THE GREAT GENE FIASCO

The Quran Defines Life

Prof. P. A. WAHID, Ph.D., FNAAS

(Former Member Secretary, Kerala State Council for Science, Technology and Environment and

Dean, Faculty of Agriculture, Kerala Agricultural University)

ADAM PUBLISHERS & DISTRIBUTORS
(Exporters & Importers)
1542, Pataudi House, Darya Ganj,
New Delhi-110002
Phone (O) : 23282550, 23284740
Tele/Fax : 23267510 (R) 95120-2413957
e-mail : apd@bol.net.in
www.adambooks.com

Edition - 2006

ISBN : 81-7435-

Price :

Printed & Bound in India
Published by :
S. Sajid Ali for,
ADAM PUBLISHERS & DISTRIBUTORS
1542, Pataudi House, Darya Ganj,
New Delhi-110002

Genetic program (biological information) is the intangible software of the living organism. It is not constituted by a chemical structure like genome, but the program is stored in chromosomes - the storage device of the cell, the biochip. The chemical structures are hardware components of the natural computer biosystems (organisms) that encode chemical information. By chasing a chemical trail to locate the source of genetic information, biologists are trying to find a hardware solution for a software problem. Genome is not genetic program, the cause of life. Particulate gene does not exist. Life can only be understood in conjunction with the Quranic revelations. Life is where science meets the religion and the phenomenon is the solid proof of God's existence.

BLANK

CONTENTS

BLANK

Preface

Modern science enjoys a high degree of credibility in the contemporary society, thanks to the advancement of technology offering a variety of facilities and amenities to make life a pleasure on the earth. In the new-age world, human life is virtually technology-driven. Generation of new information and explanation of natural phenomena have been the province of science with little or no contribution from religion. In spite of this, people irrespective of their educational status and background do have own religious beliefs although, of late, there is considerable erosion of belief in religion. Apathy of the common man to the efforts of scientists to debase the theistic doctrine is very much obvious. There is also no agency to act as a watchdog of purity of science and to guard it against the influence of pseudoscientific developments.

This book attempts to expose certain unscientific concepts that pose as stumbling block in the advancement of genetic science. The subject presented in this book is a continuation of my earlier work, "The Computer Universe: A Scientific Rendering of the Holy Quran". I have drawn materials from that book and used them lavishly in the present one. However, the aim of this book is to drive home the point that the particulate gene concept is wrong, and the whole biology including evolutionary biology has turned to be more of a junk.

Figures 3.1 and 3.3 were reproduced from the websites of PLoS Biology and http://butler.cc.tut.fi/~malmivuo/bem/bembook/02/02.htm respectively. The permission given to reproduce the materials at these portals is a great help and a model for others to emulate. This gesture is placed on record here and

acknowledged with thanks.

English translation of the Quranic verses quoted in this book is as given by A. Yusuf Ali (The Holy Quran, Amana Corp., Maryland, U.S.A.). I have however replaced words like 'thy' and verb endings like '-est' with words and expressions in common usage.

Praise be to Allah – the Creator and Sustainer of the worlds, for giving me the strength, determination and perseverance all through this work. I bow to Him in all humility.

February 1, 2006 P.A.W.

1 INTRODUCTION

Life, ever since it began, has remained as the mystery of mysteries, to borrow the Darwinian adage, of this world. Biology, the science of life, has grown at a rapid pace both vertically and horizontally. But the phenomenon of life has so far eluded definition. A living cell is a highly sophisticated irreducibly complex organic machine. If we remove any part from the cell, it will cease to function. Such is the irreducible complexity of the cell so beautifully designed and perfected by Allah. The lack of understanding the phenomenon of life has already impacted several fields in biology from cloning and bioethics to synthetic biology and astrobiology. Perhaps the most damaging consequence is the development of false concepts and theories about life leading to the generation of a large body of misleading information which the scientific community is 'blissfully' unaware of. Thus even when we do not know the kind of life which we are familiar with, efforts have been long since on to discover life on other planets. There are also allied entities like 'gene' and 'species', which remain as elusive as life itself. Although various explanations may be advanced for the failure to define them, the single most important reason is that life, the mother of all these phenomena, is not understood properly, and whatever perception we have about it is flawed. In fact this trio constitutes the fundamental basis of biological sciences. 'Life' is the very subject of biology; the 'gene' is (supposed to be) what sustains life; and 'species' is the biological unit that is supposed to undergo evolution. One wonders how biology can proceed in the right direction without understanding these phenomena.

Science has firmly established in the human psyche as the rational knowledge founded on facts extracted from meticulously carried out experiments and observations. Science is the medium for human beings to unravel the mysteries woven in the fabric of Nature. The success of technologies developed from scientific knowledge has added irrefutable testimony to this view. Unfortunately this is not the whole story. There is also the other side which, to say the least, generates junk leading to misconception of the natural realities. One such case is the particulate gene concept.

In science life and genetics are intimately linked. Genetics is the window of science to view the phenomenon of life. Genetic concepts of heredity also form the contemporary view about the cause of life. Thus 'the gene' is viewed as the entity behind the functioning of an organism and its perpetuation. Currently, it is believed that DNA is the gene and hence blueprint of life. In reality DNA molecule complex constitutes the protein synthesis apparatus of the cell. With the crowning of this molecule as the gene, problems started surfacing. A physical gene has never been the perception of the early geneticists.

This book puts the concept of particulate gene on trial and exposes the materialists' deliberate efforts that went into its making and promotion, and their reluctance to abandon the idea even when the pressure from scientific evidence is mounting. In the wake of particulate gene losing ground, the holy Quran shows the way to the true nature of the phenomenon of life. So beautifully, so elegantly, and so scientifically, the Quran explains to us the life intangible which is far beyond the confines of the physical elements.

2 GENETIC INFORMATION

Every organism carries a genetic program which is responsible for its biological characteristics and functioning. The ontogenetic development of an organism from the zygote, the first cell formed by the fusion of male gamete with female gamete, is guided by the program contained in the zygote. The program is also responsible for the moment-to-moment existence of an organism. The chromosome is the seat of the genetic program. The genetic program is conceptualized as being constituted by genes, the supposed hereditary material. Rheinberger *et al*. [1] provide an excellent review of the evolution of the heredity concepts tracing it to the present day. In the second half of the nineteenth century two alternate concepts emerged on the nature of heredity. One school regarded hereditary matter as particulate and amenable to breeding analysis. Charles Darwin called the presumed hereditary particles gemmules; Hugo de Vries, pangenes; and Gregor Mendel, elements. The other school to which Carl Naegeli and August Weismann belonged, distinguished the body substance, the trophoplasm or soma, from a specific hereditary substance, the idioplasm or germ plasm, which was assumed to be responsible for intergenerational hereditary continuity. They considered the idioplasmic substance as being not particulate, but highly organized [1].

