1958). Polyploidization in interspecific hybrids — allopolyploidization—has been linked to the restoration of sexual fertility in some natural triploid hybrids (e.g., *Senecio*, Abbott and Lowe 2004)." (Vallejo-Marin 2012, p. 2). Polyploidization may therefore be a nonrandom, adaptive event, as evidenced by the tolerance of plants and fungi to polyploidization.

But most of the work of rearrangement is accomplished during crossing-over, including the "repatterning" of the genome that follows polyploidization. In neo-Darwinism, the effect of crossing-over is to swap alleles on homologous chromosomes—the reciprocal recombination of alleles. But it is now known that crossing-over accomplishes much more than allele swapping.

In gene conversion, the transfer of DNA during crossing-over is one-way, not reciprocal. (Gardner et. al. 1993, p. 187). A sequence on one chromosome is cut out and replaced with the homologous sequence from the other chromosome. This is allele replacement, not swapping. Gene conversion is not an aberration. In fact, "gene conversion or nonreciprocal recombination is more frequent than reciprocal recombination." (*Id.*, p. 197).

Gene conversion is related to the system for repairing damage to double strands of DNA. There are several methods of repairing damage to single strands. (Brooker et. al. 2011, pp. 291-92). One is for a protein in the repair system to detect an irregularity in a DNA strand and directly convert the strand to its original structure. A second method is to detect the irregularity, remove the damaged nucleotides through excision, then use the complementary DNA strand as a template to synthesize the normal strand. All species have this repair system. A third method is similar, except that it is used to detect and repair mismatches in base pairs.

These methods work for repairing damage to single strands of DNA because the complementary strand is intact. They do not work when both strands are damaged. One way to repair a double-strand break is by copying and inserting the correct DNA sequence from the homologous chromosome, a process that is similar to crossing-over during meiosis. Like gene conversion, the net effect of this double-strand DNA repair is that the donor and recipient, rather than being heterozygous for the genetic segment that is involved, wind up being identical (homozygous). For this reason, it has been suggested that meiosis originally evolved as a device to repair DNA. (Michod et. al. 2008).

But as Bernstein points out, even if meiosis originated as DNA repair, "that is not the same thing as saying sex exists today to repair genes." (Ridley 1993, p. 42). DNA repair during meiosis would be useful only for damage that happened before crossing-over. In female mammals, crossing-over occurs while they are embryos (Arms and Camp 1987, p. 274), so this could not repair DNA damage that occurs to reproductive cells during their lifetimes. Moreover, meiosis also involves the recombination of chromosomes, which would seem to have nothing to do with DNA repair.

And even if crossing-over originated as a device for DNA repair, that is not its sole function today. Although both DNA repair and gene conversion are one-way transfers of DNA segments, gene conversion occurs not just between homologous sequences, but also between sequences that are on the same chromatid, which effectively duplicates one sequence and eliminates another. (Futuyma 1986, pp. 465-69). It also occurs between nonhomologous sequences on homologous chromosomes and even between sequences on nonhomologous chromosomes.

Another means of genetic rearrangement is unequal crossing-over. Like allele swapping, this process involves reciprocation between homologous chromosomes. But unlike allele swapping, the sites on the two chromosomes are not precisely matched, so that different sequences are exchanged. The result can be deletion of a gene or genes on one chromosome and duplication of genes on the other. (Gardner et. al. 1993, p. 587). Because of its ability to duplicate genes, repeated unequal crossing-over is believed to be one of the mechanisms responsible for the concerted evolution of multigene families and, hence, extremely important in genetic evolution.

Unequal crossing-over could be the result of random mutations—perhaps unequal crossing-over is just poorly executed DNA repair. Gene conversions could be random—just uncontrolled hyper-expansions of DNA repair gone wrong. To believe this, however, one would have to suppose that despite all the tools for DNA repair that have been discovered, and despite the fact that DNA repair has been subject to natural selection for billions of years, DNA repair devices are consistently incapable of precisely matching homologues during crossing-over, and that they cannot control themselves to repair only when repair is actually needed, and that it just so happens that the resulting unequal crossing-over and gene conversion turn out to be implicated in the kind of genetic rearrangements that are responsible for significant evolution.

More believable is the hypothesis that crossing-over, including unequal crossing-over and gene conversion, is an evolutionary tool; it is an adaptation for evolving.

As would be expected from this hypothesis, crossing-over is not random. Like sex and conjugation, when crossing-over occurs is not random. Rates of crossing-over increase in response to resource stress. (Bell 1982, pp. 413-19). Crossing-over can also be suppressed. Suppression "is most familiar in male *Diptera*, including *Drosophila*, but

it is also found in female *Lepidoptera*. No species is known in which crossing-over is suppressed in both sexes." (Maynard Smith 1989, pp. 233-34).

Where crossing-over occurs is also not random. Genes that are close together on a chromosome are linked and less likely to be split apart during crossing-over than genes that are farther apart. (Gardner et. al. 1991, pp. 159-160). Thus, contrary to Mendelian law, they will not assort independently. And thus, nearby genes are more likely to be preserved together as a "family." Genetic linkage therefore biases where crossing-over will occur.

There are also "hotspots," DNA sequences where crossing-over occurs more frequently. (Arnheim et. al. 2003). These are associated with mutation hotspots, particular regions of chromosomes that are more likely to be altered. (Shee et. al. 2012). These appear to be associated with regions that are susceptible to double-strand breaks: "Mutational hot spots exist because certain types of DNA sequence are much more prone to replication and repair faults than others. For example, short repeated sequences in and around genes tend to cause problems, because replication enzymes 'slip', missing out or duplicating some repeats. They make the region error-prone. If there is an advantage in frequent genetic change, the short repeats or other sequences that make the DNA liable to be replicated or repaired inaccurately will be selected." (Jablonka and Lamb 2006, p. 323). Barbara Wright "found that when starved of a particular amino acid, the bacteria increased the mutation rate in the very gene that might, if mutated, enable the cell to make the amino acid missing from its food." (*Id.*, p. 322). Mutational hotspots might also "promote concerted evolution (coincident mutations) within genes/gene clusters, an important issue in the evolution of protein functions." (Shee et. al. 2012). Interspersed repeats can block gene conversion.

There are two other types of events that can rearrange chromosome structure during crossing-over. In translocation, a segment of a chromosome gets attached to another. (Brooker et. al. 2011, p. 322). This can also occur as a reciprocal transfer between chromosomes, homologous or nonhomologous. An inversion is when a DNA sequence is spliced back into the chromosome in reverse order, so that DNA content remains the same, but is backwards: "Inversions have been associated with the suppression of crossing-over." (Gardner et. al. 1991, p. 492).

Duplications, amplifications, transpositions, translocations, insertions, inversions, deletions, conversions, repeats: all of these events can cause harmful results. Discussions of these events are commonly accompanied by mentions of defects and diseases that are caused by these kinds of "mutations." Gene amplifications and translocations, for example, are implicated in some kinds of cancer when they occur in somatic cells. (*Id.*, p. 295-96). If they occur in reproductive cells, they can lead to sterile gametes, miscarriage, or Down's Syndrome. (Arms and Camp 1987, p. 276). Discussions of unequal crossing-over speak of it as due to the "misalignment" of

sequences. (Futuyma 1986, p. 67).

But it must be borne in mind how rearrangements, along with the tools that cause them, have been discovered. Much of molecular genetics is devoted to the research of disease and disorders, along with cures for them. A great deal of research necessarily induces genetic novelties in the lab, as when flies are bombarded with radiation, so that the novelties can be detected. In fact, the "mutations" that are easiest to spot are harmful, like double wings in fruit flies. (Eldredge 1999, p. 123). It is not clear how a lab biologist would detect a "mutation" for a better digestive enzyme in a fruit fly or any other subtly beneficial genetic variation.

The emphasis on all the bad things that are caused by rearrangements reinforces the notion that they are random mutations, that they are abnormalities resulting from errors in biological mechanisms. This obscures the fact that every day in species across the globe, millions of offspring, who are the products of dozens or hundreds or thousands of rearrangement events resulting from crossing-over, are born quite normally and develop without defects. Cross-overs are not rare. They are frequent. In humans, there are fifty cross-overs per chromosome. (Arms and Camp 1987, p. 276). The consequences of the routine process of crossing-over, along with the recombination of chromosomes, are endless experiments in the form of genetically unique organisms.

And the emphasis on the bad things that result from rearrangements obscures the fact that over evolutionary time, in the divergence of new species and taxa, dozens and dozens of rearrangement events must have occurred in step-by-step fashion, all without fatality to the lineages in which they accumulated, all in some way beneficial.

That bad things, often fatal, can happen when rearrangements go awry should underscore the improbability of evolution through dozens of sequential, large genetic errors. It should reinforce the hypothesis that life has evolved tools to direct variation, thereby minimizing errors, reducing risks, and biasing variation towards adaptation.

Genetic Experimentation: The Continuum from Conjugation and Sex

The connection of sex to genetic experimentation through rearrangement is also evidenced by the research that has made it increasingly clear that sex descends from conjugation. If we compare bacterial conjugation to sex in our own species, or that of other vertebrates, sex seems far removed from conjugation. In vertebrates, there are morphologically distinct males and females, which have very distinct gametes—typically, small sperm and comparatively large eggs. The union of the sperm and egg results in an embryo developing in the female, eventually leading to the reproduction of an offspring, who will develop and live its life with fully diploid cells. Bacterial conjugation shows none of these characteristics.

But in between bacteria and vertebrates, there is wide range of both conjugation and sex, which illustrates the continuum from one to the other. This also illustrates that, at their core, conjugation and sex serve the same adaptive function: the acquisition of DNA, followed by the reorganization of DNA, resulting in organisms with unique genotypes.

Even bacterial conjugation bears some similarities to sex. In bacterial conjugation, one cell donates DNA to another, so the donor and recipient cells in some sense could be viewed as male and female. There is even a pili tube formed between them, like a male appendage, which is used to transmit the DNA from donor to recipient. Although there are no morphological males and females, bacteria do have mating types that signify conjugal compatibility—with the preference for conjugating with different mating types, similar to outbreeding in sexually reproducing species. Also similar to sex, bacteria employ pheromones to attract the opposite mating type: "Plasmid-free cells [in *Entrococcus faecalis*] broadcast their presence by means of an array of small hydrophobic peptide pheromones…. Plasmid-containing cells bind these pheromones by means of pheromone receptors. (Ruhfel et. al. 1997, p. 53). Likewise, "drug-resistant strains [of *Streptococcus faecalis*] were significantly more likely to be both producers of and responders to sex pheromones." (Clewell 1985, p. 24). Pheromones are also known to signal mating readiness and mating type in ciliates. (Laybourn-Parry 1984, p. 255).

Ciliate conjugation also involves mating types. (Ricci 1982). In ciliates, many species won't conjugate with a cell of the same mating type. However, if necessary, they are nevertheless capable of mating with clones; different mating types are derived from the same clones epigenetically, e.g., by asymmetrical cell division. (Miyake 1996, p. 279). Intraclonal conjugation is akin to inbreeding, whereas mating with different mating types is akin to outbreeding. (*Id.*, p. 249, 280). Species of ciliates with only two mating types have been characterized as "inbreeders." They have fewer potential mates and often wind up conjugating with close relatives. Species with multiple mating types are characterized as "outbreeders": "Many mating types allows for a wider arrange of potential mates. Outbreeding results in greater genetic diversity. These differences have been related to evolutionary adaptations." (*Id.*, pp. 303-04)(citations omitted).

Conjugation also entails crossing-over events that look similar to crossing-over during meiosis. (Gardner et. al. 1991, pp. 219-223). The donor cell transmits a fragment of its DNA. The recipient cell is then temporarily homologous for that particular fragment. It incorporates the donated fragment through two cross-over events in which its own homologous fragment is excised out and the donated fragment is inserted into its DNA strand.

The timing of meiosis in ciliates and metazoa also illustrates the functional continuum between conjugation and sex: "Austin (1965) noted another curious similarity between ciliate conjugation and metazoan [multi-celled animals with differentiated

tissues and nerves] fertilization in that often an egg is diploid when it unites with a sperm. Meoisis begins (or resumes) only after a sperm enters it as, similarly, meiosis begins in ciliates only after they pair. These striking similarities between ciliate conjugation and metazoan sexual reproduction may be viewed as support of the hypothesis that metazoan have evolved from an ancestral form of ciliates." (Miyake 1996, p. 247)(citations omitted).

"Sexual reproduction in ciliates, conjugation, differs from that of metazoan in that there are no gametes [sperm and eggs]." (Jones 1974). But even with this distinction, there is a continuum of gradations rather than a bright line. *Chlamydomonas* is a unicellular green algae that conjugates. Most conjugation occurs between isogamous pairs, meaning that there is little or no differentiation in morphology between the conjugating cells. (South and Whittick 1987, p. 137). But some *chlamydonas* are anisogamous, meaning that there is a male gamete, which is usually small, and a female gamete, which is larger. Sexually reproducing species also span from isogamous, with mating types, to anisogamous, with males and females. The *Charophyceae* are yet another green algae, but with what is thought to be a higher form of sexual reproduction almost equivalent to plants, as it has male and female structures. There are also intermediate forms: "Intermediates between isogamy and anisogamy exist in some groups of green algae. For example, the Volvacales form spherical multicellular colonies. The smaller species are isogamous, forming motile sperm. There are species of intermediate size, in which some colonies produce small motile gametes, and others larger motile gametes. Finally, in the largest species, some colonies produce sperm, and other large non-motile gametes, or eggs." (Maynard Smith 1989, p. 235).

A more definite distinction between conjugation and sex is that conjugation is decoupled from reproduction. As with bacteria, ciliates reproduce asexually by cloning, only periodically engaging in conjugation. But like sex, conjugation accomplishes the reorganization of nuclear DNA, like the sexual process in metazoa. Conjugation is just not tied to reproduction.

But even here, there is a continuum between conjugation and sex, which can be seen with the many species that reproduce by cloning during most of their life cycles, then switch to sex when stressed or at the end of growing seasons. Some degree of starvation is apparently necessary in order to induce conjugation in the ciliates *O. bifaria*, *tetrahymena*, and *Euplotes*. (Ricci 1982, p. 326). But research also suggests that starvation is unnecessary in wild ciliates, which conjugate during specific seasons. This may be triggered by the amount of light and/or degree of temperature: "Apparently environmental shock or starvation are not necessary prerequisites, as previously had been assumed. A closely-related species, *Blepharisma*, also tends towards conjugation at high temperatures (Bleyman 1975). The fact that conjugation often occurs in wild populations during some definite season in the year, for example *Nassula ornate* in May (Daikov, 1972) and *Loxodes striatus* in August (Bogdanowicz, 1930), suggests that temperature

may play an important role in initiating the sexual process, at least in some ciliates." (Laybourn-Parry 1984, p. 86).

Bacteria can evolve by genetically experimenting through conjugation. If they can do this, we should be able to infer that this ability was not lost in the evolutionary process that led to meiosis in higher species.

Point Mutations and the Rival Allele Model of Evolution: Why Have They Stuck?

The neo-Darwinian synthesis has been around so long, and is so consistently repeated as orthodoxy in texts and popular books, that one tends to assume that the evidence for it must be overwhelming. It is therefore surprising to discover that the evidence is weak and always was. It is true that some traits, including those in Mendel's peas, do assort according to Mendel's laws. Point mutations do occur, affecting single traits, as documented in the fly lab. The idea that a single gene codes for an individual trait has been a useful tool, especially in identifying genetic causes of diseases and the role of heredity in transmitting them. These are documented facts. Where the synthesis went wrong was in extrapolating from these facts to draw broad conclusions, including the following:

- That Mendel's laws are laws: all genes assort according to them.
- That all traits are the product of a single gene.
- That an organism can be understood as the sum of a string of genes coding for individual traits.
- That although the alternative traits that assort according to Mendel's laws are typically nonadaptive or maladaptive, in nature there regularly occur alleles that are adaptive.
- That although the point mutations studied and induced in the lab are nonadaptive or maladaptive, in nature there regularly occur point mutations that lead to adaptive traits.
- That the principal means of evolution is natural selection acting on alleles, so that life evolves as alleles for individual traits replace rival alleles.
- That the effects of sex are to shuffle alleles for individual traits and recombine the chromosomes containing them, which spread through the gene pool of a population.
- That what evolves is the gene pool.
- That over time, species diverge as frequencies of alleles in the gene pool change, supplemented by occasional, beneficial new alleles caused by point mutations.

