ORIGIN OF GENETIC INFORMATION AND EVOLUTION OF BIOLOGICAL SPECIES

Pallacken Abdul Wahid

Literature on the origin of life and the evolution of diverse forms of life is reviewed to provide an understanding of the current thinking in evolutionary science. There are conspicuous vagaries, inconsistencies and conflicts of ideas in evolutionary knowledgebase. Darwinism and neo-Darwinism thrive by literally sidelining and trivializing 'heretical' scientific discoveries capable of invalidating it. While punctuated equilibrium (PE) reflected in the fossil record is a strong negative evidence to the underlying principle of phyletic gradualism (PG) enshrined in the evolutionary theory, the phenomenon of cell-directed mutagenesis challenges another tenet of the theory, namely, the requirement of stochastic mutations produced by extra-cellular agents to create heritable changes in the organism. No attempt has been made to re-examine the theory dispassionately in the light of the rapidly changing particulate gene concept. More importantly, our knowledge of life and its origin hinges on hypotheses. The lack of evidence for characterizing organic evolution as continuation of inorganic evolution and failure of attempts to synthesize life in the laboratory from chemicals strongly suggest the need for a new direction to the scientific pursuits towards understanding life and origin of biological species, especially in view of the changing concept of gene and growing natural evidence against the foundations of Darwinism or synthetic theory. In this paper, an attempt is made to develop a theory of creation of life and biodiversity through a combination of scientific facts and Qur'ānic revelations.

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Introduction

The origin of living and non-living things that make up the universe remains the most fundamental unresolved question. The past three centuries have been an event-rich era of active research into this issue. Darwin's theory of evolution postulated in his *The Origin of Species* in 1859 has been a landmark of sorts and has subsequently affected the entire discipline of evolutionary biology which now encompasses a wide range of issues. Advances in molecular genetics and genomics have given a new impetus to the pursuit of unraveling the mystery of life and biological diversity. In spite of this, there is a growing discontent among scientists and the public over the issue of origins. The on-going controversy over the scientific validity of Darwinism-based evolutionary theories amply testifies to this.

While addressing the question of life, distinction has to be made between the origin of life and the origin of organisms. Physically the world around us is described in terms of material entities comprised of atoms and molecules. The living system is also described likewise without any distinction from the non-living world. Consequently the bioworld is believed to have come into existence as a continuation of the inorganic evolution which preceded it. Hence, with this perspective, the phenomenon of life is looked upon as having originated from non-life. In other words, it implies that chemical atoms and molecules combined in a certain manner can create life.

In contrast, it is now well established that all living beings have a genetic program responsible for life processes and biological activities, currently viewed as being coded in a chemical structure called the genome which is nothing but an arrangement of deoxyribonucleic acid

(DNA). At the same time, attempts to synthesize life from chemicals in the laboratory remain unsuccessful. This inability raises an important question as to whether we are correctly investigating the origin of life. Coupled with that, the particulate concept of gene is also losing ground[1] and a growing body of information is challenging the monopolized role of DNA in transmission of heredity. Some of these are: the non-linear relationship between genome and phenotype among species,[2] ability of proteins to transmit information,[3] "non-nucleic acid" or cytoplasmic inheritance,[4] existence of more than 95% of DNA in the eukaryote genomes as non-coding meaningless DNA referred to as "junk DNA",[5] and epigenetic modifications which do not alter the gene sequence but still can influence the phenotype (e.g. gene silencing, paramutation, genomic imprinting, position effect, etc.).[6] The most compelling evidence against genome-genetic program equivalence is the fact that the genome is intact at the time of death of an organism but still the body loses its life. In other words, if the genome has been responsible for conferring life and biological functioning of the body, the cessation of its functioning at the time of death would be tantamount to loss of properties of the chemical structure (genome) which is scientifically untenable.[7]

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1. Shapiro, J. A., "A Third Way" in *Boston Review* 22: 1 (1997), 32-3.
2. Raff, R. A. and Kaufman, T. C. *Embryos, Genes and Evolution* (New York: Macmillan, (1983); Gibbons, A., "Which of our genes make us human?" in *Science* (1998), 281:1432-34; and Wells, J. "Homology in Biology: A Problem for Naturalistic Science", *http://www.trueorigin.org/homology.asp*, accessed on April 6, 2005.
3. Legname, G. *et al. Science*, 305:673-676, taken from Helen Pelcher "Lab-made *prions* trigger mad cow symptoms" in *Nature News*, (29 July 2004); doi:10.1038/news040726-11.
4. Beisson, J. and Sonneborn, T. M. "Cytoplasmic inheritance of the organization of the cell cortex" in *Paramecium aurelia*. *Proc. Natl. Acad. Sci. USA* (1965), 53: 275-82.
5. *http://www.psrast.org/junkdna.htm*, accessed on April 6, 2005.
6. Meyer, P. "Gene silencing in plants", *Encyclopedia of Life Sciences*, 2000; doi:10.1038/npg.els.002022.
7. Wahid, P. A., *The Divine Expert System* (Aligarh, India: MAAS, Centre for Studies on Science, 2002), 130 and "Definitions of life, death, genetic program and soul based on the Qur'ān and computer concept of the universe" in *J. Islamic Sci.* 18 (1-2) (2003): 137- 47.

Theories of the Origin of Life

As of today, there is no evidence whatsoever to believe that there is a region in the universe other than the planet earth that supports life. In the beginning, the earth was very hot and did not possess an atmosphere. But as it cooled, an atmosphere began to develop from the gas emitted from the rocks. It is believed that by chance combination of atoms, macromolecules, were formed from which self-reproducing structures were formed. The reactions leading to their formation took place when the earth had been sufficiently cooled. Several theories (or more correctly, hypotheses) have been advanced to explain the origin of life; the most popular one is the primordial soup theory. According to this theory, self-replicating entities, the precursors of life, arose spontaneously under favourable conditions in the primitive environment of the earth. There are at present two schools: one supporting a heterotrophic origin of life and the other supporting an autotrophic origin of life. The theory of heterotrophic origin assumes a primitive ocean of slowly accumulating amino acids, bases, sugars, lipids, and other organic compounds. These are seen as self-organizing to the first reproducing entity. The chemistry of this speculative process is pictured along conventional lines: solution reactions with adsorption-desorption equilibria and heterogeneous catalysis on minerals. These notions have come to be very deep-seated over the past several decades. For a "hetero-origin", therefore, the concepts of prebiotic chemistry and a broth as an arsenal of organic building blocks are mandatory. On the other hand, for an "auto-origin", the concept of a prebiotic chemistry never arises; and the primitive ocean, whatever its content, is irrelevant as an arsenal of organic building blocks of life. Theories are seen as competing with each other for survival *vis-à-vis* the facts.[8]

All attempts to assemble an integrated scheme of physicochemical processes have significant weaknesses. Problems occur with hypotheses of the earliest molecules with the properties commonly associated with "life". These include the unlikelihood of formation of complex self-replicating molecules such as RNA by chance encounters even over geological time; the difficulty of protecting such molecules following

8. Wachtershauser, G. "Life in a ligand sphere" in *Proc. Natl. Acad. Sci. USA* 91 (1994): 4283- 87.

their formation from dilution and destruction by high temperatures, hydrolysis and ultraviolet radiation; and finally the difficulty of imagining how self-organization alone could lead to encapsulation of a complex hierarchy of biochemical reactions in a membrane to form the simplest unicellular organism.[9] According to the RNA World Hypothesis, the first living system was a polymer(s) of catalytic RNA capable of self-replication that subsequently evolved the ability to encode more versatile peptide catalysts.[10] Mineral-catalyzed reactions, followed by a series of fractionations, would offer the most plausible route to RNA.[11] According to Smith *et al*.,[12] a stable cell wall is required to protect the first primitive organism. The first cell wall might have been an internal mineral surface, from which the cell developed a protective biological cap emerging into a nutrient-rich "soup". Ultimately, the biological cap might have expanded into a complete cell wall, allowing mobility and colonization of energy-rich challenging environments. All the scenarios that have been proposed for producing RNA under plausible natural conditions lack experimental demonstration and this includes the RNA world, clay crystals and vesicle accounts. No one has been able to synthesize RNA without the help of protein catalysts or nucleic acid templates, and on top of this problem, there is the fragility of the RNA molecule to contend with.[13]

The idea that life originated on its own on this planet in continuation of the inorganic evolution received a jolt when, in 1973,