In 1865, the Austrian monk Johann Gregor Mendel, discovered three laws governing heredity and his seminal paper on the subject entitled 'Experiments in plant hybridisation' appeared in 1866. But this paper remained unknown to the outside

world gathering dust in library shelves for nearly thirty five years. In the year 1900, three botanists, Hugo de Vries in Holland, Carl Erich Correns in Germany, and Erich Tschermak von Seysenegg in Austria, independently and almost simultaneously rediscovered the laws of transmission of characters from parents to offspring, which Mendel had already presented in his seminal paper. Bateson coined the term "*genetics"* for this emerging science of heredity in 1906. Subsequently, Wilhelm Johannsen introduced the notions of "*genotype*" and "*phenotype*". In addition, for the elements of the genotype, he proposed the term "*gene*". "*He had…reservations with respect to its [gene's] particulate character, and especially warned that the notion of "genes for a particular character" should always be used cautiously if not altogether be omitted"* [2, p. 147; emphasis added]. So the gene remained as a hypothetical entity as Mendelian genetics did not allow supposition of physical structure for genetic elements. Thomas Hunt Morgan and his group contributed substantially to the understanding of the mechanism of heredity. In the year 1933, on the occasion of his Nobel address, Morgan observed: "At the level at which the genetic experiments lie it does not make the slightest difference whether the gene is a hypothetical unit, or whether the gene is a material particle" [3, p. 3]. Nevertheless, many geneticists like Herman J. Muller (Morgan's student), believed that genes had to be material particles. In 1950, on the occasion of the fiftieth anniversary of the rediscovery of Mendel's work, Muller however admitted: "[T]he real core of gene theory still appears to lie in the deep unknown. That is, we have as yet no actual knowledge of the mechanism underlying that unique property

which makes a gene a gene… its ability to cause the synthesis of another structure like itself, [in] which even the mutations of the original gene are copied. [We] do not know of such things yet in chemistry" [4, p. 95-96]. Meanwhile, cytological research had also added credence to the material nature of genes on chromosomes. The growing successes of various studies relating to classical genetics led to a "hardening" of the belief in the gene as a discrete, material entity [1, 5]. It has been known since about 1913 that the individual active units of heredity - the genes - are strung together in one-dimensional array along the chromosomes, the threadlike bodies in the nucleus of the cell. It has also become apparent that the information-containing part of the chromosomal chain is the DNA molecule [6].

2.1 The molecular gene

George Beadle and Edward Tatum during the late 1930s and early 1940s established the connection between genes and metabolism. They used X-rays to cause mutations in strains of the mold *Neurospora*. These mutations affected single genes and single enzymes in specific metabolic pathways. Beadle and Tatum proposed the "one gene, one enzyme hypothesis" for which they won the Nobel Prize in 1958. Since the chemical reactions occurring in the body are mediated by enzymes, and since enzymes are proteins and thus heritable traits, it is supposed that the gene and proteins are related. George Beadle, during the 1940s, proposed that mutant eye color in *Drosophila* was caused by a change in one protein in a biosynthetic pathway [7]. These views of gene function strengthened the idea of genetic specificity leading to molecularization of the gene. In the early 1940s, Oswald Avery

and his colleagues purified the deoxyribonuleic acid (DNA) of one strain of bacteria, and demonstrated that it was able to transmit the infectious characteristics of that strain to another, harmless one [1].

The elucidation of the structure of DNA as a macromolecular double helix (Fig. 2.1) by Francis Crick and James D. Watson in 1953 (both received Nobel Prize for this discovery) and *in vitro* characterization of the process of protein biosynthesis led to the idea that it was the linear sequence of ribonucleic acid derived from one of the DNA strands that directed the synthesis of a linear sequence of amino acids, or a polypeptide, and that this process was mediated by an adaptor molecule (RNA template). The relation between these two classes of molecules was found to be ruled by a nucleic acid *triplet code* or *codon*, i.e., three bases at a time specified one amino acid. Based on these, Francis Crick in 1958 formulated the "sequence hypothesis" and the "central dogma" of molecular biology. The sequence hypothesis implies that specificity of a piece of nucleic acid is expressed solely by the sequence of its bases; the sequence being a simple code for the amino acid sequence of a particular protein. The central dogma states that once 'information' has passed into protein *it cannot get out again*. That is, the transfer of information (the precise determination of sequence, either of bases in the nucleic acid or of amino acid residues in the protein) from nucleic acid to nucleic acid, or from nucleic acid to protein may be possible, but transfer from protein to protein, or from protein to nucleic acid is impossible [8, p. 152-153]. A remarkable feature of the structure is that DNA can accommodate any sequence of base pairs – any

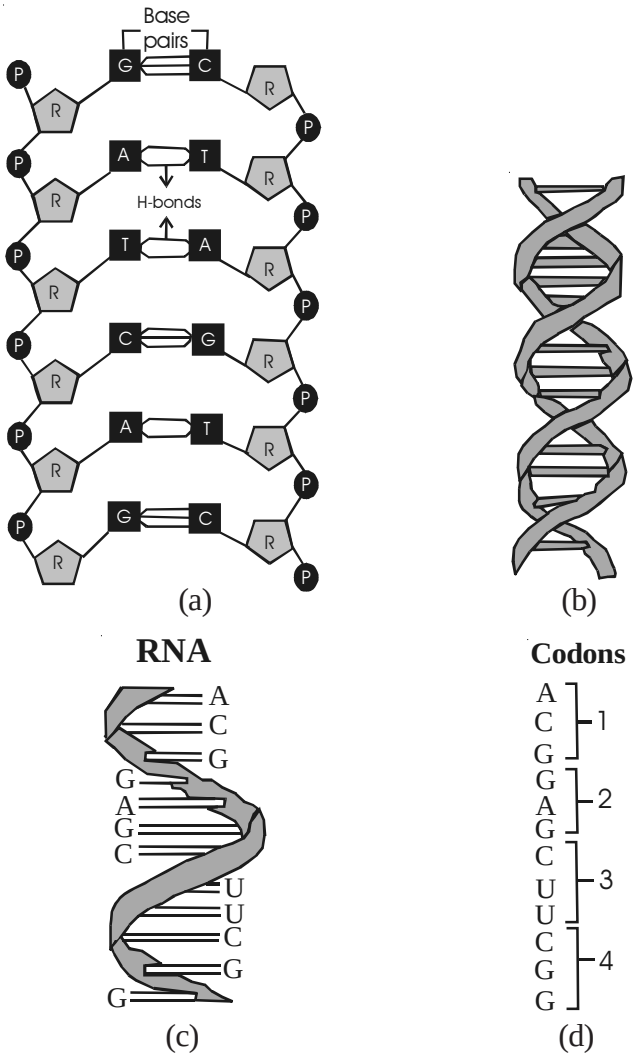

Fig. 2.1. Double helical model of DNA, structure of RNA and codon concept.