The fact that species divergence, and therefore significant evolution, is due to

transpositions, translocations, insertions, inversions, splicing, deletions, additions, amplifications, and duplications of DNA sequences—which I have lumped together under the term "genetic rearrangements"—blows the entire Mendelian/population genetics model.

Over the past several decades, evolutionary biology has developed a kind of schizophrenia. On one hand, because of the findings of molecular genetics, it is doubtful that any biologist today would mount an intentional argument that the evidence supports anything like the original Mendelian concept of the gene (allele) that codes for a particular trait. Nor would anyone argue that the genome consists of genes for traits strung out at loci on chromosomes that, when added together, constitute an organism. Jablonka and Lamb observe:

> One of the things that molecular studies have reinforced is something that had already been accepted by modern geneticists: the popular conception of the gene as a simple causal agent is not valid. The idea that there is a gene *for* adventurousness, heart disease, obesity, religiosity, homosexuality, shyness, stupidity, or any other aspect of mind or body has no place on the platform of genetic discourse. Although many psychiatrists, biochemists, and other scientists who are not geneticists…still use the language of genes as simple causal agents…the geneticists themselves now think and talk (most of the time) in terms of genetic networks composed of tens or hundreds of genes and gene products, which interact with each other and together affect the development of a particular trait. They recognize that whether or not a trait…develops does not depend, in the majority of cases, on a difference in a single gene. It involves interactions among many genes, many proteins and other types of molecule, and the environment in which an individual develops.

(Jablonka and Lamb 2006, p. 6).

Nor would anyone today claim that Mendel's laws of heredity are generally valid. Stebbins pointed out thirty years ago:

> The entire history of Mendelian genetics has consisted of discoveries that have modified these laws as stated by Mendel. Genetic linkage, crossing over, genes located in organelles rather than nuclei, pleiotropy, multiple locus or "polygenic" inheritance, multimer enzymes having unitary functions but coded by two or more genes, and epistatic interactions between genes at different loci—these are the principal variations, and variations of variations, that have complicated the genetic picture and rendered unrealistic a simple, direct interpretation of Mendelian laws.

(Stebbins 1982, p. 3). In fact, "[t]he most basic concept that emerged from them, that of the gene as a discrete particle, is now known to be false." (*Id.*).

Likewise, no one would mount an intentional argument that the causes of most significant genetic variations—the raw material of evolution—are point mutations, either in the original sense of a change in a gene that creates a new allele for a particular trait, or in the sense of a single change in a base pair of nucleotides.

But on the other hand, evolutionary theory remains wedded to this model. Basic textbooks in genetics, biology and physical anthropology still discuss Mendelian genetics with enthusiasm, as though it unlocked the ultimate secrets of evolution. Population genetics is still taught as fundamental to Darwinian theory. So is the Hardy-Weinberg Law. The most widely accepted model of speciation, which requires reproductive isolation, is premised on Mendelian/population genetics. (Bush 1982, p. 120). The theory of kin selection, which until recently was almost universally accepted as explaining the evolution of altruism, is a mathematical equation (Hamilton's rule) based upon the rival allele model, postulating alleles for altruism opposed to alleles for selfishness at the same slot on a chromosome. (Hamilton 1964). Trivers' theory of reciprocal altruism is a mathematical equation with the same rival allele premise (Trivers 1971), as are modern theories of group selection. (See, eg., Wilson, D.S. and Sober 1994). Mendelian genetics formed the premise of the theories of the adaptive function of sex that were adopted by the framers of the neo-Darwinian synthesis. Mendelian genetics continues to be the premise of other theories as to how sex might be adaptive (as will be discussed below).

In theoretical biology, not only have Mendelian gene-centered theories continued to exist in the age of molecular genetics, they have flourished. Richard Dawkins' selfish gene theory has taken gene-centered theory to a whole new level of popularity and influence. Not only does it heighten the notion of single genes coding for single traits, but it diminishes the concept of an organism; an organism becomes a mere vehicle, manipulated by wily selfish genes. Dawkins has even expanded his selfish gene concept to human culture through his concept of the selfish meme: a discrete idea that selfishly replicates itself in human minds for no other purpose than spreading itself. (Dawkins 1989, pp. 189-201).

Based on selfish gene theory, some scientists have seriously claimed that repetitive DNA is "junk," that these genes are selfish "parasites" of their host organisms. (Smith 1982, p. 379). This was always a poor hypothesis built on top of a bad theory. (*See* Chapter 3, *Dynastic Theory: The Evolution of Altruism in Animal Societies*). It has now been thoroughly debunked. (*See* Encode Project Consortium 2012.) Noncoding DNA is functional.

So why in the face of well-known evidence, which continues to mount, has

Mendelian genetics, and all the theories and concepts built on it, survived?

A first reason is that the framers of the synthesis were extraordinarily confident that, based on Mendelian genetics, they had gotten evolutionary theory completely, utterly right. Mayr: "The essentials of the modern theory are to such an extent consistent with the facts of genetics, systematics, and paleontology that one can hardly question their correctness." (Campbell, J. 1982, p. 190, quoting Mayr). Confidence is contagious.

The historical context is crucially important. Many biologists who embraced Darwin's theory of evolution from common ancestry nevertheless doubted or rejected his theory of natural selection. The debate centered on the nature of genetic variation, with doubters being skeptical that small chance mutations could produce new species. One skeptic, Goldschmidt, argued that "[t]he decisive step in evolution, the first step toward macroevolution, the step from one species to another, requires another evolutionary method [that is, the origin of hopeful monsters] than that of sheer accumulation of micro-mutations." (Mayr 1982, p. 562)(quoting Goldschmidt). The proposed alternatives were saltation or Lamarckian directed variation, which were supposed to render natural selection superfluous or of minor importance, but which also had no persuasive evidence to back them up.

In contrast, the neo-Darwinian synthesis dovetailed with Darwin's theory of natural selection and gradualism. Confirming Darwin, and silencing skeptics, was an invigorating intellectual breakthrough. Neo-Darwinism became synonymous with Darwinism, which created not only a powerful intellectual framework, but also made for a powerful polemic. Any criticism of the synthesis could be treated as anti-Darwinian, just like creationism. The synthesis took hold and has dominated evolutionary biology.

The enthusiasm for Mendelism led to a bias in what organisms and traits were studied and what results were reported. In fact, long before the synthesis, the genetic variations in de Vries' new species of evening primroses were known to be rearrangements, not point mutations. But these facts were shunted aside and kept in a separate mental compartment. As Jablonka and Lamb explain,

> The Synthesis was based on genetic research that focused on traits that could be studied using the methods of Mendelian analysis. Mendelian analysis depended on discrete qualitative traits that showed fairly regular segregation. Traits that did not behave like that were pushed aside. It was easy to believe that they were the consequences of experimental mistakes, or the complexity of the system. If there are a lot of genes and they interact, it was said that the trait is obviously too difficult to analyze. Extra genes, called "modifiers", which interact with the main gene, were readily invoked whenever there were problems of interpretation. As early as 1949, Lindegren was pointing out that in the bread mold *Neurospora*, two-thirds

> of the mutations he found did not show Mendelian segregation. But most scientists ignored these cases, even though they were in fact the majority. They were considered part of the "noise" of the system. When these deviant traits were acknowledged at all, they were excused, not studied. And even when there was agreement that there are indeed some strange phenomena—jumping genes in maize, for example, or strange inheritance of cortical structures in unicellular organisms—they were brushed under the carpet. At best they were considered to be eccentric cases that did not alter the general picture, and at worst they were simply ignored.

(Jablonka and Lamb 2006, pp. 43-44).

Discoveries of structural changes in the genome led Muller to lobby for limiting the term "mutation" to point mutations. He did so perhaps in part to avoid confusion in terminology, but mainly because only point mutations fit the concept of the gene that had emerged from Mendelian genetics. (Carlson 2011, p. 51). Muller was not successful. The result was confusion in terminology:

> As the fly work increased and as geneticists sought to expand their knowledge by studying new organisms for their modes of inheritance, the terminology used by different groups could be misleading and confusing. The term mutation was being applied to events that with more careful genetic analysis could be described as polyploidy (the gain or loss of a complete set of chromosomes), aneuploidy (the gain or loss of one chromosome in an otherwise diploid organism), and structural rearrangements. They could also involve an exchange of pieces of nonhomologous chromosomes resulting in translocations. Although all of these chromosomal events could be considered of evolutionary interest in some species…they were neither the Darwinian variations nor the "point mutations" of the fly lab.

(Carlson 2011, p. 51).

The confusion has continued. "Mutation" and "gene" are such core terms of evolutionary biology that one expects that they must have definite meanings, but they do not:

> "Mutation" is as difficult to define as "gene". Until recently, a gene was defined as a DNA sequence that codes for a polypeptide, but we may now argue whether or not introns count as part of genes, or whether the term gene should also embrace nontranslated regulatory regions and nontranscribed sequences. "Mutation" is similarly a vague term. It is often defined as a change in a base pair sequence of a gene, but sometimes the

> term is broadly used to include changes in the number and structure of chromosomes (the karyotype).

(Futuyma 1986, p. 60).

Ironically, this confusion in terminology has helped to prop up population genetics. Mendelian genetics gave birth to the concepts of mutation and gene, but with specific meanings. Those meanings have been abandoned. "Gene" is now used to describe a discrete sequence of DNA molecules. This can be useful and accurate. The genome is not an indivisible sequence of DNA. It consists of modules of molecules, with points of beginning and end, like the domains previously described. But these modules are not discrete particles that code for particular traits, with alleles for alternative traits, which is the concept integral to the Mendelian model. The continued use of the term "gene" keeps alive the illusion that the original meaning—and thus the synthesis—remains viable. Likewise, although "mutation" is now used to describe any change in the genome, the continued use of "mutation" masks the fact that the concept of point mutation is of minimal importance and maybe not viable at all. And using "mutation" in connection with the immune system ("hypermutation"), with conjugation, and with the results of crossing-over erroneously suggests that these processes are random, producing errors in line with the original concept of the synthesis.

Another reason that Mendelian genetics has continued to stick is because it is, in scientific parlance, elegant. It is elegant in its simplicity. It is elegant in the way it can be used to weave together many concepts, models, and theories. It is mechanical. Wedded with the concepts of random mutation and the genetic program, it fits the philosophical premise of determinism—and eliminates the teleology that might be lurking in saltationism or neo-Lamarckian directed variation.

In fact, Mendelian genetics is so mechanical that, with the binary nature of the rival allele model, it lends itself to math. R.A. Fisher, a founder of population genetics, asserted that "[t]he object is…to state the principle of Natural Selection in the form of a rigorous mathematical theorem." (Campbell 1987, p. 75). Mendel's laws are so mechanical and so precise that they can be put into mathematical equations, allowing evolutionary theory to be placed on the same quantitative plane as physics. With assumptions, rates can be calculated for everything: selection, gene flow, fixation of alleles, drift, sex ratios, and all the other outputs of population genetics. Point mutations complicate things, but at least they affect individual alleles, so that by factoring in rates of mutations, the basic model can remain intact. "Mutations" that are structural rearrangements blow the whole thing. They don't fit the population genetics math or any other formula.

People outside the field of evolutionary biology may be mostly unaware of the prominent role of math in theoretical biology. The mathematical formulas and math-

based studies are seldom discussed in any length in basic texts and popular books. That's because they are dense, obtuse, and indecipherable to all but the handful of mathematical biologists. However, the *conclusions* that are reached in these studies *can* be understood, and these can be cited by other biologists, even if the methodology is incomprehensible.

I discovered this when I began to examine the theoretical basis for kin selection. The theory, which Hamilton called "inclusive fitness," was set forth in two papers full of mathematical formulas, proofs, and predictions. (Hamilton 1964). Ordinary mortals (including myself) who read these two papers would come away with little or no understanding of the theory's basis, except possibly the conclusion that because close relatives share many genes by common descent, altruism is more likely to evolve among close relatives. Indeed, this is how the predictions of kin selection are commonly reported in texts. (*See, eg.*, Gadagkar 1997, ch. 6; Freeman 2011, p. 1032).

This loose statement of kin selection's basic prediction is overwhelmingly supported by the patterns of altruism in nature. Animal societies almost always consist of kin groups. Societies are formed through natal philopatry: offspring remain with their parents even after they have matured. One therefore is led to believe that kin selection has succeeded in explaining the very difficult problem of the evolution of altruism.

But as set forth in a separate book, *Dynastic Theory: The Evolution of Altruism in Animal Societies,* the actual math contains a prediction that should be implausible on its face: to evolve, altruism requires startling leaps of benefits to costs, depending on the Mendelian degree of relatedness between altruist and beneficiary: 2 to 1 (siblings); 4 to 1 (aunts, uncles, nephews, nieces); 8 to 1 (cousins); 32 to 1 (second cousins); *ad infinitum*. Even to explain the altruism of parents to offspring—i.e., basic parental care—kin selection requires 2-to-1 leaps of benefits to costs.

I understood this not from Hamilton's own papers, but through a more lucid exposition by Richard Dawkins in *The Selfish Gene* and, to a lesser extent, from E.O. Wilson's explanation in *Insect Societies*. (Dawkins 1989, p. 93; Wilson 1971, pp. 182, 328-34). However, neither of these biologists (or others) appeared troubled in the least by the extraordinary leaps of benefits to costs—or even that the very idea of any leaps makes the evolution of altruism a special case, at odds with the evolution of every other kind of trait and with Darwin's maxim that nature makes no leaps. My guess is that once one buys into the core idea that evolution can be mathematicized, and that an equation follows from Mendel's laws, one can be blinded by the equations; one can overlook obvious implications that, in the real world, would be seen as extremely implausible. I don't know how else to explain the fact that so many biologists have been perfectly comfortable with the notion that altruism requires leaps to evolve—or that sex, and all the intricate molecular events that are involved in it, must hurdle 2-to-1 leaps in order to evolve. This just follows from the math, which derives from Mendelian genetics.

Problems with kin selection's logic have been explained away with more obscure math, which can illustrate how math that hardly anyone understands can nevertheless be used to support a conclusion. Kin selection hinges on the percentage of genes two individuals share by common descent—their degree of Mendelian relatedness. No one has been able to demonstrate why this percentage should be evolutionarily significant. It is sometimes said that the degree of relatedness is the probability that two individuals share a particular gene for altruism. (*See.,eg.*, Mock et. al. 2010, p. 239; Pinker 2002, p. 400). But this doesn't hold up. Most genes (however defined) in a species are fixed. They are shared by all members of a species. Thus, degree of relatedness has nothing to do with the probability of sharing any particular gene, including a gene for altruism. Dawkins avoids this problem by assuming that a gene for altruism is very rare, which he admits is a bit of a cheat. To explain away the broader problem with degree of relatedness, he states in an end note that "Alan Grafen gives what may be the definitive solution to the problem in his 'Geometric View of Relatedness', which I shall not attempt to expound here." (Dawkins 1989, p. 288).

Grafen's geographical view of relatedness is not something that anyone other than his fellow mathematical biologists can begin to comprehend. But if one is inclined towards a confirmation of kin selection, one can tell oneself that although the math is incomprehensible, at least some professionals are satisfied with it, so one can be confident that the problem with the significance of degree of relatedness has been solved.

The denouement to kin selection and the math is the *Nature* article in which E.O. Wilson and colleagues disturbed the world of sociobiology by declaring that kin selection is flat-out wrong. (Nowak et. al., 2010). There are many logical and evidentiary problems with kin selection, which I have detailed in *Dynastic Theory.* Wilson and his colleagues hardly mention these. Instead, they focus on problems with kin selection's math. Their alternative solution to altruism is then detailed in supplements to the article containing highly complicated math. The article touched off heated exchanges between the authors and defenders of kin selection, with Dawkins calling the article a disgrace. According to a Boston Globe reporter, "Nowak explained, the critics don't understand the math…[and] many of the people who signed letters disputing his paper have never actually done the math. 'That's like alchemy,' Nowak said. 'There is no other theory than math. Mathematics is the only theory.'" (Neyfakh 2011).