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9. Smith, J. V., "Biochemical Evolution I. Polymerization on Internal Organophilic Silica Surfaces of Dealuminated Zeolites and Feldspars" in *Proc. Natl. Acad. Sci. USA* 95 (1998): 3370-75.
10. Gilbert, W. in *Nature* 319 (1986): 618; quoted from Sowerby, *et al. Proc. Natl. Acad. Sci. USA* 98 (2001): 820-22.
11. Boyce, G. E. and Orgel, L. E., *The RNA World* (Plainview: Cold Spring Harbor Lab. Press, 1993), 1-25 and Parsons, I., Lee, M. R. and Smith, J. V., "Biochemical Evolution II: Origin of Life in Tubular Microstructures on Weathered Feldspar Surfaces" in *Proc. Natl. Acad. Sci. USA* 95 (1998): 15173-76.
12. Smith, J. V., Arnold, F. P., Jr., Parsons, I. and Lee, M. R., "Biochemical Evolution III: Polymerization on Organophilic Silica-rich Surfaces, Crystal-Chemical Modeling, Formation of First Cells, and Biological Clues" in *Proc. Natl. Acad. Sci. USA* 96 (1999) 3479-85.
13. *http://www.astrobio.net/news/article428.html* accessed on April 6, 2005.

Nobel laureate Francis Crick and L. Orgel proposed a new theory called the "directed panspermia".[14] According to them, spores of life might have been sent to the earth in an unmanned spaceship by a more advanced civilization evolved billions of years ago on a planet of another star. In effect, the theory only shifted the venue of the origin of life from this planet to another planet but did not explain how life originated. The original panspermia theory did not say that the spores were intentionally sent to other planets, but merely said that microbes in space brought life to planets like the earth. Notable advocates of panspermia theories besides Crick and Orgel are Hermann von Helmholtz, William Thomson Kelvin, Svante Arrhenius, Fred Hoyle, and Chandra Wickramasinghe. In different versions of the theory, the microbes are supposed to have been transported by light pressure (Arrhenius's radio-panspermia), meteorites (ballistic panspermia), or comets (modern panspermia).[15]

Theories of Organic Evolution

Perhaps the most discussed topic in science as a whole is the theory of evolution proposed by Charles Darwin. He believed that species were mutable and could give rise to newer forms if beneficial heritable variation occurred. In this way species evolved as descent with modification. Darwin assumed that variations occurred in species by chance. He further assumed that there was severe competition between species which led to a struggle for existence. If the variation that occurs in an individual gives an advantage in some way to overcome the competition, that individual survives and the variation is transmitted down to future generations. In this way the variation gets preserved in the population through a process called natural selection. Natural selection is a purposeless, unconscious mechanism driven by chance whose result can be manifested only on time scales of the order of millions of years.

In the latter part of the nineteenth century Darwinism was challenged by an alternative evolutionary theory known as neo-Lamarckism. This hypothesis agreed with Lamarck's original theory on

14. Crick, F. H. C. and Orgel, L. E. . "Directed panspermia" in *Icarus* 19 (1973): 341.

15. *http://www. iscid. org/encyclopedia/panspermia*, accessed June 7, 2004.

the importance of use and disuse in the development and obliteration of organs, and it added the notion that environment acts directly on organic structures, which explained their adaptation to the ways of life and environments of each organism. Adherents of this theory rejected natural selection as an explanation for adaptation to the environment.

In the Netherlands, Hugo de Vries advanced a new evolutionary theory known as mutationism which essentially rejected natural selection as a major evolutionary process.[16] Mutationists believe that the driving force of evolution is mutation and not natural selection. "…the mutationist school did not, of course, regard mutations as random. They thought that the body had a built-in tendency to change in certain directions rather than others, though they left open the question of how the body 'knew' what changes would be good for it in future." [17]

Mutationism was opposed by many naturalists, particularly biometricians like Briton Karl Pearson who defended Darwinian natural selection as the major cause of evolution.[18] The work of theoretical geneticists like R. A. Fisher and J. B. Haldane in Britain and Sewall Wright in the United States contributed to the downfall of the theory of mutationism. The biologists were slow starters to accept the new developments particularly because of the involvement of mathematics and the omission of many issues such as speciation that were of great importance to evolutionists.

With the advancement of a reasonably comprehensive account of the evolutionary process by Theodosius Dobzhansky in his book *Genetics and the Origin of Species,*[19] the evolutionary theory started being understood and appreciated as the genetic change in populations. This led to the development of the "synthetic theory" which is not just one single hypothesis or theory but a multidisciplinary body of knowledge cutting across genetics, embryology, zoology, botany, paleontology, and

16. Ayala, F. J. and Fitch, W. M., "Genetics and the origin of species: An introduction" in *Proc. Natl. Acad. Sci. USA* 94 (1997): 7691-97.
17. Dawkins, R., *The Blind Watchmaker* (Middlesex: Penguin Books, 2000), 377.
18. Ayala, F. J. and Fitch, W. M. (1997), op. cit.
19. Dobzhansky, T., *Genetics and the Origin of Species* (New York: Columbia University Press, 1951).

molecular biology. The "synthetic" epithet is now often omitted and it is known as the Theory of Evolution. T. Dobzhansky, together with Ernst Mayr, Julian Huxley, the paleontologist George G. Simpson, and the botanist George Ledyard Stebbins are considered the architects of the synthetic theory.[20] The synthetic theory (modern synthesis) is also referred to as neo-Darwinism. According to Futuyma, genetic variations arise in population by random mutation and recombination. Changes in gene frequency brought about by random genetic drift, gene flow, and natural selection lead to the evolution of populations. Most adaptive genetic variants have individually slight phenotypic effects so that phenotypic changes are graded.

Diversification occurs through separation among populations which in turn results in reproductive isolation among populations. These processes continued over long periods give rise to changes of such great magnitude as to warrant the designation of higher taxonomic levels (genera, family, etc.).[21] Compared to Darwinism the modern synthesis gives more emphasis to random genetic drift than to natural selection. It recognizes that *genes are discrete entities* through which characteristics are inherited and the existence of multiple alleles of a gene is responsible for variation within a population. Speciation occurs as a consequence of gradual accumulation of small genetic changes. In other words, macroevolution is nothing but multiples of microevolutions.

According to Motoo Kimura, the vast majority of evolutionary changes are neutral or not selective. His neutral theory of molecular evolution accepts that, for any gene, a large proportion of all possible mutants are harmful to their carriers; these mutants are eliminated or kept at very low frequency by natural selection. The theory assumes, however, that many functional mutants can occur at each locus that are adaptively equivalent to one another. These mutants are not subjective to selection relative to one another because they do not affect the fitness of their carriers (nor do they modify their morphological, physiological, or behavioural properties). Evolution at the molecular level consists for the

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20. Ayala, F. J. and Fitch, W. M., "Genetics and the origin of species: An introduction" in *Proc. Natl. Acad. Sci. USA* 94 (1997): 7691-97.
21. Futuyma, D. J., *Evolutionary Biology* (Sunderland, MA: Sinauer Associates, 1986), 12.

most part of the gradual, random replacement of one allele by another that is functionally equivalent to the first. The theory assumes that favourable mutations occur, but are sufficiently rare that they have little effect on the overall evolutionary rate of nucleotide and amino acid substitutions.[22]

Species Concepts and Descent with Modification

In reality, organisms present a mosaic of characters with specific and overlapping non-specific characters. Defining 'species' has been recognized as a problem since Linnean time. This leads to a very complicated situation in the field of evolutionary biology because species is the unit of evolution. There are as many definitions of species as there are authors who have written about them. They are known by numerous terms: the morphological species concept, biological species concept, evolutionary species concept, recognition species concept, cohesion species concept, phylogenetic species concept, Greek species concept, tyological species concept, Darwin's species concept, ecological species concept, phenetic species concept, etc.[23] Mayr further admits that "the conclusion that there are concrete describable objects in nature which deserve to be called "species" is not unanimously accepted.