(a) Structural components of DNA; (b) Double helix; (c) RNA structure; (d) Codon. Note: Codons shown in (d) are based on the RNA base sequence given in (c).
P: Phosphorus, R: Deoxyribose, A: Adenine, C: Cytosine, G: Guanine, T: Thymine, U: Uracil
(Source: Wahid, P.A. 2006. *The Computer Universe – A scientific Rendering of the Holy Quran.* Adam Publishers, New Delhi)

combination of the bases adenine (A), cytosine (C), guanine (G) and thymine (T) – and, hence any digital message or information [9]. The two strands of the DNA are complementary to each other with respect to bases, i.e., base A on one strand pairs with base T on the other strand and, base C with base G. If the base sequence is AGCTTT in one of the strands, the other strand will have the corresponding sequence TCGAAA. In computer parlance, a base pair A-T or C-G is equivalent to two bits of information. Human genome has about 3.3 billion base pairs (6.6 gigabits or 825 megabytes). Each gene encodes a complementary RNA transcript, called messenger RNA (mRNA), made up of A, C, G and uracil (U) instead of T [10]. The sequence of three bases in the structure forms a code (triplet code or codon) which determines the amino acid and hence the protein. That is, sequence of three letters in a gene encodes one amino acid [11]. There are 64 possible triplet combinations (4^3) or codons of which 61 encode an amino acid (there are 20 amino acids) and three serve as 'punctuation' for signaling the termination of the protein chain (i.e., stopping the translation process). The genetic code is thus degenerate in the sense that more than one codon code for the same amino acid. For example, GGU, GGC, GGA, and GGG codons encode glycine [7]. The entire genome sequence is considered as forming a precisely definable digital core of information for an organism. The genome encodes two main types of digital information – the genes that encode the protein and RNA molecular machines of life, and the regulatory networks that specify how these genes are expressed in time, space and amplitude. An informational hierarchy can be developed thus: gene ➔ RNA

Protein ➔ protein interactions ➔ protein complexes ➔ networks of protein complexes in a cell ➔ tissues or organs ➔ individual organism ➔ populations ➔ ecosystems. At each successively higher level in the informational hierarchy, information can be added or altered for any given element; for example, by alternative RNA splicing or protein modification [9]. Organisms are characterized by three processes – replication, transcription and translation. Replication, the basis of inheritance, is the faithful copying of the DNA sequence. Transcription implies copying the DNA sequence into an RNA sequence composed of ribonucleotides (ACGU where U, uracil, replaces T, thymine) similar to the DNA sequence. Ribosomal RNA (rRNA) combines with proteins to form the ribosomes, the site of synthesis of proteins from amino acids. During synthesis of protein, transfer RNAs (tRNAs) diffuse throughout the cell carrying the amino acids and anticodons for codon recognition. This process is termed translation. The translation process takes place in two steps; a) the preparation of a messenger RNA (mRNA) that codes for the successive amino acids in the polypeptide chain, and b) the 'reading' of the mRNA into protein. This involves pairing of each amino acid-specific codon with its anticodon triplet in the tRNA. The pairing gives rise to peptide bonds between the amino acids as they are released from the tRNAs [12].

The '*sequence hypothesis'* and the '*central dogma'* form the two basic assumptions on which molecular 'information transfer' is founded. Thus the moluclar gene, stretches of DNA (or RNA in some viruses), became the carrier of information for the synthesis of a particular protein. The two fundamental properties

thought to be required by the gene namely, autocatalysis and heterocatalysis, were perceived as relying on the base complementarity (C/G and A/T and U in RNA) supposed to be responsible for the faithful duplication of genetic information (the '*replication'* process), and via the genetic code, for the transformation of genetic information into biological function through '*transcription'* and '*translation'*. The 'genotype' thus became the repository of 'genetic information' or the '*genetic program'*. These ideas emerged largely from the work of François Jacob and Jacques Monod - the so called operon model. Based on this three classes of genes namely, structural genes, regulatory genes, and signal sequences which provided the framework for viewing the genotype as 'genetic program' were recognized [1]. According to François Jacob, the genetic program is very peculiar in the sense it requires own products for being executed: "There is only the incessant execution of a program that is inseparable from its realization. For the only elements being able to interpret the genetic message are the products of that message" [13]. The whole conception looks like a circle and has been criticized as such [14].

With molecular biology, the classical gene went "molecular" [15]. A gene is defined in molecular terms as "a complete chromosomal segment responsible for making a functional product" and a genome "as the entire collection of genes encoded by a particular organism" [16]. Thus the hypothetical non-physical hereditary unit first proposed by Johansson at the beginning of the twentieth century assumed the particulate status with the elucidation of the chemical structure of DNA.

2.2 Junk DNA

The assumption of "one gene, one protein" makes the genes generally synonymous with proteins. Thus the term "gene" refers to the gene that codes for protein. The picture of gene expression became even more complicated with the advancement in molecular biology since the 1960s. It has been observed that an overwhelming 95% of genome consists of non-coding DNA in eukaryotes whereas only less than 5% is constituted by the coding DNA or genes. The non-coding DNA (ncDNA) is referred to as "junk DNA" which may encode RNA molecules capable of performing a variety of regulatory functions. Discussing the ncDNA, John S. Mattick, Director of the Institute for Molecular Bioscience at the University of Queensland, comments: "Biologists assumed that proteins alone regulate the genes of humans and other complex organisms. But an overlooked regulatory system based on RNA may hold the keys to development and evolution…Assumptions can be dangerous, especially in science. They usually start as the most plausible or comfortable interpretation of the available facts. But when their truth cannot be immediately tested and their flaws are not obvious, assumptions often graduate to articles of faith, and new observations are forced to fit them. Eventually, if the volume of troublesome information becomes unsustainable, the orthodoxy must collapse" [17]. There exist promoter and terminator sequences; upstream and downstream activating elements in transcribed or non-transcribed, translated or untranslated regions; leader sequences; externally and internally transcribed spacers before, between, and after structural genes; interspersed repetitive elements and tandemly repeated sequences

such as satellites, LINEs (long interspersed sequences) and SINEs (short interspersed sequences) of various classes and sizes. Given all the bewildering details of these elements, it comes as no surprise that their molecular function is still far from being fully understood [1, 18, 19]. "The excised intronic RNA, serving no apparent purpose, has been presumed to be degraded and recycled. But if introns do not code for protein, then why are they ubiquitous among eukaryotes yet absent in prokaryotes? Although introns constitute 95 percent or more of the average protein-coding gene in humans, most molecular biologists have considered them to be evolutionary leftovers, or junk" [17].

According to Mattick, "The genomes of complex organisms must also contain all of the information required to specify the timing, patterns, variations and amounts of expression of these components during development, and therefore must also program the overall design of the organism and individual variations. This is no trivial matter. Every cell in *C. elegans* has a defined ontogeny and fate, and this is likely to be true for most cells in animals, except those that clonally expand under (e.g.) immune pressure or nutritional conditions. Traditionally it has simply been assumed that the programming of animal and plant development is embedded in cis-acting control sequences (promoters and enhancers), which regulate gene expression in conjunction with various combinations of transacting proteins that relay environmental cues. This assumption is not necessarily correct. On the contrary, the massive amount of ncRNA that is expressed from the genomes of higher organisms, and the complex genetic phenomena that involve RNA, suggests that ncRNAs may constitute an endogenous control system that

regulates the programmed patterns of gene expression during their development" [20].

With the realization that junk DNA does have functional roles, the perception that coding DNA alone is important is rapidly changing. Eddy mentions at least nine classes of non-coding RNA genes [21]. He asks: "Could it be possible that a large class of genes has gone relatively undetected because they do not make proteins?" and concludes: "Non-coding RNA (ncRNA) genes produce functional RNA molecules rather than encoding proteins. However, almost all means of gene identification assume that genes encode proteins, so even in the era of complete genome sequences, ncRNA genes have been effectively invisible… Non-coding RNAs seem to be particularly abundant in roles that require highly specific nucleic acid recognition without complex catalysis, such as in directing post-transcriptional regulation of gene expression or in guiding RNA modifications." According to Mattick: "We may be witnessing such a turning point in our understanding of genetic information. …Proteins do play a role in the regulation of eukaryotic gene expression, yet a hidden, parallel regulatory system consisting of RNA that acts directly on DNA, RNAs and proteins is also at work. This overlooked RNA-signaling network may be what allows humans, for example, to achieve structural complexity far beyond anything seen in the unicellular world. Some molecular biologists are skeptical or even antagonistic toward these unorthodox ideas. But the theory may answer some long-standing riddles of development and evolution…" [17].