I certainly can't disprove the math. I can't begin to evaluate it. All I can say is that if Darwin's theory had turned entirely on an obscure mathematical proof, no one would have celebrated the 200th anniversary of *The Origin of Species.*

The simple math inherent in Mendel's laws apparently can give rise to exceedingly complex math. But at least it's susceptible to math. And Mendel's laws of inheritance can form the basis of a concept of the simple gene, the concept of alleles, and the concept of point mutations, which can be extended to a model of an organism and a model of

evolution through rival alleles.

In contrast, not only do rearrangements not fit the models of the synthesis, they haven't led to models of any kind, not yet. Although significant and multiple rearrangements are known to have occurred, and that these differentiate species, it is still not clear how these play out in the incremental differentiations, additions, subtractions, and recombinations of traits. Discussing the remarkable discoveries that have accompanied the human genome project, Jablonka and Lamb remark:

> But the geneticists themselves, now in possession of the coveted "book of life", have shown a curious and almost schizophrenic response. On the one hand the excitement and sense of achievement are so overwhelming that prophecies about the newly promised land have been even more daring. On the other hand there is a new sense of humility. And ironically, it is the achievements of molecular biology that are causing the humility. The discoveries that are being made show how complicated everything is…. [T]he revelations of molecular biology cannot be neatly slotted into the existing framework of thought. They do not make the old genetics more complete; rather, they highlight the simplifying assumptions that have been made and reveal vast areas of unanticipated complexity. Genes and genetics can no longer be looked at in quite the same way as the past.

(Jablonka and Lamb 2006, p. 6).

That, perhaps, is the ultimate reason that genetic rearrangements have mostly been placed in an intellectual corner. Absent a model with which to replace the synthesis, evolutionary biologists have been reluctant, perhaps unconsciously, to let go of the existing framework, or to fully acknowledge the evidence that contradicts it. The certainty of an entire academic field that it thoroughly answered complex, long-debated questions does not easily give way to uncertainty, much less disavowal and the reopening of debates. As Thomas Kuhn observed in *The Structure of Scientific Revolutions*, "once it has achieved the status of paradigm, a scientific theory is declared invalid only if an alternate candidate is available to take its place." (Kuhn 1970, p. 77). Until then, "defenders [of a paradigm] will do what we have already seen scientists do when confronted by anomaly. They will devise numerous articulations and *ad hoc* modifications of their theory in order to eliminate any apparent conflict." (*Id.*, p. 78).

But although there is not yet a model demonstrating how genetic rearrangements result in new phenotypes, the fact that they are responsible for speciation cashiers the neo-Darwinian model of evolution through point mutations and rival alleles. This knocks down a barrier to the solution of the puzzle of sex.

And this, in turn, has opened the door to a fresh look at the connection between

sex, rearrangements, and directed variation.

Directed Variation and Rearrangements

The fact of genetic rearrangements undercuts one of the primary rationales against directed variation, which has been incredulity. Recall Dobzhansky's comment that "only a vitalist Pangloss could imagine that the genes know how and when it is good for them to mutate." (Futuyma 1986, p. 76, quoting Dobzhansky). Similarly, Dawkins writes, "how on earth is *mutation* supposed to 'know' what will be good for the animal and what will not? Of all possible changes that might occur to an existing complex mechanism like an organ, the majority will make it worse." (Dawkins 1986, p. 305)(emphasis added).

Given what is now known about the complexity of the genome, the incredulity should be turned around. How could rearrangements possibly be random?

With point mutations, one can at least imagine that these could occur randomly, as minor mistakes in copying DNA. This was particularly true when the gene was conceived as a particle and mutations were thought to be minor disturbances to the particle. Even with the extension of point mutation to nucleotide substitutions, one could imagine that this, too, could occur through random copying errors. One could then imagine that, occasionally, a point mutation might result in something that was actually functional.

But in the face of genetic rearrangements through transpositions, translocations, insertions, inversions, splicing, deletions, additions, amplifications, and duplications, one can no longer even imagine that these could occur randomly—at least not in a way that would be functional and beneficial. It is simply too improbable. And for sequential rearrangements through random mutations to add up over time to a new species would be even more miraculous: "Neither Darwin, Dawkins nor any other biologist has ever calculated the probability of a random search finding in the finite time available the sorts of complex systems which are so ubiquitous in nature. Even today we have no way of rigorously estimating the probability of even one functional protein. It is surely a little premature to claim that random processes could have assembled mosquitoes and elephants when we still have to determine the actual probability of the discovery by chance of one single functional protein." (Denton 1998, p. 61).

To suggest that organisms can interpret their environments, project a "theory" as to what might be adaptive, then genetically self-manipulate in a way that is better than random, does seem to assign extraordinary abilities to organisms which, after all, are collections of mere molecules. But this can be put in perspective by pointing out that the human brain is also a collection of mere molecules. It is, however, a highly evolved

collection of molecules. We are well aware of the marvels of which it is capable. Human minds have invented writing, numbers, computers, and many other devices, all of which aid human cultural evolution. Routinely, while approaching an intersection in a car, we can concurrently perceive stoplights and pedestrians, estimate the speed of other autos approaching the same intersection, and formulate our own response, all while listening to music. We seldom pause to reflect on the stunning sequence of chemical reactions that flow through our physiological system, which enable us to perform this routine wonder. Yet at some level, it is mere molecules at work. It is mere molecules that know how to store information in the brain because it might be useful in the future. It is mere molecules that devise new cultural adaptations.

We ought to be able to put aside incredulity that mere molecules can be so remarkably intelligent and instead acknowledge the possibility that intelligence, including theory-making, is not the sole prerogative of human brains, or even of brains in general. Other collections of molecules can also possess these abilities.

In the same vein, we should also recognize that asking how mutation is "supposed to 'know' what will be good for the animal" and statements such as "mutation is random, but this only means that it can't see into the future and plan what would be good for the animal" (Dawkins 1986, p. 309) are merely polemic devices that make the hypothesis that organisms are adapted to evolve too incredible to be plausible because they imply consciousness. Intelligence does not require mental consciousness. Organisms to which we do not ascribe human-like consciousness nevertheless exhibit conduct that is highly intelligent. Ant colonies build remarkable nests and orchestrate a series of organized activities in which some members help build the nest, others forage for food, others defend the colony, others nurse the young, some develop into various castes of workers, and others develop as virgin queens—all exquisitely coordinated and timed to successfully establish colonies. Yet they never hold a group meeting to coordinate it all, much less consciously tell themselves why they are doing it or visualize the outcome.

For that matter, the development of the simplest organism, from egg to adult, is so remarkably complex that despite years of investigating the process, we have only rough ideas as to how organisms accomplish it. It would take a great deal of intelligence to invent it from scratch. Yet it has been invented, refined, and re-engineered during the evolutionary process, all without conscious design. Consciousness accompanies our own human intelligence, but it is a blinding conceit to suggest that it is a necessary component of all forms of intelligence.

We need to acknowledge that organisms do in fact direct variation. Even under the population genetics model, sex produces genetically unique organisms—nonrandom genetic experiments. As illustrated by the immune system and conjugation, organisms are capable of genetic manipulation. This genetic manipulation results in rearrangements, using a variety of tools. Sex appears to descend from conjugation. Crossing-over during

meiosis results in genetic rearrangements. Even if it is not known how these rearrangements affect the phenotype of offspring, it is known that the end results are millions of genetic experiments in the form of unique offspring.

Thus, the question should no longer be whether crossing-over, meiosis, and the reproductive union of gametes can produce genetic experiments; the question is how organisms do these things and how they aid the evolutionary process.

Organisms as Epigenetic Systems: Perceptive and Flexible

To understand how organisms can genetically self-manipulate, it is useful to first replace the string of genes model of an organism with a model acknowledging that organisms are perceptive and intelligent. This began in two previous books, which introduced the model of an organism as an epigenetic system. This model is not as mechanical as the Mendelian model. It doesn't result in equations. However, it is a more accurate depiction of organisms as adaptively flexible—and intelligent. The epigenetic model helped to explain phenomena that had remained intractable under the string-of-genes model, including the problem of altruism, group adaptations, and the transition of humans to cultural evolution.

In the epigenetic model of an organism, an organism's DNA contains a repertoire of adaptive and developmental possibilities. Moreover, DNA builds an intelligent organism. An organism can perceive its environment and reach into its repertoire of DNA for an adaptive response.

In fact, the epigenetic process of organism development, previously summarized, is a key demonstration that organisms know how to perceive their environment, that they know how to genetically self-manipulate, and that they know how to direct rearrangements. All the genetic manipulations that must occur in genetic experimentation are known to occur during development: amplifications, transpositions, splicing DNA, joining it together, switching on some DNA, switching off other sequences.

Organisms are thus capable of directing the genetic manipulation of *somatic* cells. As Jablonka and Lamb put it, "No one can deny that directed DNA changes are possible, because they occur during development…. What does disturb many evolutionary biologists is the idea that some of the mutations that are the raw material of evolution are not the result of blind accidents." (Jablonka and Lamb 2006, p. 88).

During organism development, in order for cells to differentiate into arms, legs, and livers, cells must genetically manipulate in response to the organism's *internal* environment. A cell's cytoplasm serves as the intermediary to nuclear DNA and as the information link between somatic cells.

But it is also known that cells can perceive the environment *external* to the organism and genetically self-manipulate to alter their development. For example, the Mexican salamander, the axolotl, will pass different generations in completely different morphological forms. (Gould 1977a, p. 178). It may live and reproduce in water as a tadpole for several generations, but if the pond dries, one or more offspring will pass through the larval stage to become a salamander. Parasitic trematodes (flatworms) can occupy many different hosts. One such species, *Hymenolepsis diminuta*, is sufficiently flexible that it can infest species of insects belonging to five different orders. (Matsuda 1987, p. 39). To do this, the germ-line cells of salamanders and trematodes must be able to perceive the physical environment surrounding them—a dry or wet pond, or which host—then absorb this information and transmit it to nuclear DNA, in order to evoke the appropriate genetic configurations to steer the development of the organism accordingly.

This ability is not uncommon. To the contrary, it is ordinary. In ants, bees, and wasps, female larvae can develop into queens or any one of several castes of workers, all with greatly different morphological and behavioral traits. The division of the castes is not due to genetic differences among the larvae. The divisions are due to epigenetic (external) influences, such as diet and pheromones. (West-Eberhard 1987). (Wilson 1971, p. 152, 190). To do this, these larvae must be able to perceive their external environment, absorb its influences, genetically self-manipulate, and develop into one caste or another.

Entire colonies, and whole populations of social species, can epigenetically adjust to varying environments. Species of voles can range from mostly solitary to highly social, depending on available resources and population density. Some species of ants can switch from colonies with a single queen to colonies with multiple queens, with highly divergent morphology and behaviors, when resources temporarily become abundant. (Herbers 1993, pp. 280-81). In honeybees, the roles of workers typically change as they age, but the roles are flexible, depending on the environment: "Bees can accelerate, retard or even reverse their behavioral development in response to changing environmental and colony conditions. For example, favorable environmental conditions in late spring might cause a surge in worker birth rates, and that could result in a colony with a reduced percentage of foragers. Under these circumstances, young bees compress their period of hive work from three weeks to one week and become 'precocious foragers.'" (Robinson 2010, p. 329).

In all of these cases, and in all the numerous instances of epigenetic responses, the question is not whether organisms are capable of perceiving the external environment and genetically self-manipulating, thereby causing differential expression of nuclear DNA. The question is *how* they do it. In the case of bees switching between castes of nurses and foragers, researchers recently determined that the switch is due to DNA methylation, an epigenetic device that can switch genes on and off. (Herb et. al. 2012). But this is a breakthrough. On the whole, very little is known about the epigenetic process at the

molecular level. As in the process of epigenetic development, cell cytoplasm is presumably the intermediary between the external physical environment and nuclear DNA.

Organisms as Epigenetic Syst*ems:* The Genetic Library

The fact that organisms can epigenetically differentiate their phenotype depending on the environment means that their DNA contains a repertoire of adaptive and developmental alternatives. Butterfly color patterns can change with seasonal photoperiods and temperatures. (Matsuda 1987, p. 39). Bristow describes a fungus, an aquatic mold, in which gender can be epigenetically determined. If two fungi are placed side by side, one will become male and the other female. (Bristow 1978, pp. 77-78).

We could say that an organism's DNA is a genetic library of adaptive possibilities.

During its lifetime, an organism does not express all the possibilities contained in its genetic library. Many of traits will remain latent in one or even many generations. To perpetuate a line of descent, it is useful to have a repertoire of adaptations available for different environments that may be encountered by any given generation.

In the population genetics model, the gene pool of a species has been described as a genetic library, consisting of a variety of alleles for alternate traits. (Ruse 1998, p. 11). It is true that variation does exist in a population, which is why organisms prefer to outbreed. But in the epigenetic model, it is also true that each organism's DNA contains a genetic library of adaptive possibilities, accumulated by the organism's line of descent.

The Genetic Library: Atavism and Homoplasy

The concept of DNA as a genetic library is also implicated in the phenomena known as "atavism" and "homoplasy." Ancient traits that have long been lost in a lineage sometimes curiously reappear, as when a whale develops hindlimbs. This phenomenon is known as atavism, or "throw-backs" to ancestral forms. Developmental biologists can induce them in laboratory experiments. For example, a chick embryo can be manipulated to develop a leg and foot structure similar to that of the ancient archaeopteryx. If placed on the jaw mesoderm of a mouse, a chick's jaw epithelium will develop teeth, "a striking example of the conservation of a response to induction that has not been expressed for more than 80 million years." (Futuyma 1986, p. 436).

Darwin was fascinated with these reversions to ancestral forms and not just because they are curiosities. Reversions often occur adaptively. Traits may appear in a species, then disappear in a descendant species, then reappear in a further descendant

species after a long span of evolutionary time—then disappear, then reappear again. He called this “reversion”:

> But on the doctrine of reversion... the germ [reproductive cell] becomes a far more marvellous object, for besides the visible changes which it undergoes, we must believe that it is crowded with invisible characters, proper to both sexes, to both the right and left side of the body, and to a long line of male and female ancestors separated by hundreds or even thousands of generations from the present time: and these characters, like those written on paper with invisible ink, lie ready to be evolved whenever the organisation is disturbed by certain known or unknown conditions.

(Darwin 2011, ch. XIII).

An example of adaptive reversion is the plant *Dalechampia.* When it colonized Madagascar, this plant reverted its form to a primitive, ancestral state, from pollination by resin-collecting bees: “It is not as improbable as it at first seems, however, because the resin gland is derived from the sterile fourth, or fourth and fifth arms of the staminate pleiochasium. Hence the coding for the primitive arrangement of flowers, bracts and bractlets may have been preserved in the genome as suppressed information, and this chunk of DNA may have been reactivated when a mutation altered a regulatory gene….” (Armbruster 1996, p. 239).

Modern systematists refer to the repeated gain, loss, re-gain, and re-loss of traits in a lineage as homoplasy. It contrasts with homology, in which it is assumed that when two species share a trait in common, they've inherited it from their most recent common ancestor. (Wake 1996, p. xvii). If a trait is homoplastic, this assumption does not hold. The shared trait is derived from a common ancestor, but the common ancestor may be very distant on the family tree, yet more recent common ancestors do not have the trait. Consequently, homoplasy is also sometimes referred to as “latent homology” (Wake 1996, p. xix) or “leap-frog radiation.” (Chase and Palmer 1997, p. 331).

Homoplasy is a source of frustration for systematists in their efforts to pin down the relationship of species on evolutionary trees. (Armbruster 1996, p. 227). Historically, systematists had attempted to establish the genealogy of species based on the number and kinds of traits that they shared. But when traits appear, disappear, and reappear in taxa and species which, by other criteria, seem to have been long separated both in time and by common ancestor, two species may share the same trait that one of their common ancestors did not. Distant species may share more traits than they do with more closely related species.

Adding to the frustration, many traits can be homoplastic, making the task of establishing phylogenetic trees based on shared traits extremely confusing: “In

cyclomorphosis in Rotifera (chap. 15), Claocera (Sect. 23A), and some Collembola (Sect. 23D1) great ranges of environmentally induced variation are perplexing to taxonomists…." (Matsuda 1987, p. 39). Three different mating systems occur in "each major subdivision of the higher fungi, and there are many genera in which all three mating systems occur…and this situation obtains in many other groups at all levels of phylogenetic divergence." (Raper 1966, p. 247).