There has been a widespread view that species are only arbitrary artifacts of the human mind, as some nominalists, in particular, have claimed." [24] In *The Origin of Species* Darwin states "… I look at the term species, as one *arbitrarily given for the sake of convenience* to a set of individuals closely resembling each other, and that it does not essentially differ from the term variety, which is given to less distinct and more

22. Kimura. M., *The Neutral Theory of Molecular Evolution* (Cambridge: Cambridge University Press, 1983). This book is no longer available, but there is a collection of papers by Kimura entitled *Population Genetics, Molecular Evolution, and the Neutral Theory: Selected Papers* (Chicago: University of Chicago Press, 1994). See also Ayala, F. J. "Vagaries of the molecular clock" in *Proc. Natl. Acad. Sci. USA* 94 (1997): 7776-83.
23. "Process of Evolution", *www.tulane.edu/~admincat/pdfcat/section1/eeob_05.pdf* accessed April 6, 2005.
24. Mayr, E. "What is species and what is not?" in *Philosophy of Science* 63 (1996): 262-77.

fluctuating forms. The term variety, again, in comparison with mere individual differences, is also applied arbitrarily, and for mere convenience sake" (emphasis added).[25]

Besides the problem of defining the species, the concept of descent with modification is also fraught with several difficulties.[26] Given the confusions and vagaries in determining the hypothetical common ancestor necessitated by the assumption of descent with modification, such views leave much to be desired. For instance, the question of homology of the structures like heart, eyes, and other organs still remain unanswered. The assumed common ancestor of arthropods and vertebrates is the so-called *Urbilateria*. According to De Robertis and Sasai, we have no anatomical knowledge of this common ancestor[27] which is also presumed to be extinct. It was, therefore, generally concluded that these structures arose independently in the two phyla. The eye, for example, was judged to have evolved independently up to forty times. Eyes from different phyla were thus considered analogous rather than homologous.[28]

Besides the so-called structural, anatomical, morphological, or traditional homology, another type of homology called molecular homology also exists. This homology is based on DNA sequence. Genes from two different species are considered homologous if they are related in sequence due to common descent from an ancestral gene present in a shared ancestor. Comparisons of the genes encoding ribosomal RNAs of the microbes suggested that life began with some primitive bacteria. These then branched into Archaea, modern bacteria and later to eukaryotes. However comparisons of DNA sequences of other kinds of genes had led to varied versions of the evolutionary tree making the tree

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25. Darwin, C., *The Origin of Species* (New York: Bantam Books, 1999), 46.
26. Gaunt, S. J., *http://people.we.mediaone.net/sarima/dinosaurs/ philosophy/ linnean.html* accessed on August 24, 2001, and Gaunt, S.J., "Evolutionary developmental biology: Homologous regulatory genes and processes" in *Encyclopedia of Life Sciences*, doi:10.1038/npg.els.0001064.
27. De Robertis, E. M. and Sasai, Y. "A common plan for dorsoventral patterning in Bilateria" in *Nature* 380 (1996): 37-40, quoted from Gaunt, S. J. op. cit.
28. Gaunt, S. J., doi:10.1038/npg.els.0001064, op. cit.

of life more confusing. "More genomes have only further blurred the branching pattern of the tree of life. Some blame shanghaied genes; others say the tree is wrong". These observations prompted Elizabeth Pennisi to ask the most obvious question, "Is it time to uproot the tree of life?"[29] Pennisi presented an impressive cross-section of the growing body of evidence which challenged the veracity of the evolutionary tree. In the case of bacteria, lateral gene transfer has been considered to be so widespread that it renders the concept of species among bacteria meaningless and makes it impossible to construct an evolutionary tree.

This aspect was addressed by Daubin *et al*.[30] Philippe and Forterre[31] demonstrated that the phylogenies were highly confusing due to the combining effects of gene duplication, gene loss, lateral gene transfer, and tree reconstruction artifacts. According to them, the genes tRNA synthetase, ATPase, and carbomyl phosphate synthetase could not be used confidently to root the tree of life because of the difficulty to choose between different evolutionary scenarios, knowing that gene duplication, gene loss, and lateral gene transfer have been frequent during prokaryotic evolution. The results of a study of the patterns of a certain type of genomic change, called transposon insertions, among thirteen vertebrate species supported an earlier proposal of evolutionary trees showing that primates (human, chimpanzee, baboon) are more closely related to rodents like the mouse and rat than to carnivores like the cat and dog or artiodactyls like the cow and pig.[32] This placement had earlier triggered off a heated controversy in the field of evolutionary genomics as the new sequence data refutes alternative evolutionary tree that place rodents much farther away from primates. There are other similar cases. "Bacteria and archae look very much alike and, prior to genetic sequencing, they were classified together even though their genes now tell us they are as different as elephants and pond scum—

29. Pennisi, E., "Is it time to uproot the tree of life?" in *Science* 284 (1999): 1305-07.
30. Daubin, V., Muhamad, R. and Watts, D. J. "Phylogenetics and the cohesion of bacterial genomes" in *Science* 301 (2003): 829-32.
31. Philippe, H. and Forterre, P., "The rooting of the universal tree of life is not reliable" in *J. Mol. Evol*. 49 (1999): 509-23.
32. "Gene menagerie" in *Astrobiology Magazine* (November 4, 2003).

maybe more so." [33]

The construction of the evolutionary tree based on genetic parameters is clearly a departure from the expected morphological classification. A particularly unexpected finding in this respect is that structures traditionally viewed as being analogous are regulated in their development by genes that are clearly homologous. Some biologists hold that traditional conclusions about the relatedness of certain structures should now be revised in favour of homology whereas others stress the need for caution. How accurate then is the use of gene sequence and expression data to shed light on structural homology? In practice, we have to reconstruct the evolutionary history of the gene, its role, and the structures in which it is expressed. We also need extensive taxonomic sampling. "Finally, we must appreciate that the only clear cut evidence for morphological homology remains in the identification of transitional structures in species, either living or as fossils, that are known to be related. Since ancestors are rarely available for direct examination, we must accept that homology is usually a hypothesis about evolutionary history rather than a deduced matter of fact."[34] All these results clearly reveal the ambiguity and uncertainty associated with the origin of species as descent with modification from a common ancestor.

Punctuated Equilibrium

The use of palaeontological data in evolutionary biology proved to be a crucial landmark for the theory of evolution. Darwin believed in gradualism and a fairly constant rate for evolution. Phyletic gradualism (PG) treats species as part of a continuum of gradual change in anatomical characteristics through time. In spite of the absence of transitional forms in the fossil record, the idea of gradualism was not questioned for over a century until 1972 when Niles Eldredge and Stephen Jay Gould proposed a different model called "punctuated equilibrium" (PE) to explain evolution in the light of fossil evidence.[35]

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33. *http://www.peripatus.gen.nz/paleontology/CamExp.html*, accessed February 13, 2005.
34. Gaunt, S. J., op. cit.
35. Eldredge, N and Gould, S. J. "Punctuated equilibria: an alternative to phyletic gradualism" in T. J. M. Schopf (ed.) *Models in Paleobiology* (San Francisco: Freeman, Cooper, 1972), 82-115.

The essence of the theory is that there is sudden appearance of new species in the fossil record punctuated by long periods of species stability (stasis). "Eldredge and Gould not only showed that paleontologists had been out of step with biologists for decades, but also that they had been unconsciously trying to force the fossil record into the gradualistic mode…. Most species appear suddenly in the fossil record and show no appreciable change for millions of years until their extinction."[36]

In 1980, an historic conference attended by a wide spectrum of researchers including geologists, paleontologists, ecologists, population geneticists, embryologists, and molecular biologists was held at Chicago's Field Museum of Natural History to discuss macroevolution in the light of modern synthesis. The central question of the conference was whether the mechanisms underlying microevolution, seen as changes within a population, can be extrapolated to explain the phenomenon of macroevolution, seen as changes above species level leading to the origin of new species. The observation of stasis in the fossil record and the theory of punctuated equilibrium were the main focus of the deliberations. In a generous admission Francisco Ayala, a major figure in propounding the modern synthesis theory in the United States, said: "We would not have predicted stasis from population genetics, but I am now convinced from what paleontologists say that small changes do not accumulate."[37] The PE does not support gradualism which is the backbone of Darwin's theory. Naturally, the gradualists started a frontal attack at PE. The debate still goes on; it is a fight between two evolutionist groups, one upholding natural evidence (i.e., supporters of PE) and the other (i.e., supporters of PG) rejecting the natural evidence. PE demolishes the very foundation on which Darwinism has been built, the natural selection of gradual accumulation of beneficial chance variations resulting in a new species.