2.3 Limitations of the molecular gene

The operon model of Jacob and Monod marked the end

of the simple, informational concept of the molecular gene. By 1960, the picture of the gene expression has become highly complicated [1]. Based on the molecular definition, it should be possible to identify genes in the DNA sequence of a genome. Although five criteria are in use to identify the genes, their application has not been straightforward; besides, issues like overlap, alternative splicing, and pseudogenes are also involved [16]. "Pseudogenes are similar in sequence to normal genes, but they usually contain obvious disablements such as frameshifts or stop codons in the middle of coding domains. This prevents them from producing a functional product or having a detectable effect on the organism's phenotype…. The boundary between living and dead genes is often not sharp. A pseudogene in one individual can be functional in a different isolate of the same species… and so technically is a gene only in one strain…. there are other pseudogenes that have entire coding regions without obvious disablements but do not appear to be expressed…. Ultimately, we believe that identification of genes based solely on the human genome sequence, while possible in principle, will not be practical in the foreseeable future" [16].

The variations observed in the use of triplet codes among organisms still remain unexplained. The degenerate nature of the biological code implies several triplets coding per amino acid. Further, two amino acids have only one mRNA codon each; AUG for methionine and UGG for tryptophan. Hence 59 degenerate triplets code 18 amino acids; these 18 have two to six synonymous codons each. Choices between synonymous codons are not random; some codons in the set specific to an amino acid are

used more than the others [12]. The 'genome hypothesis' which tries to explain the variation in codon use states that codon use is species specific, i.e., each genome or type of genome shows a particular pattern of choices between synonymous codons. Thus overall codon usage differs between taxa; but codon bias is also influenced by other factors like gene length, gene expressivity (the amount of protein made per gene), environment and lifestyle of the organism [22]. The codon bias gives rise to the paradox whether protein evolution determined DNA sequence or DNA commanded protein evolution. Many such dilemmas remain in molecular evolution. The origin of bias in codon and anticodon frequencies continues to elude researchers [12]. A surprising pattern involves the clear inverse relation between G+C bias in synonymous codons and base substitution (mutation) rate at silent (synonymous or untranslated) sites in *Drosophila* genes [23].

There are many kinds of DNA repairs. Rosenfeld gives a detailed account of the self-healing strategies of the master molecule [24]. If a base is put in wrong place during replication, there are enzymes to correct the mistake. Purines, without any errors and without any damages drop out by the thousands every day presumably due to wear and tear of existence in the chromosomes only to be promptly replaced by insertases. A base can spontaneously undergo change. A cytosine, for example, will lose an amino group and become uracil. Uracil is perfectly at home in RNA but not in DNA. The enzymes called uracil glycosylases recognize the uracil, remove it and replace it with a new cytosine. Suppose that an error has occurred in one of the DNA strands say, a T has been put across from a G, where a C really belongs.

This would give rise to two strands one with a G and the other with a T. The enzymatic apparatus 'knows' that cannot be correct, but how does it know whether to replace the C with a T on one strand, or the C with an A on the other? If the replacement takes place not on the right strand, the result would be either death of the cell or a mutation. How does it know which is the authentic original? Rosenfeld gives a couple of explanations for the existence of a protective recognition system in the chromosomes [24]. But still the question of how a chemical structure (DNA) is *aware of* the change in its composition or how the wrong one is corrected remains a mystery.

In 1988 molecular biologist John Cairns and his colleagues at the Harvard School of Public Health reported induced mutations of various elements of the lac operon changes in *Escherichia coli* bacteria [25]. Their results showed that bacteria could induce specific mutations depending on their environmental conditions. Discussing the overall implications of these discoveries, Chicurel points out that the molecular biologists view the increased mutation rate as an engine of change as it generates diversity and that it did not evolve for the purpose of tuning evolution. But then most random mutations are harmful and how can it help the organisms survive overall? [26]. Existence of the built-in tendency to mutate by a chemical structure goes against the fundamental principles of chemistry. It is the kind of mutation whose name one dare not speak for fear of being guilty of heresy. Susan Rosenberg mentions the various names being used to describe the cell-directed mutagenesis. These are: adaptive, directed, Cairnsian, selection-induced, stationary-phase, stressful lifestyle-associated mutations

(SLAM), and even "Fred" which a researcher gave with the hope that it would not inflame critics. [27].

Even while treating DNA (a chemical molecule) as genetic program, the source and origin of biological information and how biological information can be superimposed on a chemical structure have not been addressed in science. It is just not possible to change a hemoglobin gene into an antibody gene based on chemical principles. "Dobhzhansky's view [is] that much of the variation needed to accomplish the transition *was already present* in the gene pool …(italics in the original)" [28]. The view that random changes in existing information can create new information is also wrong. This assumption implies that 'information' was already present in the gene pool just waiting to be changed. Where did that previous information come from? Presumably it came from modifying other existing information. But where did that existing information come from? As Jones put it: "Just the first 50 letters of the monocyte chemoattractant protein 1 receptor gene contains about 100 bits of information. That whole gene contains about 1166 bits of information. But that gene represents just 583 of the 3 billion base pairs in a single human DNA molecule. If you find a message that contains information, someone had to write it. Random chance does not produce information… an intelligent source must have put it there. There is no scientific evidence that even a small amount of information can be generated by chance. There is scientific evidence that random changes to a message can remove information. Mutations might remove information, but they will never create it. To believe that a DNA molecule evolved by chance, you have to reject science" [29].

References

1. Rheinberger, Hans-Jörg, Müller-Wille, Staffan, "Gene", *The Stanford Encyclopedia of Philosophy (Winter 2004 Edition)*, Edward N. Zalta (ed.), URL = http://plato.stanford.edu/archives/win2004/entries/gene/ Accessed 11 December 2005.

2. Johannsen, W. 1911. The genotype conception of heredity. *The American Naturalist* 45, 129-159.

3. Morgan, T. H. 1935. The relation of genetics to physiology and medicine. *Les prix Nobel en 1933*. Imprimerie Royale, Stockholm, 1-16.

4. Muller, H. J. 1951. The development of the gene theory. *In* Leslie C. Dunn (ed.), *Genetics in the 20th Century. Essays on the Progress of Genetics During its First 50 Years.* MacMillan, New York 1951, 77-99.

5. Falk, R. 2000. The gene – a concept in tension. *In* Peter Beurton, Raphael Falk, and Hans-Jörg Rheinberger (eds.), *The Concept of the Gene in Development and Evolution. Historical and Epistemological Perspectives*. Cambridge University Press, Cambridge, 317-348.

6. Benzer, S. 1962. The Fine Structure of the Gene. *Scientific American*, January, 1962 (reprint: p. 2); cited from: Craig Holdrege. 2005. The Gene: A Needed Revolution. *In Context* No.14 (Fall, 2005, pp. 14-17). http://natureinstitute.org/pub/ic/ic14/gene.htm Accessed 9-1-2006.

7. http://www.emc.maricopa.edu/faculty/farabee/BIOBK/BioBookPROTSYn.html Accessed 29-1-2006.

8. Crick, F. 1958. On protein synthesis. *Symposium of the Society of Experimental Biology* 12, 138-163.

9. Hood, L. and Galas, D. 2003. Digital code of DNA. *Nature* 421:444-448. Jan 23, 2003, issue. Doi:10.1038/nature 01410.