Frustrations aside, one interpretation of homoplasy is that it is adaptive, as Darwin suggested. It is as though, in addition to their expressed traits, organisms retain a genetic library of other unexpressed traits, stored for the potential use of their descendants when once again they prove adaptive: "[A] significant component of organismal diversity consists of species that exhibit traits that are similar to those found in near or even distant relatives, despite their absence in a common ancestor." (Sanderson and Hufford 1996, p. 327).

Is it really possible that latent traits could be "stored" in the genetic library, transmitted down a line of descent through several or many speciation events, then "triggered" when once again the traits became adaptive? The adaptive radiation of the three-spined stickleback suggests that this is not just a hypothetical possibility.

A coastal marine fish that feeds on plankton, the three-spined stickleback radiated from saltwater into the numerous freshwater lakes of northern North America created by the deglaciation following the last ice age. (Foster et. al. 1996; Taylor et. al. 1997). The freshwater sticklebacks have two distinct morphologies and behaviors. One is a limnetic (open water) form, with a suite of specialized adaptations for feeding on plankton in open water. Traits include a narrow mouth, long snout, large eyes, closely-spaced gill rakers, and group feeding. The benthic (deepwater) form, which feeds on benthic invertebrates, is characterized by a large mouth, small eyes, and widely-spaced gill rakers. Since the lakes that support the freshwater stickleback are not connected to one another, biologists believe that each lake was populated independently by coastal marine sticklebacks. Thus, each of the two suites of characters must have evolved independently in each lake: "These results argue that divergence into Benthic and Limnetic morphologies and life-styles has occurred independently many times." (Taylor et. al. 1997, p. 527).

This suggests that the suite of traits is genetically intercorrelated. (*Id.*, p. 514). As Foster et. al. put it, "many of the phenotypes are not independent, and have evolved in concert in response to the same selective regimes." (Foster et. al. 1996, p. 263). Moreover, lakes that can ecologically support both forms have evolved both distinct forms, even though the evidence demonstrates that each lake was "invaded" by the coastal marine form only once and despite gene flow within each lake. (Taylor et. al. 1997, pp. 519-521).

In short, the adaptive radiation of sticklebacks required no novel traits, only the

iterated evolution of similar phenotypes:

> In the case of behavioral characters, our efforts have uncovered no derived states that are a consequence of the evolution of novel motor patterns. Similarly, we know of no clear cases in which a novel morphological structure has appeared in a postglacial population. Thus, the pattern that emerges in the postglacial radiation of threespine stickleback is one in which adaptive homoplasy is extremely common, and the derived characters are the products of expression shifts or loss of ancestral states....

(Foster et. al. 1996, p. 258). It is as though, as Darwin suggested, "these characters, like those written on paper with invisible ink, lie ready to be evolved whenever the organisation is disturbed by known or unknown conditions." (Darwin 2011, ch. XIII). In the case of sticklebacks, they are "disturbed" by their encounters with fresh water lakes and different ecological opportunities within the lakes.

Biologists studying the sticklebacks speak of the two forms as due to speciation events. But this kind of speciation appears strikingly similar to ordinary epigenetic differentiation, cued by different environmental conditions, which is thought of as occurring within a species. (Nor does this kind of speciation appear to be a throw-back). The distinction between ordinary epigenesis and environmentally-cued homoplastic speciation may be a graded one, not a bright line. Homoplastic traits can be cued by the same kinds of environmental "disturbances." (Matsuda 1987). In either case, a potential adaptive response is stored in the genome, is transmitted down a line of descent, and is triggered by exposure to an environment that renders it adaptive.

The number of generations that pass between environmental disturbances that trigger the use of epigenetic traits and reinforce their adaptive utility may affect the ability of organisms to access their accumulated, stored genetic and developmental repertoire. Organisms are constrained by the pathway of their development (ontogeny). The pathway of development may diverge over time. Depending upon constraints and degree of divergence, accessing the stored repertoire may be simple, difficult, or impossible. But as the extreme cases of atavism illustrate, DNA stores a wide and interesting range of phenotypes—a genetic library of evolutionary possibilities.

The concept of the genetic library, and induced epigenetic responses to varying environments, could also account for patterns of speciation when mainland species colonize islands. For example, "despite historical contingencies and ecological differences among the four islands of the Greater Antilles, morphologically convergent species of these lizards have evolved on each island that fill the same set of ecological roles; furthermore, species filling different roles appear to have evolved in the same sequence on each island." (Givnish 1997, p. 36). It is also common for relatively small mainland birds, when they colonize an island, to become quite large, lose the power of

flight, and occupy the ecological niche that mammals ordinarily occupy on the mainland. The now-extinct giant Moa of New Zealand is an example. This kind of iterated evolution may entail relatively small changes in development through heterochrony. (*Id.*, p. 35). Relatively simple heterochronic changes in development could likewise account for the repeated evolution of "gigantism" in other island-colonizing species, such as giant turtles, rodents, and other species.

Evidence of the genetic library, and the interplay with environmental cues, can be found in the silversword alliance, which consists of over fifty species in the composite (sunflower) family found in the Hawaiian islands. (Baldwin 1997, p. 104). All of these species are believed to have evolved from a common ancestor that migrated from North America. The Hawaiian species are remarkably diverse—trees, shrubs, plants, vines, and others—and occupy highly diverse habitats, from wet to dry, lowland to highland. Some of the species are believed to have evolved independently on different islands. Yet the genetic differences among these species are relatively small, suggesting that all of their widely diverse traits existed in the DNA of the common ancestor, with many being latent, but expressed and cobbled together in myriad forms in the myriad environments offered by the geologically recent Hawaiian islands.

That an organism's DNA contains a genetic library is supported by a breeding experiment conducted by a Russian biologist, Dmitry Belyaev. He successfully bred tameness into silver foxes. Other characteristics evolved along with tameness, including droopy ears, white spots, curly tails, shorter legs, and a longer reproductive season. (Jablonka and Lamb 2006, pp. 259-260). The researchers concluded that selection for docility co-selected for reduced hormone levels, which affected development of these other traits. They also concluded that no new DNA was involved: "[T]he new phenotypes appeared too frequently to be the result of new mutations, and the mating scheme allowed very little inbreeding, so these two alternative explanations were ruled out…. Belyaev…attributed the appearance of new phenotypes to the arousal of what he called 'dormant' genes. According to Belyaev, animals have a large reservoir of dormant genes…. Belyaev suggested that in stressful situations, such as during domestication, the effects of selection on the hormonal systems cause these inactive genes to become heritably active. The result is a dramatic increase in the amount of variability seen in the population. So, according to Belyaev's interpretation, the new phenotypes that accompanied tameness were the consequence of epigenetic changes rather than genetic changes." (*Id.*).

The Genetic Library: Genomic Imprinting

Genomic imprinting is a phenomenon found in diploid species in which genes are epigenetically expressed, or suppressed, depending on whether they are inherited from

the mother or the father. (McEachern and Lloyd 2011). The genes from the mother and father might be identical, but the epigenetic imprint that suppresses the sequence in, say, the mother but not the father is also inherited. Thus, "in genomic imprinting it is the allele's parent-of-origin, and not the underlying DNA sequence, that determines its activity." (*Id.,* p. 44). The epigenetic mechanisms that cause imprinting are the same as those that cause epigenetic regulation of expression during development: DNA methylation, histone modifications, chromatin structure, noncoding RNA, and RNA interference.

Genomic imprinting is widespread in mammals, insects, and plants. The epigenetic mechanisms are similar, suggesting that these mechanisms are highly conserved over time and across divergent lineages. (*Id.*, p. 62). Genomic imprinting is thus presumably functional and adaptive. Significantly, although the mechanisms are highly conserved, which genes are imprinted differs from species to species. This "may indicate that imprinting of genes can evolve rapidly…." (*Id.*, p. 63).

In diploid organisms, imprinting could affect phenotype by halving the protein products from a particular gene due to suppression in either the mother's or father's line. In species in which males are haploid and females are diploid (eg., ants, bees, and wasps), imprinting could contribute to different phenotypes in males and females. In species that switch between haploid and diploid stages during their life cycles, imprinting could differentiate phenotypes in the two stages.

Beaudet and Jiang point out that another adaptive advantage of epigenetic imprinting is that the traits it affects can be highly evolvable. Traits that are dependent on the dosage of the protein product, eg., growth hormones, can be alternately reactivated and silenced. It is as though the genome is storing two alternate traits, which can be switched on or off. This would permit epigenetic responses to varying environments across generations: "A species is likely to encounter cyclical changes in the environment, such as intervals of drought and abundant rainfall. Similarly, there are likely to be periodic and recurring variations in the abundance of food, the prevalence of specific predators, and other environmental components. Imprinting-dependent evolution can provide reversibility of phenotype, such as the ability to vary back and forth between smaller and larger body size…." (Beaudet and Jiang 2002, p. 1393).

Genomic imprinting is a subset of a broader phenomenon of epigenetic inheritance. For example, Linnaeus had classified a kind of toadflax, a flowering plant, as a separate species due to a very different floral structure from other toadflax; however, it was later determined to appear separate due not to a difference in DNA, but to an epigenetic "mutation"—the pattern of methylation marking that was transmitted from generation to generation. (Jablonka and Lamb 2006, p. 142-43). It is also known that unicellular organisms can transmit epigenetic inheritance from generation to generation. (Jablonka and Lamb 2006, p. 138).

The Genetic Library: The Contextual Shift Hypothesis

In *Dynastic Theory*, I outlined Mary Jane West-Eberhard's contextual shift hypothesis, which explains the origins of social behavior, including altruism towards other members of an animal society. West-Eberhard observed that in social insects, the altruistic traits of sterile workers are exhibited in solitary species as normal mothering. Nest-building, provisioning of the young, and the other helping behaviors of sterile workers are essentially the same as mothering behaviors: "A 'worker' social insect is a female that behaves like a mother but rears no offspring of her own. She can be regarded as an ordinary female *minus* the ability or opportunity to reproduce...." (West-Eberhard 1988, p. 126).

The same is true of social behaviors in other kinds of species—things such as grooming, babysitting, and feeding the young, originate as parental care. Parental care necessarily implies natal philopatry—offspring remain with one or both parents for some period of time after they are born. Larger societies are formed when philopatry becomes extended over time—perhaps because a nest is re-used or new territories are hard to find, so that offspring do not disperse. When this occurs, a context develops in which parenting behaviors are extended to other members of the social group, such as siblings and cousins. There is no need for a specific mutation "for" new social behaviors—just a new context for an existing behavior.

West-Eberhard developed the contextual shift hypothesis primarily to explain the origins of social behaviors, but the basic concept—that old traits in new contexts can result in new traits—applies more broadly to the origins of many diverse traits. Darwin employed a similar concept to explain gradual, successive, and intermediate "gradations" of morphological traits in the evolution of species, as well as to explain the similarities in structures across species:

> [I]f a man were to make a machine for some special purpose, but were to use old wheels, springs, and pulleys, only slightly altered, the whole machine, with all its parts, might be said to be specially contrived for that purpose. Thus throughout nature almost every part of each living being has probably served, in a slightly modified condition, for diverse purposes, and has acted in the living machinery of many ancient and distinct specific forms.

(Gould 1980, p. 26 (quoting Darwin)).

What the findings of molecular genetics are suggesting is that this is true not only of the traits themselves, but of DNA. DNA consists of sequences of molecules that are stored as modules, which can be deployed for very different purposes and traits, depending on the context: when they are activated, whether they are duplicated and

amplified, in conjunction with other DNA sequences or gene products, etc. A gene that is involved in developing an insect leg doesn't have information encoded in it that says "make an insect leg"; it doesn't program for a leg; it's not even a recipe for a leg. It can be used to create a variety of traits, depending on the context. It can be suppressed by being placed in a deactivated region of a chromosome so that it makes nothing at all—at least not in that particular organism in that particular generation. But the module continues to exist, perhaps to be re-deployed at some future time, either to make a leg or for some other purpose. It is part of a genetic library of phenotypic possibilities.

The Genetic Library: Its Significance for Genetic Experimentation

As an epigenetic system, an organism possesses a wide array of adaptive and developmental possibilities, stored in its genetic library, that can be epigenetically expressed. But the concept of the genetic library also means that DNA contains an enormous amount of experimental possibilities. Sex and conjugation are the tools employed to "access" and experiment with these possibilities. As Ridley said of the evolution of antibiotic resistance in bacteria, "many of the bugs seemed to have the resistance genes already in their chromosomes; it was just a matter of reinventing the trick of switching them on." (Ridley 1993, p. 71).

Similarly, sex is implicated in homoplasy. For example, while homoplasy is rampant in sexually-reproducing lizards (Jackman et. al. 1997), parthenogenetic lizards show no homoplastic tendencies. (Sanderson 1991).

As detailed in *Dynastic Theory*, the neo-Darwinian model of an organism inhibits thinking of organisms as adaptively flexible. That model also does not allow for the concept of an organism's DNA as containing a genetic library of adaptive or experimental possibilities.

Other neo-Darwinian concepts inhibit thinking of DNA as containing latent, generation-skipping traits. As also detailed in *Dynastic Theory*, Neo-Darwinian definitions calculate the "fitness" of a trait based on its contribution to the number of offspring or genes in the *next generation* of the *individual.*[7] These definitions therefore

[7] *Eg.*, [N]atural selection leads organisms to become adapted as if to maximize their inclusive fitness." (Abbot et. al. 2011). "Fitness: A measure of genes contributed to the next generation by an individual, often stated in terms of the number of surviving offspring." (Alcock 1993, p. 576). "Natural selection": "[t]he differential contribution of offspring to the next generation by individuals of different genetic types but belonging to the same population." (Wilson 1980, p. 316). "Natural selection": "the differential capacity of individuals to transmit copies of their genes to the next generation." (Alcock 1993, p. 578). "Fitness": "The contribution to the next generation of one genotype in a population relative to

do not account for latent traits because these traits contribute nothing to the reproductive success of an individual in that generation. I illustrated this point with the lac operon in *E.coli* bacteria. The lac operon gene complex allows bacteria to metabolize glucose in their more normal environments, but switch to lactose on those more rare occasions when they are in a lactose-rich environment. (Gardner et. al. 1991, p. 392). Compare two *E.coli* bacteria, one without the lac operon and one with it. Suppose both are in a glucose environment. The fact that one is able to metabolize lactose, and one cannot, is immaterial in the glucose environment. All other things being equal, each will survive just as well as the other and leave the same number of offspring.

Thus, according to neo-Darwinian theory, these two bacteria are equally fit. But they are not. If it is asked which is most likely to leave descendants, the bacterium with the lac operon will prevail. Sooner or later, descendants of the two bacteria will find themselves in a glucose-poor, lactose-rich environment. Bacteria descended from those with the lac operon will thrive; those without it will perish.

To understand the difference in fitness over multiple generations, one must use line-of-descent thinking, which I introduced in *Dynastic Theory.* In analyzing whether a trait is adaptive, dynastic theory's line-of-descent thinking asks not whether a trait propagates more genes or offspring, but whether it is useful in perpetuating a line of descent. Latent, generation-skipping traits are useful in the survival of a line of descent.

The rationale follows a basic Darwinian premise: all genes, and all traits, are transmitted down lines of descent through reproduction with inheritance. Hence, what survive over time are not individual organisms. What survive are not individual genes, or genotypes. What survive are not specific traits. What survive are not even whole species. What does survive are lineages. Through repetition over the long haul of evolutionary time, the kinds of organisms that continue to exist are those that are adaptively designed to leave descendants.

The fundamental difference between dynastic theory and neo-Darwinism was summed up as this: whereas neo-Darwinism holds that individuals are selected and species evolve, dynastic theory holds that lineages are selected and lineages evolve. But the selection of lineages doesn't occur in discrete generations; it occurs over a continuum of time.

Line-of-descent thinking thus accounts for the genetic library, which allows for greater possibilities in genetic experimentation, and more adaptive possibilities over

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the contributions of other genotypes…." (Wilson 1980, p. 312). "Adaptation": "[A]ny structure, physiological process, or behavioral pattern that makes an organism more fit to survive and to reproduce in comparison with other members of the same species." (Wilson 1980, p. 305).

generations. The concept of the genetic library is also significant because of the modular way in which alternative traits are stored in DNA, which provides easier "access" to alternate possibilities, and thus further aids in experimentation.