Cell-directed Mutagenesis

The phenomenon of cell-directed mutagenesis was discovered in 1970 by

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36. Prothero, D. R. "Punctuated equilibrium at twenty: a palaeontological perspective" in *Skeptic* 1 (1992) 3: 38-47.
37. Lewin, R. "Evolutionary theory under fire" in *Science* (1980), 210 (4472): 883-87.

Miroslav Radman, a molecular geneticist at the Universite Rene Descartes in Paris. He demonstrated that bacteria harboured a genetic program to make mutations. At that time, no one believed this heretical proposal.[38] Obviously, the scientists refuse to think beyond Darwinism. In 1988 molecular biologist John Cairns and his colleagues at the Harvard School of Public Health observed induced mutations of various elements of the lac operon changes in *Escherichia coli* bacteria.[39] Their results were even more shocking than Radman's idea. "…depending on their environmental conditions, bacteria might be able to direct mutations to particular genes…. Outraged, a number of evolutionary biologists quickly embarked on their own studies to test the notion."[40] These discoveries were quickly used to evolve a new concept called 'adaptive mutation' instead of rejecting the idea of stochastic mutation.

The concept of adaptive mutation leans heavily on the Lamarckian view. Clearly the genetic conservatism of species would be jeopardized if the Lamarckian idea were true, because this idea makes the species too plastic and unstable. The observation made by Cairns *et al*. on directed mutagenesis in certain bacteria belittles the importance of natural selection in the evolutionary process particularly because no one expected that beneficial mutations could be induced from within the cell. It is also important to note that the change in genetic make-up resulting from directed mutations is target-oriented and result-oriented. It would be therefore more appropriate and straightforward to interpret these results as due to the built-in program to bring about specific mutations to suit the need. Instead, the evolutionists preferred to look for explanations from within the framework of Darwinian model. This religious attitude of the evolutionists towards Darwinism has done more harm than good to the progress of evolutionary science. Goodman decisively stated, "No one in this debate about mutation is abandoning natural selection as the prime shaper of evolution. But Cairns and supporters suggest that evolutionary theory must incorporate a new

38. Chicurel, M. "Can organisms speed their own evolution?" in *Science* (2001), 292 (5523): 1824-27.

39. Cairns, J., Overbaugh, J. and Miller, S. "The origin of the mutants" in *Nature* (1988), 335: 142-45.

40. Chicurel, M. (2001), op. cit.

wrinkle. They say that some mutations may occur more often when they are advantageous than when they are not."[41] The remark of Fred Hoyle, a knighted astronomer who coined the term "Big Bang" and who fought against neo-Darwinism using mathematics is all the more revealing: "The Darwinian theory is wrong and the continued adherence to it is an impediment to discovering the correct evolutionary theory."[42]

Despite such confirmation of preferential production of advantageous mutations, scientists are not ready to accept a truly directed mechanism, but keep on asking the question whether such mutation could still be due to random process. In this context, Elizabeth Pennisi's remarks resound clearly: "Genetic change, and hence the evolution of new species, is commonly thought to result from small, random mutations in individual genes, but a growing wealth of data emphasizes that the perception is wrong. Indeed the mutations leading to evolutionary change can involve the wholesale shuffling or duplication of the genetic material, changes that can affect the expression of genes or free up duplicated genes to evolve new functions. What's more, these changes may not be totally random….mainstream biologists need to consider genomes, and the kinds of evolutionary changes they undergo, in a much different light."[43] As rightly pointed out by Motoo Kimura "Looking back, I think that it is a curious human nature, that if a certain doctrine is constantly being spoken of favourably by the majority endorsed by top authorities in their books and taught in classes, then a belief is gradually built up in one's mind, eventually becoming the guiding principle and the basis of value judgement." [44]

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41. Goodman, B. "Directed mutations: Heredity made to order." in *Mosaic* 23(1) (1992):24-33.
42. *http://home.wxs.nl/~gkorthof/kortho46.htm* accessed on February 9, 2005.
43. Pennisi, E., "How the genome readies itself for evolution" in *Science* (1998), 281(5380): 1131-34.
44. Kimura, Motoo, *The Neutral Theory of Molecular Evolution* (Cambridge: Cambridge University Press, 1983), 22. This book is no longer available, but there is a collection of papers by Kimura: "Population Genetics, Molecular Evolution, and the Neutral Theory: Selected Papers" available from the University of Chicago Press, 1994.

The Need for a Non-Darwinian Theory

Prof. J. A. Shapiro, a bacterial geneticist at the University of Chicago, remarks, "Our current knowledge of genetic change is fundamentally at variance with neo-Darwinist postulates. We progressed from the Constant Genome, subject only to random, localized changes at a more or less constant mutation rate, to the Fluid Genome, subject to episodic, massive and non-random reorganizations capable of producing new functional architectures….Nonetheless, neo-Darwinists writers like Dawkins continue to ignore and to trivialize the new knowledge and insist on gradualism as the only path for evolutionary change."[45] He adds, "…the debate about evolution continues to assume the quality of an abstract and philosophical "dialogue of the deaf" between Creationists and Darwinists.

Although our knowledge of the molecular details of biological organization is undergoing a revolutionary expansion, open-minded discussion of the impact of these discoveries are all too rare. The possibility of a non-Darwinian scientific theory of evolution is virtually never considered." Shapiro stresses the need for a non-Darwinian theory. "Although such purists as Dennett and Dawkins repeatedly assert that the scientific issues surrounding evolution are basically solved by conventional neo-Darwinism, the ongoing public fascination reveals a deeper wisdom. There are far more unresolved questions than answers about evolutionary process, and contemporary science continues to provide us with new conceptual possibilities." Our knowledge of molecular genetics and cell biology has advanced so much that the concepts of gene and its function have undergone a quantum change. The "one-gene one-enzyme" hypothesis of the 1940s and 1950s which portrayed the gene as a unit that encodes a specific protein molecule linked to a particular phenotype is now replaced by a much wider concept in which a genetic locus is treated as a modular assembly of regulatory and coding motifs. Most of these motifs are shared among many loci, suggesting that genomes are assembled like Lego blocks from a repertoire of more basic sequence elements, many of which do not encode proteins but other important functions such as transcription,

45. Shapiro, J. A., "A Third Way" in *Boston Rev.* 22(1) (1997): 32-3.

translation, RNA processing, DNA replication, and chromatin condensation. Many genetic loci are active at different times, participating in the expression of more than one phenotypic trait.[46]

Needless to say, the Darwinism-based theories which invariably rely on the particulate concept of gene, DNA base sequence (genome, a chemical structure) as the genetic program and a hypothetical mechanism called natural selection are facing a frontal attack from scientists and the public alike, if the current website debates on Darwinism, the increasing number of books questioning the validity of the theory, and the efforts to remove Darwinism from the school science curriculum are any indication.

Programmed Evolution as a Probable Divine Mechanism of Creation

Organism as a Natural Computer Biosystem

The general picture that emerges from contemporary cell and developmental biology is that essentially all cellular functions are regulated by interactive 'signal transduction' networks composed of information transfer molecules, such as G proteins, protein kinases, second messengers and transcription factors.[47] They form, in effect, cellular computation systems allowing cells to evaluate multiple internal and external inputs in order to make appropriate decisions (e.g., which enzymes to synthesize, when to divide, where to move).[48] These new ideas and concepts are taking molecular biology into the domain of computer science.

An organism is treated here as a natural computer biosystem (NCB).

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46. Ibid.
47. Alberts, B., Bray, D., Lewis, J., Raff, M., Roberts, K. and Watson, J. D., *Molecular Biology of the Cell*, 3rd ed. (New York: Garland, 1994).
48. Bray, D. "Intracellular signaling as a parallel distributed process" in *J. Theoret. Biol.* 143 (1990): 215-31. See also Gerhart, J. and Kirschner, M., *Cells, Embryos and Evolution: Toward a Cellular and Developmental Understanding of Phenotypic Variation and Evolutionary Adaptability* (Malden: Blackwell Science, 1997).