10. Brenner, S., Jacob, F. and Meselson, M. 1961. An unstable intermediate carrying information from genes to ribosomes for protein synthesis. *Nature* 190:576-581.

11. Crick, F.H.C., Barnette, L., Brenner, S. and Watts-Tobin, R.J. 1961. General nature of the genetic code for proteins. *Nature* 192:1227-1232.

12. Grantham, R.L. Codon usage in molecular evolution. doi: 10.1038/npg.els.0001806.

13. Jacob, F. 1976. *The Logic of Life. Vanguard,* New York., p. 297.

14. Keller, E. F. 2000. Decoding the genetic program: Or, some circular logic in the logic of circularity." *In* Peter Beurton, Raphael Falk, and Hans-Jörg Rheinberger (eds.), *The Concept of the Gene in Development and Evolution. Historical and Epistemological Perspectives.* Cambridge University Press, Cambridge: 159-177; cited from: Rheinberger, Hans-Jörg, Müller-Wille, Staffan, "Gene", *The Stanford Encyclopedia of Philosophy (Winter 2004 Edition)*, Edward N. Zalta (ed.), URL = <http://plato.stanford.edu/archives/win2004/entries/gene/>.

15. Waters, K. C. 1994. Genes made molecular. *Philosophy of Science* 61: 163-185.

16. Snyder, M. and Gerstein, M. 2003. Genomics: Defining genes in the genomics era. *Science* 300: 258- 260.

17. Mattick, J. S. 2004. The hidden genetic program of complex organisms. *Scientific American.* Oct 2004 issue, p. 60-67.

18. Fischer, E. P. 1995. How many genes has a human being? The

analytical limits of a complex concept. *In* E. P. Fischer and Sigmar Klose (eds.), *The Human Genome.* Piper, München, 223-256.

19. Rheinberger, Hans-Jörg. 2000. Gene concepts: Fragments from the perspective of molecular biology. *In* Peter Beurton, Raphael Falk, and Hans-Jörg Rheinberger (eds.), *The Concept of the Gene in Development and Evolution. Historical and Epistemological Perspectives.* Cambridge University Press, Cambridge: 219-239.

20. Mattick, J.S. 2003. Challenging the dogma: the hidden layer of non-protein-coding RNAs in complex organisms. *BioEssays* 25:930–939.

21. Eddy, S.R. 2001. Non-coding RNA genes and the modern RNA world. *Nature Reviews Genetics* 2(12): 919-929.

22. Grantham, R., Gautier, C., Gouy, M, Jacobzone, M. and Mercier, R. 1981. Codon catalog usage is a genome strategy modulated for gene expressivity. *Nucleic Acids Res.* 9: 43-47; cited from Grantham, R.L. Codon usage in molecular evolution. doi: 10.1038/npg.els.0001806.

23. Sharp, P.M. and Li, W-H. 1989. On the rate of DNA sequence evolution in Drosophila. *Journal of Molecular Evolution* 28: 398-402; cited from Grantham, R.L. Codon usage in molecular evolution. doi: 10.1038/npg.els.0001806.

24. Rosenfeld, A. 1981. Master molecule heal thyself. *Mosaic* 12(1).

25. Cairns, J., Overbaugh, J. and Miller, S. 1988. The origin of mutants. *Nature* 335: 142-145.

26. Chicurel, M. 2001. Can organisms speed their own evolution? *Science* 292(5523):1824-1827.

27. Rosenberg, S. M. 1997. Mutation for survival. *Genetics and*

Development 7(6):829-834.

28. Christopher Wills. *The Runaway Brain: The Evolution of Human Uniqueness*. New York:Basic Books, 1993, page 64; cited from: Do-While Jones http://www.ridgecrest. ca.us/~do_while/sage/v2i12f.htm Accessed on 11-6-2005.

29. Do-While Jones http://www.ridgecrest.ca.us/~do_while/sage/v2i12f.htm Accessed on 11-6-2005.

BLANK

3 THE GENE FIASCO

Molecular biology opened the floodgates of boundless optimism about the ability of the super molecule DNA to decipher the mechanism of life as well as the potential of gene for genetic manipulation. In his classic and influential textbook, *The Molecular Biology of the Gene*, James Watson stated: "We have complete confidence that further research of the intensity given to genetics will eventually provide man with the ability to describe with completeness the essential features that constitute life" [1]. But he was grossly wrong. Peter Cook at the University of Oxford, U.K., reflects: "Watson and Crick must have thought that the sequence was everything. But life is much more complicated than that" [2]. Instead of throwing more evidence in support of the particulate nature of the gene, molecular biology is now questioning the very concept. Writing in *In Context*, Craig Holdrege observes: "The complexity at the molecular level reveals that the simple mechanisms one imagined in the 1960s simply do not exist in that form. It has become less and less clear what a gene actually is and does. And although the deterministic gene is still the gene that lives in the minds of many students, lay people, and - at least as a desire - in the minds of many biologists, *the findings of late twentieth century genetics show one thing clearly: the simple deterministic gene, the foundational "atom" of biology is dead.* There is no clear-cut hereditary mechanism - no definite sequence of nitrogenous bases in a segment of a DNA molecule that determines the make-up and structure of proteins, which in turn determine a definite feature of an organism" [3, italics added].

The contemporary gene looks quite different from the gene of the 1960s. It has also become an indefinable entity!

3.1 The gene is indefinable

Biochemists Maxine Singer and Paul Berg defined the gene thus: "A [eukaryotic] gene is a combination of DNA segments that together constitute an expressible unit, expression leading to the formation of one or more specific functional gene products that may be either RNA molecules or polypeptides. The segments of a gene include (1) the transcribed region (the transcription unit), which encompasses the coding sequences, intervening sequences, any 5' leader and 3' trailer sequences that surround the ends of the coding sequences, and any regulatory segments included in the transcription unit, and (2) the regulatory sequences that flank the transcription unit and are required for specific expression" [4].

According to geneticist Peter Portin: "The gene is no longer a fixed point on the chromosome, producing a single messenger RNA. Rather, most eurkaryotic genes consist of split DNA sequences, often producing more than one mRNA by means of complex promoters and/or alternative splicing. Furthermore, DNA sequences are movable in certain respects, and proteins produced by a single gene are processed into their constituent parts. Moreover, in certain cases the primary transcript is edited before translation, using information from different genetic units and thereby demolishing the one-to-one correspondence between gene and messenger RNA. Finally, the occurrence of nested genes invalidates the simpler and earlier idea of the linear arrangement of genes in

the linkage group, and gene assembly similarly confutes the idea of a simple one-to-one correspondence between the gene as the unit of transmission and of genetic function...." [5].

Richard M. Burian, philosopher of science, remarks: "There is a fact of the matter about the structure of DNA, but there is no single fact of the matter about what the gene is. [Genetics today] provides strong, concrete support for the claim that the concept of the gene is open rather than closed with respect to both its reference potential and its reference" [6].