Line-of-descent thinking also provides a framework for understanding how the genetic library can not only store alternate traits, but can also accumulate a "memory" of how to access them and join modules together. Natural selection is not just a negative weeding out of mutations, or less fit alternatives, through the sieve of death. It is also a process of positive reinforcement. In every generation, each sexually-reproduced organism is a genetic experiment. In every generation, countless organisms pass the survival test. Each organism that passes this test positively reinforces a genetic experiment. It reinforces what is adaptive—what works. This information can be passed on to the succeeding generation.

This information is not acquired just by the next generation. It accumulates. All organisms are embedded in a line of descent. They are embedded in a line of descent in the sense that their genetic constitution, and hence their repertoire of traits, is the product of the evolutionary history of a long line of ancestors. The cumulative, repetitive process of natural selection can be a form of learning through positive reinforcement. It can be a basis for knowledge. This knowledge of what works can be stored in DNA.

"What works" includes specific traits, such as heads, arms, legs, livers, flower color, digestive enzymes, and the DNA that causes the development of these traits. But "what works" also includes the entire epigenetic system that regulates the genome, the interaction of its sequences, and the process of development. Furthermore, "what works" includes the most efficacious ways of storing hereditary information. As with the human brain, the genetic library compartmentalizes information, arranging it in "comprehensible" modules that can be readily accessed.

"What works" includes the tools for arranging these sequences, and re-arranging them, during organism development to help ensure that the process produces functional organisms and minimizes defective ones. "What works" can include the regions in the genome for crossing-over during meiosis; for transposition; for adding and subtracting proteins, hormones, and the like. It can also include molecular devices for recognizing that something went wrong in transcribing DNA, and fixing it. But it can also include devices for recognizing that the organism is under stress, that resources are lacking, that what has worked in the past is not presently working, and then ramping up the process of genetic experimentation and taking greater gambles. What works can include narrowing the "search options" as to what experiments are unlikely to produce an organism that develops functionally—and also what might possibly work.

All of these ways of storing, processing, and rearranging DNA, and the tools for experimenting with them, have been tested again and again, through thousands and

thousands of generations. Each sexually produced offspring is an experiment, a hypothesis. But genetic experiments also include experiments in the process of experimentation itself. Those that do not work are rejected in the sieving process. Those that improve the process of storing, retrieving, splicing, transposing, joining, and rearranging DNA are positively reinforced.

They accumulate thousands and thousands of generations of genetic history. The result may be said to be an accumulation of hindsight. The process of genetic experimentation thus may be said to be applied hindsight.

This can minimize the risk of a failed experiment. When the immune system engages in trial-and-error experimentation, a certain number of failed experiments will occur, but the system learns from these failures in trying to find the right antibody. Likewise, in conjugation, a bacterial colony can absorb a certain number of failed cells during the trial-and-error process. The same would be true of plants, fungi, and animals that produce prodigious numbers of offspring. But in more slowly reproducing animals, such as mammals, a high ratio of failed offspring would be extremely costly, so risky experimenting must be minimized. Accumulating a memory of what works, and what does not, reduces risk.

In short, line-of-descent thinking, together with the concept of the genetic library, allows an understanding of how the process of genetic experimentation—sex and conjugation—can evolve. Jablonka and Lamb sum it up well: "It would be very strange indeed to believe that everything in the living world is the product of evolution except one thing—the process of generating new variation." (Jablonka and Lamb 2006, p. 101).

Communicating Environmental Information to Reproductive Cells

This has been a conceptual outline as to how an organism can perceive the environment, acquire information, communicate it to reproductive cells, and genetically manipulate DNA in order to devise a nonrandom genetic experiment.

This process, or something like it, must happen. As stated, even in the population genetics model of the effects of meiosis, "determinations" must be made as to how many cross-over events occur and where they occur. The cause of this cannot in any sense be random. The cause must reside somewhere in the organism. The same is true for unequal crossing-over and gene conversion. The same is true for double-strand DNA repair. Somewhere, cells must be able to sense the break, communicate the problem, and send in molecular agents to make the repair. Rates of crossing-over and transposition can vary in respond to stress. Thus, organisms must be able to sense the stress, communicate it to reproductive cells, and trigger the appropriate increase in crossing-over and transposition.

But if we look for the molecular genetics and epigenetics that might explain how any of this occurs, we find that the evidence trail grows fairly cold.

As mentioned, the cytoplasm of cells, including germ line and reproductive cells, must somehow be implicated in interactions with cells' nuclear DNA. It is known that cytoplasm contains a lot of ingredients: organelles, such as mitochondria, plastids, and the Golgi apparatus, not to mention cytosol, which contains proteins and an assortment of other molecules and complexes. Cytoplasm can be exchanged between paramecia cells. Cytoplasm affects fertility in flowering plants, maize, and other crop plants.

It is also known that the initial conditions of egg cytoplasm must be important in development. In the much-studied *Drosophila*, development is controlled by a cascade of regulatory genes that cause different patterns of gene expression in various cell lineages. (Gardner et. al. 1991, p. 413). However, development actually begins before the egg is even fertilized, "with molecular gradients being established in the mature egg." (*Id.*). This is due at least in part to maternal effect genes, which are transcribed prior to fertilization. In one lab experiment, embryos with mutant maternal effect genes, which were known to prevent development of a head or thorax, could "be rescued by injecting them with cytoplasm obtained from the anterior segment of a wild-type [normal] embryo." (*Id.*, p. 417). In all higher organisms that have been studied, fertilization by the sperm is known to trigger a dramatic increase in protein synthesis and cell division, thereby initiating development. However, as with *Drosophila*, the components for protein synthesis must have already existed in the egg prior to fertilization because protein synthesis is not accompanied by RNA synthesis: "Gene transcripts, in the form of mRNA or pre-mRNA molecules, must therefore be stored in the egg in a dormant state." (*Id.*, p. 425). If the molecular gradients in the egg or the maternal effect gene products can be influenced by the environment external to the organism, this would allow the initial conditions of development to be affected, which could in turn greatly affect the cascade of gene expression and subsequent organism development.

Other maternal effects of cytoplasm have been discovered. The previously discussed genomic imprinting and chromatic marking of DNA must necessarily be caused by something external to the nuclear DNA.

I could mention a host of other facts, but the in the end, very little is known about the epigenetic interactions between cytoplasm and nuclear DNA. They remain very much a mystery. This is true not just of reproductive cells, but of germ-line cells, cells during organism development, and cells in fully-developed adults. As Jablonka and Lamb have pointed out, part of the reason is that genetics has turned out to be extremely complicated, far more complex than was envisaged when genes were viewed as particles that somehow caused traits. Another reason is that the gene-centered neo-Darwinian synthesis has tended to emphasize genes and thus ignored epigenetic mechanisms.

In fact, the Weismann doctrine—that germ cells are segregated from somatic cells—theoretically precluded any communication of external information to reproductive cells. The technical rationale for the Weismann doctrine was that deleterious mutations in somatic lines accumulate during an organism's life; segregation of the germ line prevents these mutations from infecting nuclear DNA. The philosophical rationale for the doctrine is that if the soma cannot influence germ cells, this would preclude any kind of Lamarckian inheritance. (Jablonka and Lamb 1995, p. 43). Given what is now known about the way that the genome works, the technical rationale is no longer necessary, and it is further known that germ lines are not segregated from somatic cells, as was postulated by Weismann: "In spite of the widespread belief in the importance of Weismann's doctrine, for many years it has been clear that for *most* organisms it simply is not true." (*Id.*, p. 39). Plants don't segregate the germ line from somatic lines. Even in animals, which do have segregated germ lines, germ-line segregation occurs late in development: "It is clear from the information collated by Nieuwkoop and Sutasurya and Buss that only a minority of groups have early determination of the germ line. For the majority, Weismann's doctrine is not true." (*Id.*, p. 43).

The Weismann doctrine never could be applied to prokaryotes, since their chromosomal DNA is not even segregated in a nucleus. Their chromosomal DNA is part of the "somatic" cell itself, along with all the other contents of cell cytoplasm. As the experiments with bacteria conjugation demonstrate, information from the environment kicks up the level of experimentation. This information includes stress. And as also discussed, the information gleaned from the environment might even include the particular kind of stress that the bacteria are suffering from, e.g., the kinds of resources it is lacking or the kinds of antibiotics that are killing it. This enables the bacteria to focus its experiments on the regions of its DNA that might overcome the stress.

The Weismann doctrine is no longer a theoretical barrier to directed variation. As the grip of the Neo-Darwinian synthesis has begun to loosen, research into epigenetics has correspondingly increased. (*See, eg.*, Jablonka and Lamb 2006; Hallgrimsson and Hall, eds. 2011). But the fact remains that research is presently insufficient to piece together even a conjecture about the molecular process of absorbing information from the environment and communicating it to reproductive cells, along with how this information can be used to manipulate DNA during meiosis. But we ought to be able to predict that these connections exist and eventually will be found. Although it is likely that so-called Epigenetic Inheritance Systems—in which epigenetic inheritance via the cytoplasm directly causes differences in phenotype—will play a role, I think it is more likely that the more significant role for epigenetics will be cytoplasm as the repository of environmental information and as the conduit for signaling nuclear DNA. My reasoning is that DNA is a better tool for stable inheritance over the long haul of evolutionary time.

Criteria for Evaluating Theories of Sex

Thus far, I have focused on establishing that sex produces genetic experiments. But how are these experiments adaptive?

There is no shortage of theories as to the function of sex. Before analyzing them, it is useful to establish criteria for evaluating them. A theory should account for the phenomenon it is supposed to explain. That is, it should fit the facts. To recapitulate, with sex, these phenomena include:

1. In sexually-reproducing species, all offspring are genetically unique—all are genetic experiments.

2. There are three effects of sex: a) crossing-over, b) the recombination of chromosomes that occurs during formation of gametes, and c) the recombination of chromosomes that occurs when gametes unite.

3. With crossing-over, a theory should account not just for allele swapping, but also for gene conversion and unequal crossing-over.

4. There is a "preference" for outbreeding. And, as discussed, the rationale for outbreeding cannot be simply that organisms avoid inbreeding.

5. In species that switch between sexual and asexual reproduction, sex is cued by stress, seasons, or overcrowding.

6. Sex appears to descend from conjugation. Thus, the benefits of sex ought to be consistent with conjugation and vice-versa.

7. Conjugation is cued by the same patterns as the switch between sexual and asexual reproduction.

8. Just like any other trait, sex, and all the intricate mechanisms that it comprises, can evolve even if it is only slightly advantageous.

This last criterion merits an explanation, as it should be obvious that to be consistent with Darwin's theory, a theory should propose that an adaptation can evolve if it is slightly advantageous. However, as mentioned at the outset, many theorists have insisted that whatever the advantage of sex, it must be a two-for-one advantage over cloning. They thus dismiss any theory that posits only slight benefits. For example, in dismissing the tangled bank theory (discussed below), Ridley argues that "It is easy to identify an individual case where sex would have some advantage, but to raise it to a general principle for every habitat of every mammal and bird, for every coniferous tree, a principle that can give a big enough advantage to overcome the fact that asex is twice as

fecund as sex—nobody can quite bring himself to do that." (Ridley 1993, p. 61).

Theorists have based the two-for-one advantage of asex partly on the previously discussed notion, derived from kin selection, that organisms have evolved to propagate their own genes, and thus sex throws away half of their investment. (Williams 1980, pp. 11, 382). But they confuse and conflate this notion with another supposed two-for-one advantage to asex, which is that a population of asexual organisms could produce twice as many offspring as a sexual population. (Ridley 1993, p. 40). The reasoning is that all asexual organisms reproduce offspring, whereas only females reproduce in sexual organisms. If males make up half of a sexual population, only half of the population will reproduce. Therefore, sex must have twice the advantage in order to have evolved.[8]

Dynastic theory dispenses with the first two-for-one problem, but it doesn't speak to the second one. I'm not sure how seriously this second two-for-one problem is still taken, but it still pops up often enough (eg., the Wikipedia article on the evolution of sex) to muddy the waters that its superficial logic should be addressed.

The error can be seen in several ways. First, populations of the same species don't really compete with one another. A "population" is defined as a group of organisms of the same species that are either reproductively isolated or semi-isolated from other members of the same species. (Futuyma 1986, p. 554). If a sexual population is isolated on one side of the river, and an otherwise comparable asexual population is on the other side, it doesn't really matter whether the asexual population could reproduce at twice the speed. Hypothetically, it would matter only if an asexual organism "invaded" a sexual population of the same species.

Second, even then, asexual organisms wouldn't really reproduce at twice the speed. This can be seen most easily when considering a species that reproduces by cloning, occasionally engaging in conjugation. Like sex, conjugation takes time and effort by two organisms as they exchange or transfer DNA. Unlike sex, conjugation produces no offspring. Thus, in such a species, the cost of conjugation is simply the time and effort involved. This is undoubtedly a cost, but it isn't a two-for-one loss of reproductive power. In fact, it isn't a loss of reproductive power at all, since conjugation doesn't involve reproduction. Sexual reproduction accomplishes the same thing (for purposes of this exercise) as conjugation, except that sex combines genetic manipulation with reproduction. The time and effort is a cost, which is why many species reproduce asexually in habitats with temporary resource abundance, switching to sex when resources become limited. But the cost of sex is not a two-for-one loss of reproductive power.

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[8] If one follows the logic of both two-to-one advantages, asexual reproduction should be four times as advantageous as sex. Not only would an asexual organism reproduce twice as many offspring, but it would avoid throwing away half of its genes in each offspring.

Likewise, that there is no double advantage to asexual reproduction can be seen when considering monoecious plants, which bear both male and female flowers and can self-pollinate. This form of sex is barely a step away from asexual reproduction through parthenogenesis. Yet there is no logical reason to think that a monoecius plant could double its reproductive capacity by dispensing with male flowers, instead switching to asexual reproduction.

Third, the two-for-one logic presumes that the only function of males is to reproduce, but otherwise they are waste. This is false. Males take up space and consume resources, the same as females. If an asexual bear showed up in a population of normal sexual bears, the asexual bear wouldn't produce any more offspring than female bears. And when she did reproduce, her offspring would face the same problem as any other juvenile bear: the habitat is saturated with bears, both male and female, adult and juvenile. Although separate populations of bears do not compete, within a population, they do. Bears are territorial. The primary challenge is surviving to maturity in a crowded, hostile habitat with limited resources, and no room to expand. In such a habitat, devoting enough resources to offspring so that one or a few survive to adulthood is of paramount importance. Diluting resources by reproducing more offspring, more swiftly, won't be an advantage—not from the standpoint of individual bears or the population.

I'm guessing that the reason that theorists fall into the trap of comparing sex and asex by sheer numbers is that so many neo-Darwinian definitions of natural selection, fitness, adaptation, and reproductive success are expressed in numbers of offspring (or genes). Using sheer numbers of offspring as the basic standard is valid only when populations (or lineages) can expand without restraint. This is not true for most organisms. For most species, most of the time, habitats are completely saturated. There is no room to expand; there is only room to replace or displace—or find a new niche. This is not a numbers game. It is a quality issue: the more fit organisms survive and reproduce, with "fitness" gauged by competitive abilities other than churning out as many offspring as possible. Again, asexual reproduction is an advantage only when resources are abundant, so that the population can expand rapidly, which is the basic pattern of asexual reproduction observed in nature. And the advantage isn't two-for-one.

Theories of Sex that Do Not Acknowledge Genetic Experimentation

I've already mentioned the theory that crossing-over evolved to repair double-strand breaks in DNA. This theory could be consistent with the fact that stress can trigger sex, conjugation, and increased rates of crossing-over since, presumably, organisms under stress might suffer greater damage to DNA. But DNA repair theory doesn't account for sex and conjugation being triggered by seasonality and overcrowding.

The theory is also limited to crossing-over, with no role for chromosome shuffling. Even with crossing-over, it doesn't explain gene conversion and unequal crossing-over. Nor does it explain the fact that the end results of sex are genetically unique organisms—unless this is just a coincidental by-product of gene repair. Nor is it apparent how outbreeding would promote DNA repair.

Kondrashov proposed that the function of sex is to purge bad mutations from a population. (Ridley 1993, pp. 49-50). He assumes that most mutations are slightly deleterious. Most organisms can live with some "load" of bad mutations, but eventually they will accumulate and cause death, unless there is a means of purging them. In an asexual population, the only way to purge bad mutations is when organisms die. According to Kondrashov, by recombining chromosomes, some sexually-produced offspring will happen to acquire many mutations, while others will happen to acquire fewer. Those with many mutations will die, thereby more swiftly purging mutations from the population, leaving those with fewer mutations to survive and reproduce. That is the advantage of sexual reproduction over asexual reproduction.