A cell, the basic unit of a living system, is a biochip. The structures in the cell (organelles and nuclear structures including DNA) constitute the hardware serving as processor, clock, decoder, memory, etc., of the biochip to execute the program (software) stored in the memory. Since these structures are intended for the execution of the program, they are produced in the cell in accordance with the program as can be inferred from the cytological differences among the tissues of the body. In computer parlance *the program may be defined as a set of instructions in the right sequence for the development of the organism, execution of various bioprocesses, its behaviour, instincts, habits and every other task performed by the NCB*. The software is not coded in a chemical structure called genome (DNA base sequence). It has no visible features and is comparable with a computer program. Every activity from the molecular level (inside the cell) to the level of the organism is treated in the NCB concept as a programmed function. The concept does not recognize the so-called "errors" or "mistakes" in the functioning of a cell including when it performs such tasks as chromosome replication, copying process, and DNA repairs. In fact the use of these terms in contemporary scientific literature is misleading because a cell cannot make mistake; it can carry out the task only as stipulated in the program. The view that the program is not constituted by a chemical structure (genome or DNA) and it has an independent existence raises the question as to how then it exists in the cell. Probably it exists as stored information in the storage medium (chromosomes and probably other structures as well) of the cell. The programs and data we store in our computer memories do not form an integral part of the chemical structure of the device but, we are only exploiting the magnetic or other property of a chemical structure for storing information. Natural evidence of such a mechanism for storage can be found in the example of brain memory. If information can be stored in human brain cells without altering the DNA base sequence, it must also be possible to store the program by a similar or a different mechanism in the biochip (cell).[49] The biomemory, is assumed to have

49. Wahid, P. A., *The Divine Expert System* (Aligarh, India: MAAS, Centre for Studies on Science, 2002), 130. See also his "Definitions of life, death, genetic program and soul based on the Quran and computer concept of the universe" in *J. Islamic Sci.* 18 (1-2) (2003): 137-47.

been organized in sectors, i.e., a group of bytes (see Fig. 1). Each sector stores a part of the program, such as a few instructions or a program bit required for a given task, enabling the system processor to read from a particular sector as required. For example, each biochemical event has its own specified steps and sequence. These steps in the right sequence form a "program bit" in the program of the species. A storage sector in the chromosome represents a "program bit".

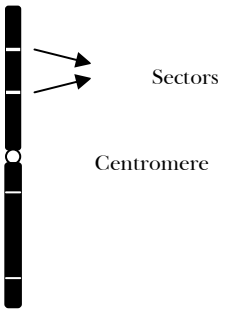

Fig. 1. Chromosome as the memory device of the biochip
Note: The chromosome is divided into many sectors which store program bits; only a few sectors are shown.

Programmed Organic Evolution

The creation of all biological species, excepting human beings, *Homo sapiens*, by Allah can be thought of as a programmed phenomenon. According to the Qurʾān man was created through a special process in heaven.[50] Hence only the evolution of other organisms is considered here. The evolution of a species could never have been a chance phenomenon driven by random mutation and natural selection. There were no gradations either between any two organisms created by Allah. All of them are perfectly designed for meeting the requirements of the overall divine scheme of things. The theory of programmed organic evolution is proposed here on the strength of the natural existence of molecular tools and systems for rearranging and reorganizing

50. *al-Baqarah*: 30-34; *al-ʿArāf* :12-25.

chromosomes in the cell and the fact that these rearrangements can be carried out as a cell-directed (i.e., programmed) phenomenon.

Insofar as each organism is a system functioning according to a specific program, the evolution of diverse species, or biodiversity, can be considered as the evolution of diverse programs. In other words, it is possible to visualize the evolution of these programs through differentiation of a divine master program referred to here as the Bioprogram. During the differentiation process the Bioprogram has been differentiated into as many programs as there are species. The resulting programs that describe the species may be called as microbioprograms. Thus each microbioprogram defines a species. *The Bioprogram is the driving force behind the organic evolution responsible for the creation of the microbioprograms of the various species. Microbioprogram is Bioprogram at the species level which determines the development of its individuals, traits and their potentials, longevity, behaviour (food habit, shelter construction, mating behaviour and instincts), etc.*

It is assumed here that the Arabic term *rūḥ* used in the Qurʾān can be scientifically interpreted as the master divine software–the Bioprogram for the creation and functioning of living beings by Allah. The following Qurʾānic descriptions were used to draw such a conclusion. Man was created from clay (Q. 6:2; 15:26) and God breathed into him His *rūḥ* (Q. 15:28-29; 17:85). *Rūḥ* mentioned in the Qurʾān can be considered as a sort of "software" and the "breathing of *rūḥ*" into the clay model, as the installation of the software. Another Arabic term *nafs* used in the Qurʾān would indicate either an individual i.e., the biological system with software (Q. 3:25) or just the software (microbioprogram) of an individual (Q. 6:93) depending on the context. *But how (will they fare) when We gather them together against a Day about which there is no doubt, and each nafs will be paid out just what it has earned without (favor or) injustice?* (Q. 3:25). … *At [the time of] death, the angels stretch forth their hands[(saying] "yield up your nafs…* (Q. 6:93). Based on these, the term *nafs* may be taken to mean specifically the microbioprogram at the level of an individual (species) whereas the term *rūḥ* may be considered as a general term to mean the divine Bioprogram. This Qurʾānic description (Q. 6:93) further tells us that the phenomenon of death is akin to deletion (removal) of the software (microbioprogram) from the body cells. In other words, *a dead body is like a computer without software*. The phenomenon of life may be therefore defined as the manifestation of the execution of the microbioprogram. These aspects have been discussed in detail

elsewhere.[51] Insofar as the proposed theory is founded on natural software engineering mechanisms and differentiation process, these phenomena are briefly discussed here before we examine the proposed concept of programmed organic evolution.

a. Natural Software Engineering Tools

Excellent reviews are available on the subject of natural genetic engineering mechanisms.[52] Advances made in molecular biology have brought to light several natural mechanisms and processes occurring in the cell which can produce tailor-made chromosome compositions. The ability of the chromosomes to store the software and the existence of cell-mediated mechanisms for cutting and splicing chromosome sectors and thereby producing different chromosome organizations meet the requirements of a possible cell-directed evolutionary phenomenon.

An important breakthrough in molecular biology is the discovery of various molecular tools and mechanisms available in the cell itself for genetic change. The view that stochastic mutations induced by cosmic radiation, chemicals, and other means are primarily responsible for bringing about genetic mutations is now quickly yielding to the view of more extensive, non-random, cell-mediated mechanisms. Several genetic engineering mechanisms and systems have been identified within the cell. It is to be noted that although the terms 'genetic sequence', 'nucleotide sequence', 'genome sequence' and any other term involving or referring to DNA are retained in this discussion to match the usage in contemporary scientific literature, they should be taken to imply a chromosomal region or a chromosomal sector, but not specifically the DNA structure, that stores a program bit.

Genetic recombination: This occurs during meiosis. Through a process of 'crossing over', the segments of non-sister chromatids of a

51. Wahid, P. A., *The Divine Expert System* (Aligarh, India: MAAS, Centre for Studies on Science, 2002), 130. See also his "Definitions of life, death, genetic program and soul based on the Quran and computer concept of the universe" in *J. Islamic Sci.* 18 (1-2) (2003): 137-47.

52. Shapiro, J. A., "Transposable elements as the key to a 21st century view of evolution" in *Genetica* 107 (1999): 171-79. See also his paper "A 21st century view of evolution" in *Proc. Fourth Intl. Conf. Biological Physics*, Kyoto, Japan, July 30-August 3, 2001.

homologous pair of homologous dyads are exchanged. This swapping of portions leads to alteration of genetic information content in the resulting chromosomes. Major genetic differences observed between siblings are the result of genetic recombination.

Chromosomal aberrations: Aberrations are changes encountered in the chromosomes during cell division. Although many types of aberrations are found, the more commonly observed are deletion (loss of a small segment of a chromosome usually in only one homologue) leading to loss of information, translocation (a segment of one of the two homologous chromosomes breaks and binds to the other), duplication (occurrence of the same sectors twice on the same chromosome), inversion (a particular sector is reversed in the chromosome), insertion (a new sector is inserted into the chromosome) and substitution (a certain chromosome sector is replaced with another). Duplication of the whole complement of the chromosomes in the same cell (polyploidy, a consequence of lack of disjunction between the daughter chromosomes following replication) is also seen in nature. This phenomenon is widespread in the plant kingdom.[53] Mitosis and meiosis, two kinds of cell divisions that we find in the living beings are in fact examples of other types of software differentiation process.