Scientists like Thomas Fogle and Michel Morange concede that there is no longer a precise definition of what could count as a gene [7, 8]. An important objective of genome projects is the identification of genes. Current estimates of human genes emanated from genome sequencing is 30,000–40,000, with occasional excursions to 100,000 or more. One reason for the continuing ambiguity is that genes are neither well defined nor easily recognizable [9]. Horace Freeland Judson writing in *Nature* notes: "The phrases current in genetics that most plainly do violence to understanding begin "*the gene for*": the gene for breast cancer, the gene for hypercholesterolaemia, the gene for schizophrenia, the gene for homosexuality, and so on. We know of course that there are no single genes for such things" [10]. The autocatalytic property once attributed to the gene as a unit has been relegated to the DNA at large as it can no longer be taken as specific for the gene as such [11]. Insofar as the process of DNA replication is not punctuated by the boundaries of coding regions, it is not surprising that many researchers are finding it harder to define

clear-cut properties of a gene as a heterocatalytic entity. It has become a matter of choice as to which sequence elements are to be included and which ones to be excluded. There have been different reactions to this situation [5, 7, 12, 13, 14]. A former MacArthur fellow and a professor of history and philosophy of science at MIT, Evelyn Fox Keller makes the case for a radically new thinking about the nature of heredity in her book *The Century of the Gene*. In her articulate and insightful history of genetics and molecular biology, she suggests that most of our common assumptions about genes are either too simplistic or simply incorrect. It turns out, for example, that a single functioning gene may be split and found in several locations on a chromosome, and it is rare that a gene can be determined to have caused any particular trait, characteristic or behavior. Keller argues that scientists have gained a great deal by refocusing their attention from individual genes to the concept of an integrated genetic program [15]. These facts notwithstanding, there is no visible change in the perception of gene as is evident from the research papers being published in this field. The term 'gene' finds its place in the same sense and contexts even in the so-called 'high impact' journals as before. Insofar as the very concept of particulate gene is wrong, what is the significance and relevance of studies based on the contemporary gene concept?

According to Hardison, "A complete genome sequence of an organism can be considered to be the ultimate genetic map, in the sense that the heritable characteristics are encoded within the DNA and that the order of all the nucleotides along each chromosome is known. However, knowledge of the DNA

sequence does not tell us directly how this genetic information leads to the observable traits and behaviors (phenotypes) that we want to understand" [16]. Ultimately, we want to understand the relationships between heritable units, and their phenotypes. But, it appears that genome concept would not deliver this information. The genome organization is extremely complex. Genes reside within one another, share some of their DNA sequences, are transcribed and spliced in complex patterns, and can overlap in function with other genes of the same sequence families. "Today, in the era of genomic sequencing and intense effort to identify sites of expression, the declared goal is to search for genes, entities assumed to have physical integrity. Ironically, the sharper resolving power of modern investigative tools make less clear what, exactly, is meant by a molecular gene, and therefore, how this goal will be realized and what it will mean", observes Fogle [7]. Geneticist William Gelbart writing on databases in genomic research notes: "For biological research, the twentieth century has arguably been the century of the gene. The central importance of the gene as a unity of inheritance and function has been crucial to our present understanding of many biological phenomena. Nonetheless, we may well have come to the point where the use of the term "gene" is of limited value and might in fact be *a hindrance to our understanding of the genome*. Although this may sound heretical, especially coming from a card-carrying geneticist, it reflects the fact that, unlike chromosomes, genes are not physical objects but are merely concepts that have acquired a great deal of historic baggage over the past decades" [17, emphasis added].

In one of the classical genetics papers presented in the International Congress of Plant Sciences held in August 1926, E.

M. East of Bussey Institute, Harvard University, stated: "Nearly fifteen years ago I attempted to defend the thesis that the Mendelian method of recording the facts of inheritance was simply a notation useful as a description of physiological facts. The argument was an elaboration of the proposition that the germ-cell unit of heredity, the gene, was an abstract, formless, characterless concept used for convenience in describing the results of breeding experiments….[He concluded] We arrive, therefore, at the same port from which we departed when our discussion began. The genes are units useful in concise descriptions of the phenomena of heredity. Their place of residence is the chromosomes. Their behavior brings about the observed facts of genetics. For the rest, what we know about them is merely an interpretation of crossover frequency. In terms of geometry, chemistry, physics or mechanics, we can give them no description whatever" [18]. Sadly, this holds true for the gene even after eighty years! The fact that DNA is involved in the synthesis of protein is no justification to treat the molecule as the genetic material. We have certainly enriched our knowledge about the roles of DNA in the biochemical activities of a cell, but that is no reason to say that this has increased our knowledge of heredity and the phenomenon of life. Even though the views presented are not explicit rejection of the particulate gene, all of them in one way or the other imply that particulate gene does not exist. This conclusion may sound heretical, but that is the truth albeit embarrassing to the scientific community.

3.2 The genome-genetic program incompatibility

Three elements namely, structural genes, regulatory genes, and signal sequences offered the framework for viewing the

genotype itself as an ordered, hierarchical system, as a 'genetic program'. The totality of DNA or the genome thus forms the genetic program. This perception bestows the genetic program a particulate existence. The peculiarity of this program is that it requires its own products for its execution [19]. The human genome has been labeled the "Book of Man" [20]. The particulate nature of the genetic program implies that millions of instructions and their sequences are the properties of the DNA structure. Although such a notion is nurtured to account for the phenomenon of life, non-correspondence of genomic identity with genetic program is becoming increasingly evident from several investigations. Results from several studies as well as certain observations do indicate that a chemical structure cannot form the genetic program. Some of these are:

a) Studies at the molecular level fail to demonstrate the expected correspondence between changes in genome structure and the changes in the organism in accordance with the Darwinian notion of descent with modification from a common ancestor. Evolution by DNA mutation is largely uncoupled from morphological evolution [21]. The most spectacular example of this is the morphological dissimilarity of humans and chimpanzees despite a 98.7% similarity in their DNA [22]. Although evolutionary biologists speak of genomes of chimp and man as being almost identical in support of their argument of human evolution from an animal, and for establishing chimpanzee as the closest animal ancestor of human being, they have not enumerated so far the phenotypic similarities between human and chimp in terms of anatomy, physiology, development and other biological features.

In fact there is none. A chimp is not 98% human being nor is a human being, 98% chimp (Fig. 3.1). The chimp has a head, a

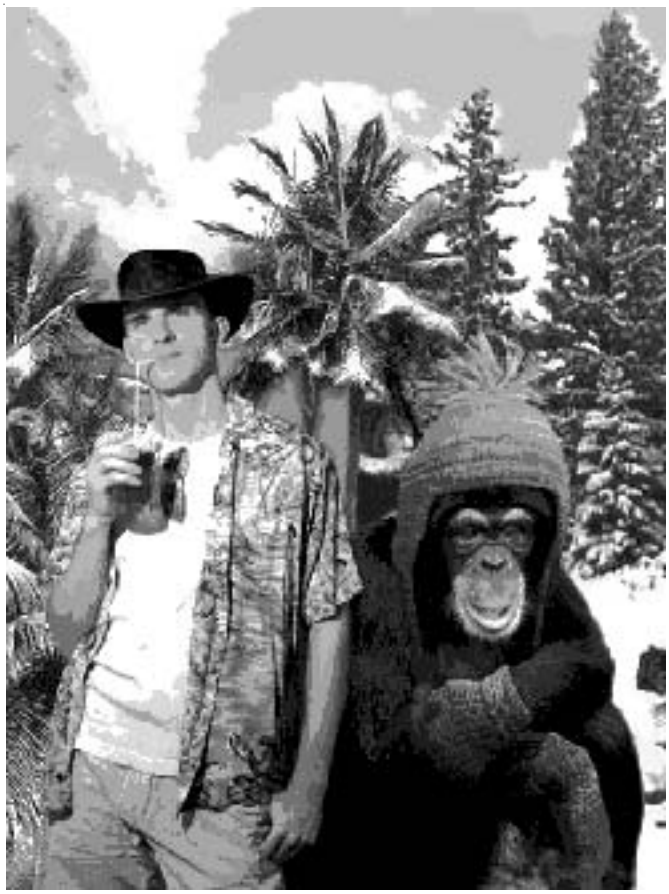

Fig. 3.1. The phenotypic contrast between man and chimp

Source: (2004) A DNA Recombination "Hotspot" in Humans Is Missing in Chimps. PLoS Biol 2(6): e192.

nose, two eyes and several other organs, which man has. The similarity ends there in the names of the organs and perhaps in their numbers as well. Many other animals also have these organs.