At best, this theory could account for only one of the three effects of sex, which is chromosomal shuffling during meiosis. It doesn't account for crossing-over. I don't even think it accounts for mating—the union of gametes—as the hypothetical purging could be accomplished without it. Nor does it meet any of the other criteria for a theory of sex.

Ridley's Red Queen hypothesis proposes that the function of sex is to protect against parasites. (Ridley 1993, p. 71). This hypothesis received its name from the Red Queen's comment in *Through the Looking-Glass* that Alice was running just to remain in the same place. According to the hypothesis, mixing up the genetics in each generation will confound parasites. Ridley analogized the effect of sex to changing locks in each generation, forcing parasites to try to change keys to fit the new locks: "The advantage of sex can appear in a single generation. This is because whatever lock is common in one generation will produce among the parasites the key that fits it…. Rarity is at a premium." (*Id.*). In contrast, an asexual species produces a monoculture that is susceptible to parasites.

As a general theory of sex, Ridley's Red Queen hypothesis is unpersuasive. First, the benefits of changing locks through reproduction would occur far too slowly as a protection against rapidly evolving parasites. Benefits would be especially minimal for organisms with long life-spans, as parasites would have a very long time to find the key to the lock. Ridley points out that species with long life-spans show far more recombination from sex than those with short lives. He argues that this supports the Red Queen hypothesis because it shows that long-lived species change up their locks even more. (*Id.*). However, the fact that there is a positive correlation between life-span and recombination supports many theories, including sex as genetic experimentation. Moreover, this does not address the fact that organisms themselves, during their lifetimes,

could not change locks; meanwhile, parasites are evolving rapidly. Plus, immune systems, which change locks during an organism's life, are far more valuable in combatting parasites than chromosome recombination through reproduction could possibly be.

Second, any advantage changing locks through sex may have is far too narrow a theory to explain all the aspects of sex. For example, crossing-over affects many DNA sequences other than those dealing with parasites. Nor is not known how chromosome reshuffling during meiosis and the union of gametes would have a role in changing locks. Nor does Ridley's Red Queen hypothesis account for the patterns in species that switch between sexual and asexual reproduction. If asexual reproduction results in a monoculture that is susceptible to parasites, it wouldn't be adaptive to reproduce by cloning most of the time, then sexually reproduce seasonally or in response to overcrowding, as many species do. Nor does the theory relate to conjugation, which is implicated in the evolution of the "keys" of the very parasites that Ridley proposes that sex is guarding against. Nor does the theory account for the patterns of sex (and conjugation) being triggered by seasons, overcrowding, and stress, except for the limited kinds of stress induced by parasites.

Theories that Do Acknowledge Sex as Experimentation

Unlike the theories just discussed, others are based on the idea that the adaptive function of sex has something to do with producing genetic experiments. All of these theories, of course, are based on the population genetics model, which is to say that they assume the only effects of sex are to shuffle alleles and recombine chromosomes and that the recombinations are broken up in each generation. And none of them actually describes sex as directed experimentation. All of them assume that mutations are responsible for new traits. I'll outline each hypothesis, then evaluate them together.

Bell's tangled bank hypothesis argues that in a crowded habitat, it is beneficial to be different than other organisms of the same species. (Bell 1982; Ridley 1993, p. 60). Sex is thus advantageous, compared to asexual reproduction, in that it recombines genes to create unique combinations.

Darwin had used the tangled bank metaphor in the concluding paragraph in *Origin of Species*: "It is interesting to contemplate an entangled bank, clothed with many plants of many kinds, with birds singing on the bushes, with various insects flitting about, and with worms crawling through the damp earth, and to reflect that these elaborately constructed forms, so different from each other, and dependent on each other in so complex a manner, have all been produced by laws acting around us." (Darwin 1952a, p. 243). Bell analogized the strategy of an organism in such a saturated, tangled bank habitat to that of a button maker: "He could either continue selling replacements for

buttons or he could diversify the range of buttons and try to expand the market by encouraging his customers to buy all sorts of different kinds of buttons. Likewise, sexual organisms in saturated environments, rather than churning out more of the same offspring, would be better off varying them a bit in the hope of producing offspring that could avoid the competition by adapting to a new niche." (Ridley 1993, p. 60, citing Bell).

The Vicar of Bray hypothesis is named for an English cleric who adapted to the religious upheavals by changing his religious convictions. (Ridley 1993). This hypothesis proposes that sex is advantageous in rapidly changing environments because it is a tool for producing varied phenotypes. When the environment changes, an asexual species will be stuck with the same phenotype, at least until the right mutation comes along. A sexual species, on the other hand, will produce many different kinds of combinations, one or more of which might fit the new environment.

Williams suggested a variety of models in which sex could be beneficial by producing new, different phenotypes. (Williams 1975). In comparing sexual to asexual reproduction, Williams used lottery tickets as an analogy. (*Id.*, p. 15). Asexual reproduction is akin to buying lottery tickets all with the same numbers, while sexual reproduction is like buying tickets with different numbers. The sex strategy would be favored when offspring are attempting to establish themselves in new, unknown environments, with very little chance of success, but a great pay-off for any organism that succeeded. It would be advantageous to produce differently-numbered "lottery tickets" by reproducing sexually and dispersing widely, hoping that one hits the jackpot.

For example, due to crowding, oyster larvae have little chance of gaining hold in their parental habitat. They reproduce sexually, then disperse in large numbers over long distances, each with a small chance of finding a favorable surface to attach and grow. Elms and similar trees face a comparable challenge. There are very few potential spaces where a seedling can sprout and grow to maturity. Elms reproduce sexually and disperse in large numbers. Aphids and rotifers reproduce by cloning until overcrowding affects the food supply, then reproduce sexually and disperse. (Ridley 1993, p. 59). When dispersing into new environments, it is advantageous to produce many differently-numbered lottery tickets because "if your young are going to have to travel abroad, then it is better that they vary because abroad may not be like home." (*Id.*, p. 56).

The tangled bank, Vicar of Bray, and Williams' hypotheses are all based on the fact that sex produces genetically unique offspring, and thus meet that criterion for a theory of sex. None of them supposes that sex produces offspring that are necessarily *improved* compared to the parental generation or to comparable, asexually-reproduced offspring. Rather, they suppose that sexually-reproduced offspring are merely *different* from parents, one another, and asexually-reproduced offspring. In Williams' models and the tangled bank hypothesis, the advantage of sex is that in saturated environments, it is

good to be different because uniqueness might enable offspring to establish themselves in an unoccupied micro-niche. Likewise, the Vicar of Bray hypothesis proposes that because the environment is constantly changing, it is good to be different because one or more offspring might match the changed environment. Thus, there is an advantage in just producing slightly different offspring. Sex accomplishes this. Asexual reproduction does not.

All of these models and hypotheses are consistent with the other criteria for a theory of sex. Although none of them incorporates gene conversion or unequal crossing-over—and, hence, genetic rearrangements—all of them could be consistent with these phenomena.

We can dismiss Ridley's objection to the tangled bank hypothesis—that it is not sufficiently beneficial to overcome a spurious two-for-one disadvantage compared to asex. In fact, in a tangled bank, or any other saturated habitat, any enhanced speed of reproduction afforded by asex would hardly be profitable. We can also dismiss Ridley's objection that "the mathematical models suggest that these [Williams'] lottery models only work if the prize that rewards the right lottery tickets is indeed a huge jackpot…." (Ridley 1993, p. 58) since the math assumes a two-for-one disadvantage to sex. In Williams' models, it would be advantageous to churn out more offspring. We can imagine, for example, that all other things being equal, an elm that sends out a thousand seeds to find a spot to germinate is adaptively superior to an elm that sends out nine hundred seeds. But it wouldn't be adaptively superior if the thousand seeds were all asexual clones of the parent and identical to one another, while the nine hundred seeds of the sexually-producing elm were all unique.

Another objection to the tangled bank hypothesis is that it predicts "a greater interest in sex in those animals and plants that have many small offspring that then compete with one another than among plants and animals that have few large young." (*Id.*, p. 61). I'm not sure I understand this objection; or, rather, I'm not sure why the tangled bank hypothesis would yield such a prediction. Slowly-reproducing species, such as mammals, also live in a tangled bank, with the challenge of finding a way to survive in a saturated habitat. Minor differences in food preferences, digestive abilities, social behaviors, and all the other small attributes that could result from experimentation, could possibly be the key to survival in a crowded world. Perhaps Bell's prediction was predicated on a belief that it was necessary for the tangled bank hypothesis to demonstrate a two-for-one advantage, which could only possibly work in species that reproduce in prodigious numbers.

Ridley dismissed the Vicar of Bray hypothesis on grounds that it is group selectionist: the advantage accrues to the population as a whole, because the genetic diversity that the hypothesis depends on is maintained in the gene pool. But this criticism follows from the population genetics framework. The neo-Darwinian insistence that

what evolves is the gene pool of a population (or species), but what is selected are individuals, is an inherent contradiction. And this contradiction virtually seals the fate of any hypothesis that is based on the fact that sex generates diversity, which is the most obvious ramification of sex.

Line-of-descent thinking realigns how to analyze the benefits of sex-generated diversity. Instead of viewing diversity as a benefit to the gene pool of a *population* (which is not selected), it should be viewed as a benefit to a *lineage* of organisms (which is selected). The concept of the genetic library shows how sex helps maintain (and add to) the diversity that an individual can reproduce. But sex can also be viewed as maintaining (and adding to) the diversity that a lineage can reproduce—generation after generation. And as demonstrated in *Dynastic Theory*, the selection of lineages does not invoke group selection of the kind that has been deemed odious in neo-Darwinism.

Using the lens of line-of-descent thinking, the pertinent question is not whether sex or asex propagates the most offspring; the question is which alternative is the most adaptive in perpetuating a line of descent. After several billion years of evolution, what kinds of organisms fill the Earth? They are those who descend from ancestral lineages that have never once failed to leave a descendant. To have accomplished this remarkable task, what properties must organisms in these lineages have possessed? Over the long haul, the most constant feature of the environment is change. Climate, geography, and life itself—all are perpetually in a state of flux. Resources are bottlenecked. New competitors invade. Prey evolve to evade. To remain unbroken, lineages, through their organismic representatives, must change. They must be flexible, accumulating the capacity to respond to alternate environments and new challenges. Even in the short term, habitats are not typically uniform, with some best genotype and phenotype to fit them. More typically, habitats are heterogeneous, with dozens of slightly different micro-niches. Flexibility is adaptive.

After several billion years of evolution, what kinds of organisms account for the incredible diversity that we observe? They are those who descend from ancestral lineages that have branched and branched, consisting of organisms that have probed the adaptive unknown for new means of perpetuating themselves, sometimes by finding new niches to occupy. By analogy, the islands of Polynesia were populated not by those who passively sought the most conservative way of life, but by those who explored beyond known boundaries. How many outriggers and individual explorers failed to reach a habitable destination we will never know; what we do know is that those who now occupy those islands are descendants of those who did not stand still. They took risks.

The benefits of exploring the adaptive unknown cannot be understood by their utility to individual organisms in surviving. The benefits of experimentation can, however, be understood by viewing individuals as buds on branches of a line of descent. Perhaps most or even all of the experiments produced by an individual plant on the edge

of a desert will add nothing new or beneficial; most may fail. But an individual plant is only a single bud on a branching line of descent. Perhaps one of the plants will produce a successful new experiment that opens up a new niche or a new way of surviving drought in the old niche. If so, it will form the base for a successful new branch with many new buds. From the standpoint of a line of descent, taking some risk carries with it the potential for great rewards—a bonanza of descendant lineages.

We can go further. Line-of-descent thinking also sheds a different light on the Malthusian condition. For Darwinian theory, the significance of this doctrine is that in each generation, more organisms are reproduced than can survive. Because of this, the Darwinian sieve of death is a reality. Selection necessarily occurs.

According to line-of-descent thinking, however, this is not the only consequence of the Malthusian condition. The fact that the power of reproduction exceeds resources, and often results in excess reproduction, causes a selection pressure that stimulates evolutionary experimentation. This is why the rates of sex, crossing-over, conjugation, and transposition increase when organisms are stressed by the environment, including crowding and other kinds of competitive stress. These are the conditions when evolutionary innovation is needed the most.

Continuity of the lineage is first; expansion is secondary and opportunistic. This is why, in species in which the life cycle is seasonal, organisms expand as rapidly as possible through cloning when resources are abundant. But when the season ends, and resources abate, they reproduce sexually or engage in conjugation—producing the next round of genetic experiments. One or more of these experiments may be best adapted for the following season of resource abundance, which may vary subtly or markedly in timing or type from previous seasons. To perpetuate a lineage, it is best not to place all of one's eggs in one genetic basket. It is best to produce many eggs in many diverse genetic baskets.

Although specific selection pressures induce evolutionary innovation most noticeably, the inducement to experiment is always present. The Malthusian condition poses a kind of "background" selection pressure that is always present. While it would not be accurate to say that all *organisms* are on the verge of starvation, it would be accurate to say that all *lineages* are constantly on the verge of "starvation" in the sense that there are never enough resources to permit the exponential expansion of which they are capable. The struggle for branching divergence is constant. The potential rewards of experimentation through creative "breakouts" are always present. Those organisms that continue to experiment are the kind whose lineages continue to fill the Earth.

When we eliminate the notion that sex promotes and maintains diversity only in the gene pool, and instead use line-of-descent thinking, the objection that this "diversity" benefit of sex invokes species (or population) selection disappears. When we eliminate

the two-for-one issue, we find that the tangled bank, Vicar of Bray, and Williams' hypotheses all show how sex can be at least slightly advantageous. These hypotheses are not mutually exclusive, as is often assumed, but rather are complementary, depending on the species.

Sex, Recombination, and Rearrangements

Line-of-descent thinking also allows another way of looking at recombination to see how sex not only generates different phenotypes, but might even improve phenotypes over time—even using the population genetics model of allele and chromosome shuffling. Ridley points out one of the potential benefits of recombination:

> The most obvious reason to borrow genes is to benefit from the ingenuity of others as well as yourself. Sex brings together mutations, constantly rearranging genes into new combinations until fortuitous synergy results. One ancestor of a giraffe, for example, might have invented a longer neck while another invented larger legs. The two together were better than either alone.

(Ridley 1993, p. 46). But he then rejects this benefit because "[i]ts advantages are far too remote; they will appear after a few generations, by which time any asexual competitor will long ago have outpopulated its sexual rivals." (*Id.*).

But again, Ridley is erroneously assuming a two-for-one advantage to asex and that the benefits of sex accrue to a population. Moreover, the benefits of recombination accrue much more rapidly in a line of descent than they do in the gene pool of an entire population. When the two-for-one advantage is dropped, and when the benefits are viewed from the standpoint of a line of descent, this objection to the recombination benefit of sex falls away.

However, there is a second objection to this benefit of recombination, which was mentioned early on: by reshuffling alleles and chromosomes in every generation, sex will break apart any advantageous recombination.

This result has always been assumed. However, it has been assumed based on the belief that genes always segregate and assort according to Mendel's laws. As has been seen, this assumption is not accurate. To begin with, Mendel's laws could not possibly apply to species whose life-cycle is haploid, or to bacteria and other microorganisms with a single chromosome. These organisms don't have rival alleles or homologous chromosomes. Thus, in these species, there is no reason to believe that sex will break apart an advantageous combination. That might happen once in awhile, but not consistently.

Furthermore, even in diploid species, genes do not always segregate and assort according to Mendel's laws. Due to gene conversion, unequal crossing-over, genetic linkage, and other reasons, genes do not assort independently. Thus, it can't be assumed that recombination will break apart advantageous combinations.

In fact, the assumption that sex breaks apart advantageous combinations is based on a model, not on facts. There is no actual evidence that sex does this. This is not observed in nature, nor is this observed in the lab. Of course, it is extremely problematic to discern in nature, or in the lab, when favorable combinations come together, much less discern whether these are then broken apart. It is far easier to detect and study combinations that produce defective traits. To some extent, therefore, we are reliant on modeling. However, enough is known about the limitations and inadequacies of Mendelian genetics that it is dangerous to assume *a priori* that sex breaks apart favorable combinations.