Transposable elements (TEs): The discovery of built-in natural genetic engineering mechanisms dates back to Nobel laureate Barbara McClintock's pioneering cytogenetic studies on transposable elements during the late 1940s and early 1950s.[54] These mobile elements offer a powerful cut-and-splice tool in bringing about specific changes and modular organization of genomes as hierarchical systems in the cell. Without these natural genetic engineering systems, functionally significant regulatory signals and repetitive elements could not have been distributed throughout the genome to build up coordinated system.[55] Transposition plays an important role in chromosome

53. Stephan, W. "Evolution of genome organization", *Encyclopedia of Life Sciences*, doi:1038/npg.els.0001699.
54. McClintock, B., *The Discovery and Characterization of Transposable Elements* (New York: Garland, 1987).
55. Shapiro, J. A. "Transposable elements as the key to a 21st century view of evolution" in *Genetica* 107 (1999): 171-79.

rearrangements.[56] Insertion, deletion and inversion occur either as a direct consequence of transposition or by general recombination between two copies of an element present at two locations.[57] These elements are present in all prokaryotes and eukaryotes.

Several specific enzymes are involved in all these chromosome rearrangement processes. These include restriction endonucleases for cleaving DNA and ligases for joining the fragments, recombinases that can execute a large variety of DNA cleavage and joining reactions. Transposases, integrases and resolvases/invertases belong to the group of recombinases. Polymerases catalyze accurate multiplication and maintenance of genomes and helicases which accomplish unwinding of duplex DNA are some of the other enzyme systems which are present in the organisms.[58] Topoisomerases catalyze the transient breaking and rejoining of DNA strands. Two types of topoisomerases are known; type I enzymes cleave only one of two strands while type II enzymes cleave both strands simultaneously allowing one DNA duplex to pass through another. These enzymes control the degree of supercoiling and are required for undoing knots and tangles in the genetic material. These are necessary for DNA replication process. All these processes viewed in light of the computer concept produce changes in chromosome sectors and hence in the program stored in the chromosome.

b. Ontogenetic Development

The development of a human being taking place as a result of execution of the microbioprogram stored in the zygote may be considered as an example of natural software differentiation. The zygote undergoes a series of divisions and sequential transformations to produce ultimately the individual, the whole system. To start with, the zygote divides to form a ball of unseparated cells. Once there are 32 cells, it is called a morula. With additional cell division, the morula becomes an outer shell of cells with an attached inner group of cells. This stage is called blastocyst stage.

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56. Bram, L. A. M. and Reznikoff, W. S. "DNA transposition: Class and mechanisms", *Encyclopedia of Life Sciences*, doi:1038/npg.els.0000590.
57. Harshey, R. M. "Transposons: Prokaryotic", *Encyclopedia of Life Sciences*, doi:10.1038/npg/els.0000591.
58. Knopf, C. W. and Waldeck, W. "DNA-binding enzymes: Structural themes" in *Encyclopedia of Life Sciences*, doi:10.1038/npg.els.0002717.

The inner cells will become the embryo. These cells of the embryonic stage multiply through repeated divisions and initiate differentiation on time schedules prescribed by the program. Differentiation implies transformation of the cells from the more general to the particular along a pre-determined direction. Thus a neuroblast which may be indistinguishable from another cell in the beginning would become increasingly different from the others as the process of differentiation continues and eventually becomes a nervous tissue. Embryo formation is completed in about two months during which, almost all of the internal organs are well established. From the third month onwards to the end of gestation, the changes that occur in the foetus are growth and further tissue differentiation. Ultimately, through repeated mitotic division, morphogenesis and histogenesis, the baby is formed which, following birth, develops into an adult.

Although the full set of instructions, i.e., the microbioprogram carried in the zygote, is intact all through the ontogenetic differentiation process and is transferred from the parent to the daughter cells during cell divisions, the resulting cells are not structurally and functionally identical. What happens during the differentiation is probably a 'programmed suppression' of certain instructions in the microbioprogram at each step of the differentiation until the end cells (tissues) are formed. Thus even if the whole microbioprogram is present in each cell of each tissue, the cells of a tissue can execute only those instructions that are not masked. This may perhaps explain why the cells of every tissue, in spite of totipotency, can not be readily cultured (e.g., cell culture, cloning); a reprogramming to restore the cell to the original status may be required depending on the differentiation status of the tissue concerned.

The cellular structures in different tissues are developed in accordance with the 'operable' sets of instructions carried by them. The 'inoperable' instructions would remain latent and unexpressed in the tissue cells. This would perhaps explain how different tissues are programmed to function differently. The whole phenomenon may be recognized as *ontogenetic software differentiation* (OSD)[59]. Some of the

59. Wahid, P. A., *The Divine Expert System* (Aligarh, India: MAAS, Centre for Studies on Science, (2002), 130.

observations relevant to the concept of programmed organic evolution that can be made from this example are:

The origin of the system is from a single cell (zygote) which is microscopic in size.

The program required for the evolution of the system was carried in the primordial cell, zygote.

The system as such did not exist in a miniature form in the beginning but evolves from a primordial cell.

The system is composed of several organs. Each organ is made up of several functionally different tissues each of which, in turn, is composed of more or less homogeneous cells. A cell is thus the basic unit of the system.

c. Primordial Biochip and the Origin of Life

The organic evolution might have begun from a single cell as is generally believed. But, contrary to the current belief, the first cell formed on this planet could not have been a species but a cell which carried the divine Bioprogram necessary for the evolution of the various species. This first cell containing the Bioprogram may be referred to as the primordial biochip (PBC).

Woese[60] proposed the concept of "the universal ancestor" to look at the rooting of the evolutionary tree. The ancestor, according to this model, could not have been a particular organism, a single organismal lineage. It was communal, a loosely knit, diverse conglomeration of primitive cells that evolved as a unit, and it eventually developed to a stage where it broke into several distinct communities, which in turn became the three primary lines of descent. The primary lines, however, were not conventional lineages. Each represented a progressive consolidation of the corresponding community into a smaller number of more complex cell types, which ultimately developed into the ancestor(s) of that organismal domain. Molecular evolutionists have given the name LUCA (last universal common ancestor) for the common ancestor of all life. Despite the wealth of genomic data, LUCA has remained elusive. Whether it is simple or complex is not yet understood. The general thinking is that LUCA may be a pool of genes shared by a host of

60. Woese, C., "The universal ancestor" in *Proc. Natl. Acad. Sci.* 95 (1998): 6854-59.

primitive organisms. According to Gary Olsen, a microbiologist at the University of Illinois at Urbana-Champaign, "the naïve picture that a group of organisms got all their genes from a simple last common ancestor is breaking down". Moreover, the communal LUCA notion does not fit the way evolution works. "To think of LUCA in terms of a community is to remove the idea of Darwinism from early evolution", says Patrick Forterre of the Paris-Sud Unversity in Orsay and the Pasteur Institute in Paris.[61] Obviously, LUCA is a misfit in the Darwinian model, but the fact that LUCA is looked upon as a more likely launching point for the organic evolution is a disturbing signal to the supporters of Darwinism.

The concept of LUCA comes very close to the requirement and role of the PBC in the proposed theory of programmed evolution. The theory of programmed evolution does not assume that the primordial cell formed at the beginning of life is an organism (i.e., the first species) as assumed in the Darwinian model. The LUCA, however, differs from the PBC in an important aspect namely, the latter has a program to guide the evolution of millions of microbioprograms (or species) without the need of chance mutation and natural selection. The PBC is defined here as a cell carrying the *rūḥ* (the divine software—the Bioprogram, stored in the chromosomes) and necessary hardware components (organelles) to execute the divine program. The PBC which started the organic evolution is the counterpart of the Big Bang singularity that started the inorganic evolution or the zygote that started the development of a human individual in the mother's womb. The PBC with a built-in program as the driving force can explain the phenomenon of evolution of species consistent with natural evidence. The Qurʾān tells us that every living thing was created by Allah from water. This is one aspect (or perhaps the only one) of the origin of living beings in which there is consensus among biologists and that agrees with the Qurʾān …*We made from water every living thing. Will they not then believe?* [62] As Alfred Russel Wallace emphasized at the beginning of the twentieth century, the first requirement for life is liquid water; without it, as far as we know, life is

61. Whitfield, J., "Born in a watery commune" in *Nature* 427 (2004): 674-76.

62. *al-Anbiyāʾ*: 30

impossible.[63]

Robert Folk of the University of Texas at Austin described the minimal genetic set required for the first living cell. He discovered bacteria-like structures about 100 nm (a nanometer is one-billionth of a meter) in size in Italian hotspring deposits. These structures are called "nanobes" because of their very small size. Nanobes are 20 to 150 nm across, smaller than the tiniest bacteria measuring about 200 nm. Folk believes that nanobes are alive. Experts put 200 nm as the smallest size required for life and anything less than that cannot be considered as life. Recent discovery of nanobes in ancient Australian sandstone by scientists at the University of Queensland indicated that the structures were as small as 20 nm across and looked like fungi. These nanobes seemed to have the enzymatic and genetic material considered essential for life. Nanobes are now seen virtually everywhere.[64] The PBC may be likened to a nanobe with minimal hardware components (cellular structures) to store the Bioprogram and also to execute it.