A human being differs from chimp in every detail and at every point of the body. The only similarity between chimp and man is in the DNA. The differences in traits, characteristic behaviour, instincts and capabilities between human (*Homo sapiens*) and chimpanzee (*Pan* sp.) are far greater than the small degree of sequence divergence (1.3%) could account for. Further, the human gene count is only 35,000 that is much less than that of simple creatures like the lowly worm (*Caenorhabditis elegans*). The chimp-human comparison is a case of similar genomes but dissimilar phenotypes. The reverse case is also known. *Caenorhabditis elegans* and *C. briggsae* are physically very similar organisms. It takes an expert to distinguish them. The two have near-identical biology, even down to the minutiae of developmental processes. Surprisingly, however, their genomes are not so similar [23; 24]. *C. elegans* has more than 700 chemoreceptor genes when *C. briggsae* gets on by just 430. There are also many genes unique to each of them [23]. Genome comparison of the *Wolbachia* endosymbiont, the obligate alpha-proteobacterial endosymbiont required for fertility and survival of the human filarial parasitic nematode *Brugia malayi*, with the *Wolbachia* endosymbiont of *Drosophila melanogaster* (*w*Mel) shows that they share similar metabolic trends, although their genomes show a high degree of genome shuffling [25]. "Typically when people say that the human genome contains 27,000 genes or so, they are referring to genes that code for proteins," points out Michel Georges, a geneticist at the University of Liège in Belgium. But even though that number is still tentative – estimates range from 20,000 to 40,000 – it seems to confirm that there is

no clear correspondence between the complexity of a species and the number of genes in its genome. "Fruit flies have fewer coding genes than roundworms, and rice plants have more than humans," notes Mattick [26].

The absence of a linear genome-phenotype relationship is very much evident from these studies. A peculiarity of the interpretations of the genome-phenome relationships is that wherever identical genomes do not produce identical phenotypes, such cases are invariably explained as due to environmental influence; but there is not a single case where the scientists, on reverse logic, interpret a case of similar phenotypes with dissimilar genomes as being due to environmental influence.

b) A genome is capable of producing two or more different biological systems even in the absence of mutation. Consider the insect world. We observe in the life cycle of an insect, stages or more correctly biosystems that are totally different and independent of each other. The larval and adult stages of a butterfly are two living systems which have nothing in common but are different in every respect, be it anatomical, physiological or functional (Fig. 3.2). They are self-sustaining biosystems in their own right,

Fig. 3.2. Larval (a) and adult (b) stages of a butterfly

produced from a single genome. The development of two morphologically, physiologically and functionally different systems from a single genome is tantamount to a chemical compound showing different properties under identical conditions at different points of time.

Development of an organism from zygote is the reflection of sequential execution of the instructions carried in the genetic program. Even after development, the biological system is changing continuously. We can conclude with certainty that the phenotype at any given time is not the same as it was a moment ago, although we cannot resolve such subtle changes. In the life of a human individual it is the same software that produces over time the child, the youth, and the old. Such temporal differences in properties cannot be attributed to a chemical structure. An infant cannot speak; but with time it develops that ability only to lose again in the old age. Reproductive ability is another example. Many such characters develop in an individual at certain times of life, stay for a pre-determined time, and then disappear. Assuming that it is a chemical structure - the genome – at work, it will be impossible to deduce that an individual can undergo all these phenotypic, developmental and functional variations. A chemical structure cannot vary its properties (or information) with time. The genome is therefore not the genetic program (software) of the living system. Cytological and functional variations in the tissues developed from the same genome present another proof against the genetic program-genome equivalence (Fig. 3.3). The functional diversity arising from genetic homogeneity is a paradox of the particulate gene concept. Every cell in our body originates from a single cell but our body is

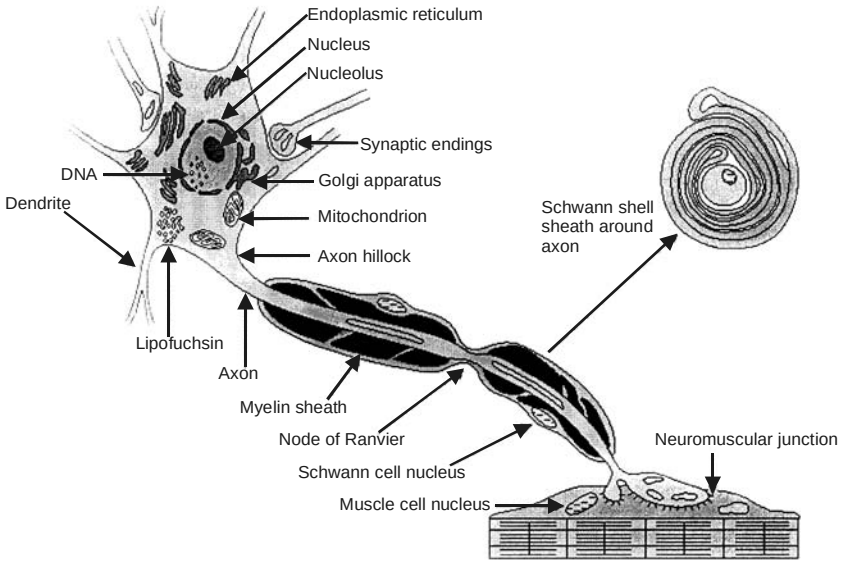

Fig. 3.3a The major components of a neuron

Source: Web-version of the book: Jaakko Malmivuo & Robert Plonsey: *Bioelectromagnetism - Principles and Applications of Bioelectric and Biomagnetic Fields*, Oxford University Press, New York, 1995.

composed of a myriad of radically different but genomically identical cells. The functional differences are explained at least partly by the epigenetic switches that regulate by turning the genes 'on' or 'off'. The epigenetic phenomenon is treated as environmentally mediated process. But this assumption is also wrong. Methylation patterns are specific and orchestrated during an organism's development, and are essential to an organism's vitality. For example, during embryonic development, the oocyte is demethlyated, then re-methylated during gastrulation; mutational loss of the enzymes that mediate this methylation process is fatal