Moreover, since sex does not break apart favorable combinations in haploid species, the conclusion that it does in diploid species presumes that in the evolution of diploid species from haploid, organisms could not "solve" this problem. And since conjugation does not break apart favorable combinations, the conclusion that sex does so presumes that the evolution of sex from conjugation created a flaw that did not previously exist. There is no logical reason, or evidence, to support these presumptions.

This is true even without taking into account the fact that sex produces genetic rearrangements. With rearrangements, there are no homologous alleles that could assort according to Mendel's laws, not even in diploid species. Instead, the homologous chromosomes in an organism will be arranged differently. This raises an interesting question as to how two such chromosomes "interact," not only during meiosis, but during organism development. The answer to this is not known. It is possible that organisms are much more tolerant of mismatched DNA sequences than has been traditionally assumed. It is also possible that organisms have other tools to "reconcile" mismatched sequences, such as gene conversion or one of the means of "turning off" a DNA sequence, such as methylation.

Then again, it bears pointing out that not all that much is really known about how homologous chromosomes interact in general. When genes were viewed as beads on a string, things were far simpler. Identical alleles produced the same traits. Alleles that varied were either dominant or recessive. Dominance and recessiveness could be thought of as characteristics that just somehow attached themselves to particular alleles, without really knowing what caused these characteristics. In some instances, at least, it has since been discovered that a recessive allele doesn't really "code" for an alternative trait. Instead, it is "defective in its ability to express a functional protein." (Brooker et. al. 2011, p. 342). For example, with flower color in Mendel's peas, the dominant allele produces enzymes that make purple pigment. The recessive allele is dysfunctional, a

mutant that produces no enzymes, resulting in white flowers if both alleles are recessive. If only one allele is recessive, the dominant allele produces sufficient enzymes by itself to color the flowers purple. Thus, two chromosomes with alleles for purple flowers are not necessary to produce purple flowers—the molecular make-up of the pea plant somehow detects the dysfunctional allele and compensates. How an organism does this is not known. And this raises the question as to why diploidy is even necessary, at least for that particular trait.

Again we are left with the dissatisfying yet poignant observation of Jablonka and Lamb, that one of the central findings of molecular genetics is that the inner workings of organisms are all much more complicated than has been supposed. And we can also say that organisms are turning out to be far more intelligent than neo-Darwinism has supposed and than its models allow. We should therefore not remain attached to those antiquated, out-of-date models just because they have been around for a long time. We should therefore not continue to assume that sex breaks apart favorable combinations. This assumption needs to be re-evaluated, especially given that it doesn't apply to genetic rearrangements, which are now known to be the primary means of evolution.

A Higher Level of Genetic Experimentation?

Thus far, the hypotheses of the benefits of sex have postulated that genetic experimentation has been beneficial simply by producing organisms that are different. This is a kind of directed variation, but it is fairly low-level. Organisms produce genetic experiments without "guessing" how any particular genetic variation might be useful or better than existing traits. They make no guesses as to the environment or attempt to produce offspring with traits to match it.

The experiments on average are thus neutral compared to the existing genotype. But experimenting is nevertheless beneficial because occasionally an experiment happens to lead to an improvement, or to an adaptation to an environmental niche, or just to a diversification of descendants in order to increase the odds of survival of the lineage. Experimenting is evolutionarily superior to remaining the same, generation after generation, as would be the case if reproduction were asexual.

This kind of experimentation is similar the neo-Darwinian concept of chance mutation in that each particular genetic variation is neutral. It differs from chance mutation in that the system of experimentation itself is not neutral; it is beneficial. The main reason that this system is better than chance mutation is that it does not produce mostly bad experiments.

In other words, essentially, the analysis thus far has followed the neo-Darwinian model of sex, except, a) line-of-descent thinking has been substituted for the notion of the

gene pool and, thus, the benefits of genetic experimentation accrue to lineages of organisms, b) sex need not hurdle two-for-one leaps of benefits to costs, but instead can evolve if it is slightly advantageous, c) sex does not necessarily break apart favorable combinations, and d) genetic rearrangements substitute for point mutations as the source of beneficial new traits.

Even this low level of genetic experimentation is beneficial. And even though it is low-level, it is still fairly remarkable. To avoid bad experiments, and to achieve neutral experiments, the system must know how to consistently avoid harmful genetic variation. To avoid harm, the system must know what parts of the genome to fiddle with; otherwise, genetic experimentation would too often result in damaged offspring. It must likewise know what parts of the genome can be fiddled with. It must have some idea of what sequences need to remain together and which can be spliced and joined with the least risk of damage.

Needless to say, if sex can do better than merely neutral experimentation, the benefits to sex over asexual reproduction would increase greatly. Can it do better?

Thirty years ago, in the concluding sentence of a paper delivered in accepting a Nobel prize, geneticist Barbara McClintock remarked that "[i]n the future, attention undoubtedly will be centered on the genome, with greater appreciation of its significance as a highly sensitive organ of the cell that monitors genetic activities and corrects common errors, senses unusual and unexpected events, and responds to them, often by restructuring the genome." (McClintock 1987b).

I am fairly confident that McClintock is correct. Organisms can perceive their external environment, perceive the particular causes of stress (or opportunities), and communicate these perceptions to reproductive cells to trigger variants in DNA that are focused on overcoming those particular problems or taking advantage of those particular opportunities. That is, search options are narrowed.

How good do they have to be at doing this? Thinking about directed variation is colored by the history of Darwinism versus Lamarckism. So it is helpful to set aside the prejudice that the alternative to chance mutations is necessarily Lamarckian in the sense that directed variation will guarantee an adaptation. There are gradations between pure chance errors and guaranteed adaptations. To facilitate evolution—and thereby to facilitate the perpetuation of a line of descent—it is sufficient that genetic manipulation produce genetic experiments that are better than random: a trial-and-error system that is biased towards adaptation but that does not guarantee it.

Bacteria seem to have this capability. If bacteria can accomplish this, it seems reasonable to infer that higher organisms can do so. Organisms possess a genetic library of adaptive possibilities, along with information about the environments in which these

would be useful. There is ample evidence that organisms can perceive their environments and genetically self-manipulate their germ-line and somatic cells in an adaptive way. This behavior is the basis for epigenetic responses that are pervasive in all cells and all species. If this can be done, it should be plausible that information from the external environment can be used to manipulate reproductive cells.

The evidence for this hypothesis is circumstantial. It requires a fair amount of conjecture, as well.

But this has been true of the neo-Darwinian synthesis, which has not stopped evolutionary theorists from declaring that it is absolutely correct—and from defending it even in the face of contradictory evidence.

For that matter, the proof of Darwin's theory of natural selection is necessarily circumstantial and requires some conjecture. We can't watch species evolve, at least not in dramatic ways. Macro-evolution, including speciation, has always been especially problematic for Darwin's theory of natural selection. The evidence marshaled by Darwin supported natural selection of genetic variation at a micro-evolutionary level. In domesticated species, individuals show variation; based on this variation, breeders have produced new varieties. In nature, individuals also show variation; selection of this variation must occur, as evidenced by the existence of subspecies and closely related species. The inference that many scientists found difficult to swallow was that this micro-evolutionary process could add up over time to the macro-evolutionary process that has resulted in dinosaurs, birds, mammals, and trees. (Mayr 1982, p. 607-08).

Complicating matters, a paleontologist looking at the fossil record, and recording the emergence of major new species and taxa, tends to view evolution quite differently than what is suggested by Darwinian gradualism. In the paleontological record, speciation of major new forms happens abruptly, with swift disappearance of older forms and entry of new forms. Once a new form emerges, it radiates into various niches; thereafter, the overall morphology typically remains the same until extinction. Mayr provides the examples of bats and birds: "Bats apparently originated from insectivores within a few million years but experienced no further major structural modifications in the 50 million years since then. The shift from thecodont reptiles to *Archaeopteryx* likewise required relatively few million years, but the class of birds as a whole has not been materially modified since the appearance of the first modern birds more than 70 million years ago." (*Id.*, p. 610). Gould and Eldredge called this pattern "punctuated equilibrium."

These patterns are not necessarily inconsistent with the micro-evolutionary process of natural selection. When major new forms emerge, they radiate in a way that is consistent with micro-evolution. Moreover, the "swift" disappearance and emergence of new forms is a relative term, occurring over thousands or millions of years. There may

be intermediate forms that, because they evolved relatively fast, did not leave much of a footprint in the fossil record.

But still, over the long haul, something has occurred that's different from a continuous, bit-by-bit, trait-by-trait evolution through natural selection. Some hypotheses invoke occasional catastrophes as suddenly throwing the doors open to large-scale evolution. Others project minor ripples in ecological systems that build into waves, thereby opening the doors to grander evolution. Some, like Gould, emphasize the importance of "body plans," with developmental architecture occasionally finding new adaptive levels; once these have evolved, they disrupt existing ecological systems, replace existing species, and morph into many descendant species. (Gould 1982).

But none of these hypotheses really contradict or nullify natural selection as the essential process of macro-evolution. Even if that process isn't smoothly incremental over time, it still must occur through the selection of traits, along with the underlying genetic variation. The basic Darwinian axiom that underlies natural selection is the Malthusian condition: the power of organisms to reproduce greatly exceeds resources. Selection of varying organisms, along with genetic variation, necessarily follows.

And what is the alternative? Saltationism isn't a theory; it's a conclusion. It doesn't purport to describe how new species come into being through giant leaps. It doesn't have anything to say about how genetic variation occurs and plays out into new species.[9]

Biologists today have far more sophisticated tools than were available to Darwin. Systematists now have the tools to compare genomes, and with these and comparative morphological traits, they can construct phylogenetic trees that enable them to guess at the structural changes in genomes that differentiate related species. Developmental biologists and molecular geneticists now have tools that are beginning to allow them to piece together the relationship between organism development and the content and structure of DNA. But combining these to arrive at a reasonable guess as to the step-by-step process whereby segments of DNA are pieced together, and how these segments substantially alter morphologies and behaviors, remains elusive. The evolutionary process can't be recreated in the lab, at least not for species other than a few

[9] One kind of saltationism is known to occur: new species via polyploidization, which was discussed previously. But the concept of saltation itself doesn't explain this kind of speciation. And even polyploidization is typically followed by "repatterning" of the genome through genetic rearrangements. (Otto 2007, p. 455). It is difficult to establish that existing species are connected by an ancient polyploidy event because, over evolutionary time, they have lost sequence homology (*Id.*, p. 454), presumably by continued repatterning of the genome. Thus, even in these speciation events, saltation is just the beginning of species evolution, not the end.

microorganisms.

However, these tools have produced clues as to what kind of variations must be involved in the evolutionary process. They aren't point mutations. They aren't alleles for specific traits that replace rivals. They are genetic rearrangements.

Rearrangements aren't as tiny as point mutations. The genome is modular. This leads to the possibility of modular changes, additions, and subtractions in morphology, which are more substantial than slight modifications of individual traits. This is not only consistent with the micro-evolutionary process through natural selection of these variations, but would also allow for swifter, more major, evolutionary events—speciation and macro-evolution.

And these tools have produced the clues and evidence that lead to the connections among sex, genetic rearrangements, and evolution.

This book has presented the evidence that sex and conjugation are responsible for restructuring the genome, which can eventually result in speciation. In addition to the evidence, it might also be asked: If not sex, what other process could be responsible for restructuring and rearranging the genome?

Even neo-Darwinians acknowledge that rearrangements occur during meiosis. But whereas neo-Darwinism insists that rearrangements are caused by inadvertent errors, the hypothesis presented in this book is that sex and conjugation direct rearrangements. Given the facts that have been discovered since the synthesis coalesced, which hypothesis is more plausible? The neo-Darwinian models and concept of chance mutation should not be the default dogma. Science is progressive: theories must give way to facts that contradict them, replaced with theories that more plausibly explain the patterns of nature.

Epilogue: Philosophical Implications of Directed Experimentation

Early on, I mentioned the philosophical importance of the doctrine of blind variation: the concept of random mutation accords with determinism, which has become the philosophical premise of scientific causation—the "ruling faith of enlightened men." (Popper 1985, p. 250-51).

In Chapter Six of *Epigenetic Evolution: A Theory of Cultural Evolution through Directed Creativity*, I trace the origins of mechanistic determinism to Descartes, Hobbes, and Newton. In Newtonian mechanics, all causation must be external to the "body." A rock does not move itself. It has no volition. It will not move unless it is struck by another object or unless some other external force, such as gravity, causes it to move.

But suppose that a rock could move on its own. We could say that it has volition. A rock could *will* itself to move. This of course is strictly a flight of fancy. We do not observe rocks and other inorganic matter to be self-moving.

However, it is not so obvious that organisms are really like rocks. Unlike a rock, a duck *does* appear to move on its own. It does not need to be struck by an object or any external force. It *may* be struck, as when a predator grabs it. A blowing wind *may* alter its flight. But these are not necessary for it to move. It will take flight before the predator actually strikes. It will fly whether or not the wind blows. Generally, it will get up, seek food, and rest without an external force causing it to do so. Unlike a rock, a duck appears to be a self-moving body. It has volition.

Before Darwin, natural philosophers frequently invoked vital forces to explain life. (Mayr 1982, pp. 51-52). Vital forces, animated spirits, sparks of life, and such were described as the forces that caused the development of organisms from egg to embryo to adult. These forces explained the features of organisms, their movements and behaviors. According to the ancient Greek philosophers, the ability to self-move was a sign of life. (Russell 1972, p. 537). Without an animal spirit, a living being would cease to move, just like an inanimate object.

Moreover, also unlike rocks, the movements of organisms appear to be purposeful. A duck flies *in order to* find food and shelter. It finds food and shelter *in order to* survive—and, in the end, perhaps reproduce. It is physically designed to fulfill these ends—it has wings *in order to* fly.

A duck's morphology and movements are patterned. Of course, rocks also have structural regularities, but as far as we can tell, there is no functional purpose for their regularities. A rock's shape and composition do not exist in order for it to do anything. Ayala illustrates the lack of purpose of the features of nonliving matter:

> The configuration of a molecule of sodium chloride contributes to its property of tasting salty and therefore to its use of food, not vice versa; the potential use of sodium chloride as food is not the reason it tastes salty. The motion of the earth around the sun is the reason why seasons exist; the existence of the seasons is not the reason why the earth moves about the sun.

(Ayala 1998, p. 188). In contrast, the wings of a bird, the leaf of a plant, and the membrane of a bacterial cell all exist *because* of their function to the organism. (*Id.*). In a word, they have a purpose.

Purposeful causation is teleological. Webster's Dictionary defines "teleology" as "the fact or character attributed to nature or natural processes of being directed toward an

end or shaped by a purpose; use of design or purpose as an explanation of natural phenomena." (Webster 1973). Ayala paraphrases: "An object or a behavior is said to be teleological or telic when it gives evidence of design or appears to be directed toward a certain end." (*Id.*, p. 187). In teleological causation, an object's movement is caused by goal-seeking behavior.

To survive and reproduce: this could be said to be the teleological goal of organisms (and their features). This is the reason why ducks have wings, dodge predators, and fly south in anticipation of winter. It is the reason why plants have leaves and bacteria have membranes. Ultimately, according to Darwin, survival and reproduction are the purposes for everything organisms do and all their features.

Thus, unlike with rocks, imagining a teleological law of causation for ducks and other living creatures does not seem fanciful. It does not seem obvious that organisms comply with Newtonian mechanics in the sense that an external cause is required for them to move. They appear to have volition.

To many scientists, the beauty of Darwin's theory of natural selection is that it paved the way for the elimination of vitalism, volition, and teleological causation, substituting mechanism as a causal force. (Lenski and Mittler 1993, p. 188; Velasquez 1994, p. 249; Mayr 1982, pp. 528-30). Neo-Darwinian theory completed the task, unifying the causation of organisms and evolution under the umbrella of mechanistic laws.

The concept of the "genetic program" eliminates the need to suppose that organisms have volition—whatever they do, they are programmed to do it. As Mayr puts it, "[t]he discovery of the existence of genetic program has provided a mechanistic explanation of one class of phenomena." (Mayr 1982, p. 48). What seems like purposeful behavior on the part of the organism really is not. It is mechanical, following cause and effect: "From the point of view of causation it is important to state that the program as well as the stimuli which elicit the goal-seeking behavior precede in time the seemingly purposive behavior." (*Id*.).