The origin of PBC has more significance than what the traditional theories of evolution give to the origin of the first organism or to the LUCA. Although the evolutionists treat organic evolution as a continuation of inorganic evolution, the phenomenon has never been thought of as a landmark changeover event from chemical principles to biological (genetic) principles. It is to be realized that biological principles are fundamentally different from chemical principles and that genetic information has not been available in nature prior to the transition from non-life to life took place with the supposed installation of the divine Bioprogram in the PBC. The installation of the divine software would have been effected *in situ* through transmission of *rūḥ* by Allah through an Angel as similar process has been mentioned in the Qurʾān in another context. For instance, the birth of Prophet Īsā is by such a process. As the Qurʾān put it: …*We sent to her Our rūḥ and he appeared before her as a man in all respects …He said: I am only a messenger*

63. Wallace, A. R. *Is Mars Habitable? A Critical Examination of Professor Percival Lowell's Book "Mars and Its Canals" with an Alternative Explanation* (London: Macmillan, 1907).

64. Leslie Mullen, "Life from scratch?" in *Astrobiology Magazine* (November 4, 2003).

from your Lord to gift a blessed son to you.[65] Another possibility is that the PBC would have been sent down as a spore to the earth by Allah's command. In practical terms, this proposition is consistent with the idea of directed panspermia. In either way, availability of the divine Bioprogram in the PBC on the earth is the cause, and manifestation of life is the result. The notion that life originated from non-life is therefore baseless. Life did not jump-start from non-life based on chemical principles; it started only when the genetic information (the divine software Bioprogram) was made available on the earth by Allah.

d. Evolution of the Microbioprograms

The program carried in the zygote, as in the human example discussed above, is intended to differentiate itself (the so-called ontogenetic development) into various subsets of operable instructions carried in the tissues at the end of the differentiation process. Each tissue is thus able to function according to the operable instructions it carries. The cell of a given tissue also has the required hardware components to suit the tasks it has to perform. The development of a human individual from the zygote illustrates how the program stored in a cell is executed with the help of cellular hardware to ultimately produce a natural computer biosystem, the adult. In other words, different kinds of tissues, or groups of homogenous cells, were produced through the execution of a program carried in the starting biochip, the zygote. It is therefore reasonable to assume that the Bioprogram carried in the PBC is such that its execution can produce a large number of end cells with different microbioprograms through a process of differentiation. The evolutionary process is supposed here as a totally programmed phenomenon to differentiate the Bioprogram into as many microbioprograms (species) as are specified in it. Software engineering mechanisms and systems like mobile elements and enzyme systems, and cell divisions, as already discussed, would have come into operation to perform a wide range of tasks like cutting and splicing of chromosomal sectors, shuffling of the sectors, replication, deletion and copying of the sectors with remarkably high fidelity to ultimately accomplish the mission. All these cellular functions are program-directed phenomena carried out with extreme

65. *al-Maryam*: 17-19.

specificity and accuracy. These processes might have been triggered into operation in the sequences and time schedules specified in the Bioprogram to ultimately produce a large number of cells each with different but viable microbioprograms carried in their chromosomes.

e. Phylogenetic Software Differentiation

We may now examine the probable pathways through which the PBC would have produced millions of microbioprograms each representing a species. The execution of the Bioprogram carried in the PBC may be supposed to have occurred through a phylogenetic software differentiation (PSD) process. *The PSD may be defined as the programmed generation of microbioprograms during which the Bioprogram stored in the PBC undergoes step by step differentiation and partioning leading to the production of as many microbioprograms (smaller packages) as specified in the Bioprogram.* Physically this would appear as a process during which the chromosomes in the PBC underwent cutting and splicing of sectors, deletion, translocation, recombination, replication, their reorganization, etc., in the specified sequential steps ultimately leading to the production of cells, each with a microbioprogram carried in specific number of chromosomes. Each of these end cells carries the microbioprogram of a species.

Taking the cue from the evolution of a human individual from the zygote, we may visualise the PSD as follows. The PBC might have undergone division initiating the biological evolution. During division, the program might have been differentiated and partitioned into as many number of mother cells as stipulated in the Bioprogram. The number of mother cells produced, or the number of cell divisions which occurred, depends on the number of evolutionary lineages (domains of life) to be created. Based on the modern phylogenetic classification, Bacteria, Archaea (microbes living in extreme environments) and Eukarya (sometimes termed Eukaryota)[66] may be recognized as the three domains for which separate mother cells had been produced from the PBC. Each domain mother cell might have undergone further differentiation of the software in successive steps in accordance with the

66. Koch, A. L. "Bacterial origins" in *Encyclopedia of Life Sciences*, doi: 10.1038/npg.els.0000445.

program representing the domain concerned. For example, the Eukarya mother cell, following PSD, would have produced daughter cells representing each kingdom in that domain. The three kingdoms—animals, plants and fungi—are just three of about a dozen extant major branches of the eukaryote domain.[67] Differentiation of the kingdom mother cell would have, in turn, directed the evolution of microbioprograms of species in the kingdom concerned. For example, the plant kingdom mother cell carried the program to direct the evolution of the species of the plant kingdom and the animal kingdom mother cell carried the program to direct the evolution of species of the animal kingdom, and so on (see Fig. 2).

67. Ayala, F. J. and Fitch, W. M. "Genetics and the origin of species: An introduction" in *Proc. Natl. Acad. Sci. USA* (1997), 94: 7691-97.

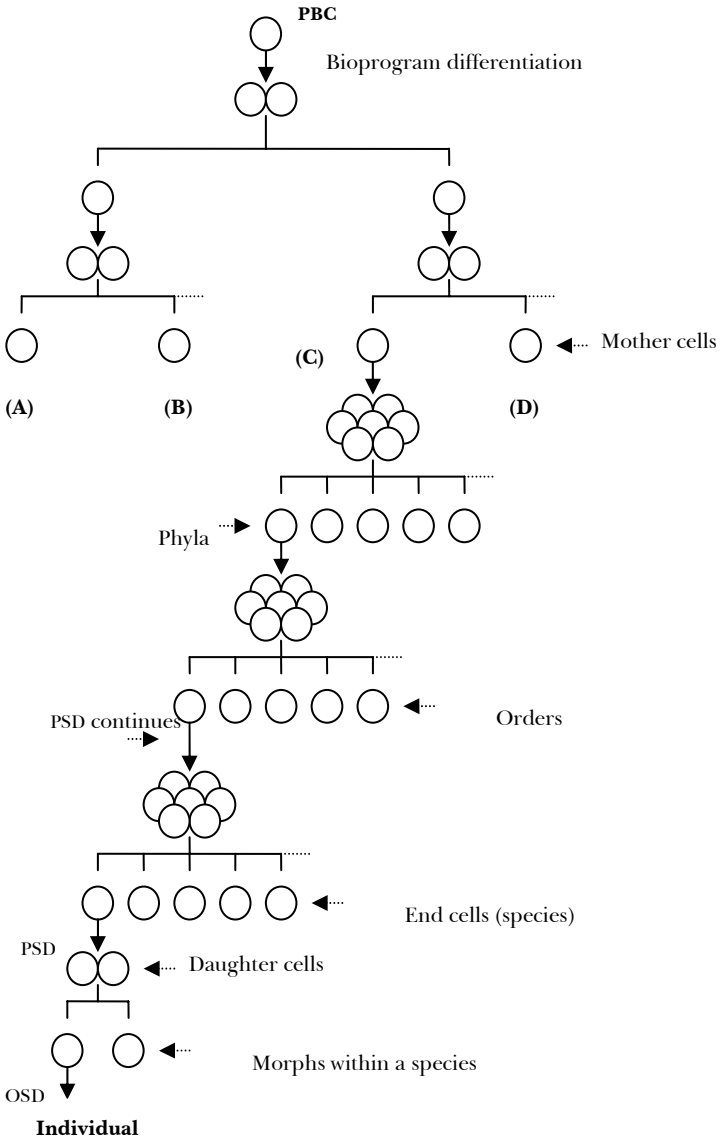

Fig. 2: Proposed phylogenetic software differentiation (PSD) pathway for the synthesis of microbioprograms (representing species) from the divine Bioprogram. Note: A, B, C and D represent the kingdoms. PBC: Primordial biochip. OSD: Ontogenetic software differentiation.

A kingdom mother cell undergoes shuffling of chromosomal sectors

through natural software engineering processes followed by repeated cleavage as specified in the program to produce something like a morula, a ball of cells. Each of the resulting cells might have become separated from the cluster to become a phylum mother cell for the evolution of the species in that phylum. The phylum mother cells might have undergone further differentiation of software through the same processes as in the previous steps and on time schedules stipulated by its program. This stage would represent the embryonic stage of the organic world. The PSD led to the production of end cells, each of which represented a species under the phylum.

An end cell is a full-fledged cell with all the hardware components (cellular structures) and the microbioprogram required for the development of various types of individuals of the species. The end cell might have undergone further software differentiation and division producing daughter cells representing sexual dimorphs, polymorphs, castes, etc., depending on the species. It is these daughter cells that developed into the first individuals of the various species via OSD. The term "phylum" is used here to denote a group of species (microbioprograms) and not exactly the taxonomic species under a phylum. If the stages of evolution in PSD and OSD are compared, each end cell (i.e., species) of the PSD may be likened to a tissue of the OSD and each cell that represented a phylum of the PSD may be likened to a blastomere of the OSD that led to the development of an organ of the body.

The end cells produced by the animal mother cell might have been in the form of eggs while those originated from the other mother cells might have been spores, seeds, or some other form. Whatever the form in which they emerged, these cells might have been dispersed over the water and land areas by natural processes resulting in the widespread distribution of the species on the earth. In fact, for all practical purposes, the evolution of species is complete with the creation of the end cells (microbioprograms). The OSD of the end cells representing species might have been programmed to take place at different time schedules. This is reflected in the sequence and chronology of appearance of the various species in the fossil record. It may be noted that programmed evolution does not need any intermediate stage to create a fully designed, perfect organism. It is creation at once through a programmed evolutionary process. Therefore the theory is consistent with the natural evidence of lack of transitional forms in the fossil record. Further the PBC does not

exist today as it has undergone PSD much like the zygote which is not to be found in the body of an individual as it has undergone OSD.

The theory of programmed evolution proposed here differs in several respects from the traditional theories of evolution based on Darwinism. These are:

(a) A divine software "Bioprogram" is supposed to be the driving force behind the biological evolution.

(b) The origin of species is viewed as the creation of diverse software packages (microbioprograms) from an original single software—the Bioprogram, through a process of software differentiation.

(c) The organisms that developed from the microbioprograms were in perfect form and required no intermediate forms whereas the Darwin mode required the physical existence of intermediate forms. In programmed evolution, the origin of a species is not through descent with modification of an existing species.

(d) Programmed evolution is a deterministic phenomenon with a purpose and a goal.

Although the existence of natural genetic engineering systems and mechanisms and the possibilities of genetic rearrangements and evolution of new genotypes are known, the process of evolution employing such engineering systems has not been conceptualized. The number of steps indicated in the software differentiation process discussed above and shown in Fig. 2 is arbitrary and is only intended to explain the process in a broad sense.

Natural Evidence Supporting the Programmed Organic Evolution

The sudden appearance of new species punctuated by long periods of stasis (PE) as revealed by the fossil record (e.g., Cambrian explosion) may be considered to reflect the time schedule specified in the Bioprogram for the appearance of the species. According to Douglas Futuyma, a prominent evolutionary biologist, "Organisms either appeared fully developed or they did not. If they did not, they must have developed from pre-existing species by some process of modification. If they did appear in a fully developed state, they must indeed have been created by some omnipotent intelligence."[68] The proposed theory of

68. Futuyma, D. J., *Science on Trial* (New York: Pantheon Books 1983),

programmed evolution supports the latter. Almost all groups at all taxonomic levels first appear in the fossil record as "type" forms and then "explode" into a large number of diverse lineages with a mix of related but not identical potentials for adaptive morphological change.[69] This pattern is suggestive of the partitioning of a very large common genetic package with a large number of alternate morphological potentials. But no known mechanism is so far available for generating such information-dense primordial source. According to Grasse, evolving species acquire a new store of genetic information through "a phenomenon whose equivalent cannot be seen in the creatures living at the present time (either because it is not there or because we are unable to see it)."[70] The primordial source of genetic information is the *rūḥ* (the Bioprogram).

The proposed theory allows great flexibility in time scales required for the evolution of the biological species. Although the time schedules stipulated by the divine Bioprogram for various stages of software differentiation cannot be reasoned out, the rapidity with which the chromosomal changes, cutting and splicing of chromosome sectors and cell division occur under normal conditions is very much indicative of the speed with which the organic evolution up to the stage of creation of

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197; quoted from *http://www.harunyahya.com/20evolution01.html*.

69. Carroll, R. L., *Vertebrate Paleontology and Evolution* (New York: W. H. Freeman and Company, 1988) See also MacFadden, B. J. and Hulbert, R. C. "Explosive speciation at the base of the adaptive radiation of Miocene grazing horses" in *Nature* 336 (1988): 466-68 and Larson, A., "The relation between speciation and morphological evolution" in *Speciation and Its Consequences* edited by D. Otte and J. A. Endler (Sunderland, MA: Sinauer, 1989), 575-98. All three references above are quoted from Wilcox, D. L., "A Blindfolded Watchmaker: The Arrival of the Fittest" in Chapter 13 *Darwinism: Science or Philosophy, Proc. Symp. Darwinism: Scientific Inference or Philosophical Preference?* edited by J. Buell and V. Herne (Texas: Foundation for Thought and Ethics, 1992).

70. Grasse, P. P., *L'Evolution de Vivant* (1973) published in English entitled *The Evolution of Living Organisms* (1977), cited from Johnson, P. E. "Darwin's rules of reasoning" in *Darwinism: Science or Philosophy* edited by J. Buell and V. Hearn (Richardson: Foundation for Thought and Ethics, 1994).

the end cells (microbioprograms of the various species) would have occurred. The OSD of the end cells might have occurred over the period and in the sequence specified in the Bioprogram. The sequences and spacing (time intervals) observed in the appearance of the species in the fossil record are a reflection of this programmed phenomenon.

The theory of programmed organic evolution based on the Bioprogram (software) differentiation and its reorganisation into millions of viable mini packages (microbioprograms) predicts the presence of identical program bits in the microbioprograms of the species. Physically these program bits will be represented by the identical chromosome sectors which store them. Since DNA is part of the chromosomal material, the existence of identical sequences in the genomes of different species is a consequence of PSD during the programmed organic evolution. Studies relating to molecular evolution provide considerable evidence of the occurrence of chromosome rearrangement, shuffling, reorganisation, etc., during the evolution of species.

These findings serve as a window to view the mechanism of PSD that was in operation during the programmed evolution of species. Studies involving comparison of genome sequences indicate wide variations in karyotypes (number, size and shape of chromosomes in a somatic cell) of organisms. Comparison of karyotypes within and between species reveals that the differences are due to chromosome rearrangements. These rearrangements had played a major role in organic evolution.[71] There is undoubtedly a correlation between the rates of speciation and chromosome rearrangement.[72] The existence of identical DNA sequences in different species is a clear reflection of the software differentiation process that had taken place during the programmed organic evolution. Little wonder that Philippe and Forterre[73] found the phylogenies as highly confusing due to the combining effects of gene duplication, gene loss, lateral gene transfer, etc. The so-called co-evolution, parallel evolution, convergent evolution, and so on are nothing but events

71. Burt, D. W. "Chromosome Rearrangement in Evolution", in *Encyclopedia of Life Sciences*, doi:10.1038/npg.els.0001500.
72. King, M., *Species Evolution: The Role of Chromosome Change* (Cambridge: Cambridge University Press, 1993) quoted from Burt, D. W. op. cit.
73. Philippe, H. and Forterre, P., "The Rooting of the Universal Tree of Life is Not Reliable" in *J. Mol. Evol.* 49 (1999): 509-23.

resulting from programmed timing and scheduling of development of individuals from the end cells representing various species. They are not a product of random process or chance event.