Next, then, is to account for the existence of the genetic program itself in a strictly mechanistic way. This requires two steps. The first step involves precise, mechanical laws of inheritance—Mendelian genetics. The second step is to account for genetic variation—new genes, new traits—through external causation, thereby eliminating any notion that organisms themselves have any role in producing variation. To do this it was necessary to eliminate Lamarckism, and to resist any form of directed variation, because organisms would then be willing themselves to evolve. (Dawkins 1986, pp. 287-306). That is why the concept of chance mutation is the linchpin of mechanistic causation. Except by accident, organisms themselves have nothing to do with causing mutations. Chance mutation thus explains new genetic variation without relying on teleology of any

sort. (Lenski and Mittler, pp. 188, 193).

Darwin's theory of natural selection does the rest. Natural selection determines which new traits and genes survive and which do not. The forces of natural selection are external to organisms. The physical environment and competition from other organisms cause differential death, survival, and reproduction. The new traits and genes that best fit the environment survive.

Thus, organisms *appear* to possess volition. They *appear* to be directed toward a teleological goal—to survive and reproduce. They can even *appear* to have foresight. If a genetic mutation happens to cause a duck to respond to environmental cues that cause it to fly south, and if this causes the duck to survive and reproduce better, the duck will be more likely to leave descendants. Life *appears* to be searching for improvements to outcompete other organisms in existing niches, for new niches, for anything that allows an organism to survive and reproduce.

But according to neo-Darwinian theory, volition, teleological goals, and foresight are illusions. Behavior results from external, mechanical causation. Life *appears* to evolve in a teleological direction. But this too is an illusion. Species evolve not because they are striving to do so. Evolution just happens. Hence,

> The theory of natural selection shows how every feature of the natural world *can* be the product of a blind, unforesightful, nonteleleological, ultimately mechanical process of differential reproduction over long periods of time.

(Dennett 1995, p. 315).

And that is where neo-Darwinism stands. Recall Campbell's comment that Neo-Darwinism eliminates vitalism, and retains Newtonian causation, by denying the behavior of the biological system any causal role in its evolution. (Campbell, J. 1982, p. 191).

As presented in this book, organisms *do* participate in the evolutionary process. They direct variation, biasing it towards Darwinian goals. This doesn't seem as though it should be all that earth-shaking. Directed variation doesn't vitiate Darwin's theory of natural selection. If organisms direct variation, the world of science wouldn't seem to crumble. But read a hardcore neo-Darwinian's account of Lamarckism, neo-Lamarckism, and teleology, and one will be treated to a parade of horribles. (*See, eg.*, Dawkins 1986, pp. 287-306).

Part of the reason for the hostility to teleology might be historical. Historically, teleology has been linked with theology—or, more broadly, teleology is linked with the idea that the cosmos has a purpose, and that life fulfills that cosmic purpose. I previously quoted Webster's definition of teleology as "nature or natural processes of being directed

toward an end or shaped by a purpose." Other definitions of "teleology" in the same dictionary entry include "a doctrine (as in vitalism) that ends are immanent in nature" and "a doctrine explaining phenomena by final causes." (Webster 1993). A philosophy textbook gives this definition: "The view that maintains the reality of purpose and affirms that the universe either was consciously designed or is operating under partly conscious, partly unconscious purposes." (Velasquez, 1994 p. 237). The online Oxford English Dictionary gives only one definition: "The doctrine or study of ends or final causes, esp. as related to the evidences of design or purpose in nature; also *transf.* such design as exhibited in natural objects or phenomena." One might say that definitions of teleology range from purpose with a small "p" to Purpose with a large "P."

The thread of the concept of "final cause" and "cosmic purpose" leads back to Aristotle. He identified four categories of causation: material, formal, efficient, and final. Material cause refers to the composition of an object. Formal cause refers to the essence of the object, its identifying characteristics. Efficient cause refers to the agents that change the object, such as external elements of wind, fire, and other environmental forces. But above all, there is an object's final cause, which is its purpose in the world, toward which the object strives. An acorn's final purpose may be said to become an oak. (*Id.*, pp. 237-38).

This kind of final purpose of an acorn is only a step away from the larger purpose of the universe. According to Aristotle, purpose and design can be seen in the overall scheme of life. Species are ranked in a scale of nature (*scalae naturae*) from lower organisms to higher—with humans at the top. (Mayr 1982, p. 129). Theories of evolution before Darwin (such as Lamarck's) reflected this scale of nature. (*Id.*, pp. 201-202). Life evolved in a direction from lower organisms to higher organisms. The end purpose of evolution was humankind.

To Aristotle's concept of final cause, add his concept of a Prime Mover of the Universe, and the result is fertile ground for Western theology. There is purpose in the universe, and it is supplied by the Creator who has designed it.

The idea that the universe has a Creator does not necessarily contravene science. Nor does the idea that the universe was created with purpose or a plan, which we now observe as it unfolds. In fact, the Creator could be conceived as the origin of scientific laws, which we are discovering.

What is the origin of the law of gravity? Where do the laws of relativity and quantum physics come from? Why do they exist?

There is order to nature. Scientific laws describe the order of nature as we perceive it. In Darwin's words: "I mean by Nature, only the aggregate action and product of many natural laws, and by laws the sequence of events as ascertained by us." (Darwin

1952a, p. 40). As Darwin implies, in addition to descriptions of the order of nature, another feature of scientific laws is that they are usually put in terms of effects following antecedent causes—not just sequences of events, but reasons why one thing follows another.

However, there is ultimately a limit to cause-and-effect methodology. Applying it to the laws themselves, we are led to ask what caused these laws to exist. Why is the universe ordered by this set of laws and not another?

No matter how meticulously documented, all laws ultimately lead back to a reason that itself cannot be explained—reasons without reasons. Science can do no more than say they are as they are. Einstein's equation $e = MC^2$ may be a descriptive model of aspects of the universe, but explaining what caused the universe to possess this property is another thing altogether. Order in the universe has origins that cannot be observed. The source of order in the universe is the original mystery.

One of the great unsolved mysteries is the origin of life itself. Organisms take in energy, metabolize it, survive, and reproduce with inheritance. Inorganic matter does not. Natural selection cannot occur without these processes. Yet Darwinian theory does not explain how the first organism—the original genetic "program" with these properties—came into existence; it explains only how life evolves once it exists. Darwin expressed this limitation in the concluding paragraph of *The Origin of Species*, in which he attributed life to "having been originally breathed by the Creator into a few forms or into one...." (Darwin 1952a, p. 243). The origin of life is still not known.

That Darwin's theory does not account for the origin of life does not invalidate it. Any theory must have a starting point. As Darwin pointed out, "It is no valid objection that science as yet throws no light on the far higher problem of the essence or origin of life. Who can explain what is the essence of the attraction of gravity?" (Darwin 1952a, p. 239).

That the origin of the law of gravity is not known does not affect its validity. It is deemed a valid concept because it is consistent with several interrelated classes of facts. It is consistent with a Copernican model of the solar system. It is consistent with the motions of the planets and moons. It is consistent with the motions of Earth-bound objects. But the origins of the universe, the solar system, and the "laws" themselves remain a mystery. So too, Darwin's theories, explain several interrelated classes of facts—given the premise that life exists, which is demonstrable.

Hence, ascribing the origins of nature, natural laws, and life to a Prime Mover or Creator—to a "reason without reasons"—is not necessarily inconsistent with science. In fact, in a way the notion of a "reason without reasons" is a necessary idea so long as humans think in terms of ordered cause and effect—the beginning of the universe must

have a cause.

Where science differs is that its methodology assumes that the "reason without reasons" is not an active agent in the unfolding universe; thus, in principle, reasons that are comprehensible to humans can be assigned to the patterns of nature. The reasons that things happen are not mysteries beyond human understanding, but are instead discoverable. Even if the reasons for the original mystery of the cosmos are beyond us, we nevertheless can peel back the layers.

This is where science, theology, and teleology can conflict. If cosmic purpose is operating in the natural world, and is the cause of events and things, then causation leaves the world of science and enters the realm of the supernatural. Causation would be unknowable.

From a scientific standpoint, a virtue of eliminating teleology is that it has been viewed as eliminating the supernatural from the explanation of evolution—resulting in a theory of the design of organisms without a Designer. In *The Blind Watchmaker*, Richard Dawkins contrasts Darwinian theory with the famous argument of the eighteenth-century theologian William Paley. (Dawkins 1986). Paley contended that the exquisite, complex design of living organisms demonstrates the existence of a Creator. If one happens upon a simple stone, one might suppose that the stone had always been there and think nothing of it. If, on the other hand, one happens upon an intricately designed watch, one would immediately conclude "that the watch must have had a maker" (*Id.*, p. 4-5), an intelligent designer and craftsman—a human. Even a well-designed watch, however, is a poor specimen compared to all the marvelous forms of life, which, in Paley's words, "exceeds all computation." (*Id.*). Therefore, argued Paley, living beings must be the work of an even more intelligent Designer, who created them with a purpose.

Paley's argument was obviously not an evolutionary one. It was tied to the traditional Judeo-Christian idea of special creation—species do not evolve; they are created whole in a specific act of creation. But that is the point. When supernatural forces are invoked as an explanation, anything is possible. The reason that events happen or that things exist need not have reasons that we can possibly discover. They just are, because it is the wish or design of a supernatural force. Darwinian theory, on the other hand, explains the reason for the design of organisms and the direction of evolution without invoking supernatural Design.

A century and a half after Darwin, this conflict has not yet ceased. Proponents of "creation science" attempt to disprove Darwinian evolution and thereby keep the door open to a supernatural creation of all living things in accordance with strictly Biblical interpretations. More recently, there has been a spate of books with *Intelligent Design* in their title, all of which present arguments for the possibility of designed evolution. Proponents usually imply or expressly state that their argument provides evidence of a

Designer.

Thus, for good reason, science has been vigilant against the intrusion of theology. But in guilt by historical association, science has also been vigilant against the intrusion of teleology—and thus against any theory that invokes intelligent, goal-directed evolution.

The theory that has been presented in this book is not a theory of design by a Designer; it is a theory of design by designers—the organisms themselves. In the words of John Campbell,

> It seems that Paley was right, in a sense. There *are* artificers of organisms; they are the organisms themselves! In my view, organisms are self-guiding artificers, as competent as the survival/evolution machines they engender.

(Campbell 1994, p. 191).

There are some who, like Reverend Paley, from a pre-set ideology, will see the Hand of a Designer in the world's marvels. But that should not count as a reason to avoid the facts demonstrating that organisms are capable of biasing variation in an adaptive direction. To the contrary, rather than undermining science, supplying a theory to solve an embarrassing gap in Darwinian theory—the puzzle of sex—aids science.

In *Epigenetic Evolution: A Theory of Cultural Evolution through Directed Creativity,* I set forth a theory that human minds cause culture to evolve. Minds create, select, and build human culture. Our creativity is directed towards the goals supplied by our bio-psychology, evolved through natural selection. This is goal-directed, teleological causation.

The human brain serves as a device for information storage and retrieval. The brain accumulates experience and arranges it in comprehensible patterns so that we can draw upon them. Some patterns are so recurrent that when we encounter them, our response is fairly automatic; those that are more rare require deliberation. But some circumstances are novel. When we encounter novel circumstances, we extrapolate. We overlay patterns on patterns, imagining what does not exist, and then attempt to adapt.

We evolve creatively, using foresight and imagination. This allows us a measure of self-determination—or, to the same effect, a measure of free will.

Another philosophical implication of the theory that organisms direct variation—they experiment—is that, like humans, other species evolve through directed creativity. If

so, do they also possess foresight, imagination, and a measure of free will?

The doctrine of chance mutation avoids these questions. But a theory that organisms are adapted to evolve *does* necessarily imply that even the simplest organisms are creative, have foresight, and possess a measure of self-determination. The tool for these qualities is the same as for human brains: applied hindsight. DNA and other contents of cells precede the mind as devices for information storage and retrieval. They contain eons of hindsight, the accumulated experience of an organism's ancestors. This is transmitted down the pathway of inheritance.

In the face of a novel environment, organisms are not slaves to their genetic program. They experiment. They might even be able to perceive their environment, observe that it is novel, know that the repertoire in their genetic program is inadequate, devise an hypothesis as to what might be adaptive, and self-engineer a genetic change that might possibly preserve the continuity of their lineage.

If organisms experiment, like humans, they are not automata. They would possess some measure of self-determination. To preserve the continuity of their lineage, they store in their DNA genetic sequences that might be useful to descendants in the future. This is a kind of foresight.

However, to say that other species possess creativity, foresight, and a measure of self-determination is not to say that these qualities are identical to those of humans. For example, the term "foresight" is very anthropocentric, referencing the way that we visualize future scenarios in our "mind's eye." To say that other species possess foresight obviously does not mean that bacteria and other organisms visualize scenarios during the process of genetic experimentation. I mean only that they retain some traits, stored in their DNA, that are not presently useful but may be adaptive to future generations and that they can extrapolate from the experience that has accumulated in their ancestral lineage.

To clarify further, to say that organisms possess foresight does not mean that the ancestors of birds could project that bird wings would be useful for flying and tinker toward that end. The kind of foresight that other organisms possess is the product of history and experience; that is also its limitation. The ancestors of birds did not have wings or flying in their ancestral lineage and thus could not project such an hypothesis.

In contrast, human minds can acquire fodder for hypothesis-making outside of the experience of our ancestors. Even though our ancestors could not fly, we can see a bird and imagine flying. That is one of the reasons that human minds have proved so remarkably adaptive in evolving culture; imaginative minds can draw on a broader range of experience and knowledge than our ancestors transmitted to us.

Another contrast, similar in effect, is that human minds can transmit experience and knowledge to other minds *outside the pathway of inheritance*. We can learn how to fly from other human minds or from documents recording the thoughts of other human minds. Or we can take such knowledge and add it our own in making new hypotheses. This is an enormous adaptive advantage. Species that evolve genetically are constrained by the fact that they have access only to experience that has been accumulated by their ancestral lineage.

Evolving through human minds also allows humans to perceive the adaptive failures of others and adjust our own hypotheses. This also makes a difference in the way that hypotheses are "tested." A genetic experiment in the form of sexually-reproduced offspring ultimately is tested by the actual events of survival and reproduction. Human minds can project the effects of hypotheses on survival and reproduction without undergoing the actual events.

From the standpoint of humans, evolving through genetic experimentation seems very limiting. It would be like climbing a mountain knowing only the terrain behind and projecting it will not be too different ahead, but ready to backtrack or sidestep when trouble arises, constantly looking for new footing and alternative routes when an impasse is reached. Many routes would be fatal. And the process never really allows for foreseeing the terrain that is ahead. Nevertheless, it is superior to clinging to the same terrain while the ground slowly erodes and crumbles. It is certainly more adaptive than waiting for a random error in copying DNA.

Another differentiating aspect of evolving through human minds is consciousness. This bears on our concept of morality. In *Dynastic Theory,* I set forth a theory that the roots of unselfishness, loyalty, fidelity, and the other traits that we associate with morality are biological. These propensities derive from the human bio-psychology that evolved in our ancestors through natural selection. These propensities are not uniquely human. All other social species have these same propensities. Our concept of morality, however, does not just entail conduct towards others. We also associate morality with awareness of our thoughts, awareness of our conduct, and awareness of our choices of thoughts and conduct—that is, we associate morality with consciousness.

This, in turn, bears on the question of free will. A theory that all organisms are adapted to evolve implies that they are creative, have volition, and therefore possess a measure of self-determination—they exercise some ability to choose among options. But when we think of free will, we are not just asking whether humans have a choice. We are really asking whether humans choose and do so while being consciously aware of the consequences. Thus, we tie the issue of free will to our concept of morality. In that sense, the human capacity for self-determination is unique.

But we inherited our tendency to be evolutionarily creative from a long, long line

of ancestors who, like us, probed the adaptive unknown, searching for ways to perpetuate themselves. Humans are unique in many respects, but we evolved from organisms that were designed to search, probe, and grope for ways to evolve.

The possibility that organisms are adapted to evolve has been criticized as an anthropocentric projection of human experience to other creatures. But perhaps it is the other way around. Perhaps the view that we are the only beings that are intelligent and creative reflects an anthropocentric bias.

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