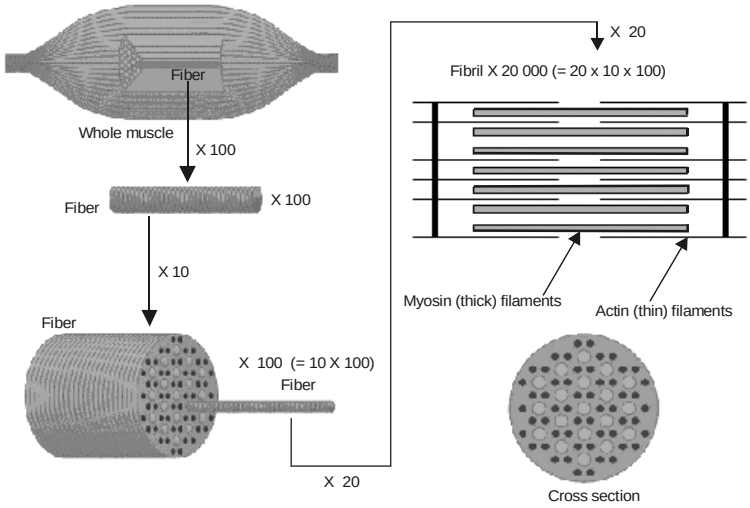

Fig. 3.3b. Anatomy of striated muscle

Source: Web-version of the book: Jaakko Malmivuo & Robert Plonsey: *Bioelectromagnetism - Principles and Applications of Bioelectric and Biomagnetic Fields*, Oxford University Press, New York, 1995.

to the developing embryo. DNA methylation is believed to be important in maintaining X-chromosome inactivation, which is a vital process that turns off one of the X-chromosomes in females and assures a proper balance of sex-linked gene transcripts [27]. To many, epigenetics is heresy as it calls into question the conventional view that DNA carries all our heritable information.

Biological information or the genetic program (software) for every activity (including epigenetic activity and any other hitherto unknown cellular function) from the moment of production of zygote to the death of the organism is available in the system and they come into operation according to the sequence and time

stipulated in the program. Thus we find actuation of the required cellular structures, production of certain chemicals (epigenetic), and even DNA mutation (cell-directed mutagenesis) taking place in the cell. All these constitute execution of the program by the cellular hardware. In this way independent existence of software and hardware can be recognized. It is the lack of distinction of these two components that led to the development of misleading concepts and terminologies in biological sciences. Phenotypic variability in space and time expressed by an organism cannot be viewed as the properties of the genomic structure.

The underlying assumption that the genetic program encoded in genome directs embryonic development has been seriously questioned by developmental biologists [28]. Goodwin noted that genes were responsible for determining which molecules an organism can produce but the molecular composition of organism does not in general determine their form [29]. In a critique of the notion of genetic program, Nijhout concluded that the only strictly correct view of the function of genes is that they supply cells, and ultimately organisms, with chemical materials [30].

c) Many insects exhibit alternative morphologies (polyphenisms) based on differential gene expression rather than genetic polymorphism (differences in genes themselves). One of the best understood insect polyphenisms is the queen-worker dimorphism in honey bees. Both the queens and the workers are females but morphologically distinct forms. Besides, the queen is fertile whereas the worker is sterile. Studies conducted with *Apis mellifera* revealed that numerous genes appeared to be differentially

expressed between the two castes [31]. The seven differentially expressed loci observed in the study belonged to at least five distinctly different functional groups. The queen and the worker castes in honey bee provide an unfailing proof of the natural existence of similar genomes exhibiting dissimilar phenotypes.

d) Besides, the ability of proteins to transmit information [32], "non-nucleic acid" or cytoplasmic inheritance [33], and epigenetic modifications [34] also go against the view of genomic monopoly as the sole carrier of genetic information.

The term 'epigenetics' literally means 'on genes' and refers to the stable alterations in gene expression that arise during development and cell proliferation without changing the DNA sequence. It acts as control system of 'switches' that turns the genes on or off. Epigenetics adds a whole new layer of information to genes beyond the DNA. The changes can be stable and passed on through mitotic cell divisions. DNA methylation, histone hypo-acetylation, chromatin modifications, X-inactivation, and imprinting are examples of epigenetic phenomenon. DNA exists in the cell in association with proteins called histones to form a complex substance known as chromatin. Chemical modifications to the DNA or the histones alter the structure of the chromatin without changing the nucleotide sequence of the DNA. Such modifications are referred to as epigenetic [35]. Changes to the structure of the chromatin influence the gene expression. If the chromatin is condensed, the factors involved in gene expression cannot get to the DNA, and the genes will be switched off. Conversely, if the chromatin is 'open', the genes can be switched on if required. This is achieved as follows. The long DNA strand with many

negative charges is wrapped around the positively charged 'histone cores' and as a result the attraction between the histone core and DNA is quite strong. Many histone cores wrapped with the DNA strand are strung together like a string of pearls; each 'pearl' in the string is a histone core with a certain length of DNA wrapped around it. Chromosomes consist of multiple strands of these strings of pearls. When a segment of DNA is tightly wound around a histone core, the genes present in that segment of DNA are locked up and not accessible. The DNA has to become slack for the genes to become accessible. When acetyl groups with negative charge are attached to the histone core, some of the positive charges of the histone core are neutralized by them, and the DNA strand is held less tightly. Removal of the acetyl groups render the histone core more positive, making it more tightly bound to the DNA strand. Addition of acetyl groups thus provides access to the genetic information on the DNA string and removal of acetyl groups makes the genes unavailable. There are two enzymes that do exactly this: an enzyme called 'HAT' adds acetyl groups (opening up the DNA/genes for consultation) and the other, called 'HDAC', removes acetyl groups (shutting off access to the DNA / genes) [36].

DNA methylation turns off gene expression (gene silencing). It is the best-understood example of stable epigenetic phenomena. Addition of methyl group to the cytosine residue of a CpG dinucleotide results in physical change of the chromatin that inhibits the expression of any genes in the methylated region. This inhibitory chromatin state is also passed on to daughter cells during cell division [37]. Methyl group acts as 'mark' to distinguish the

gene copy inherited from the father and that inherited from the mother. The mark tells the cell which copy to use to make proteins. These 'imprinted genes' do not obey traditional laws of Mendelian genetics, which describe the inheritance of traits as either dominant or recessive. The impact of an imprinted gene copy, however, depends only on which parent it was inherited from. For some imprinted genes, the cell only uses the copy from the mother to make proteins, and for others only that from the father. It is hypothesized that imprinting represents a genetic 'battle of the sexes' since many imprinted genes regulate embryonic growth. Maternally-expressed imprinted genes usually suppress growth, while paternally expressed genes usually enhance growth [38]. The epigenetic process is viewed as a phenomenon not governed by the genetic program. This assumption is an offshoot of particulate gene concept and is not correct.

e) About 95% of junk DNA in eukaryotes also has base sequences as in the coding DNA. Since the chemical principles of coding-DNA are applicable to noncoding-DNA also, it is surprising to see why certain portions of DNA do not encode protein.

The malaria parasite *Plasmodium falciparum* invades red blood cells and deposits the virulence factor PfEMP1 on their cell surface. This is how the parasite evades the immune system. PfEMP1 is encoded by a family of 60 *var* genes. However, only one of these is transcribed at any one time. How *Plasmodium* brings about this antigenic variation is not clear. Voss *et al*. showed that one active *var* promoter was sufficient to initiate the transcription of one gene while shutting off the others [39]. The paper reports 60 *var* genes for a single function. In other words,

the same information is repeated 60 times in the genome of the parasite! Take another example. *Pseudomonas syringae pv. Phaseolicola* causes Halo blight in bean plant. By simulating an outbreak, microbiologists Dawn Arnold and Andrew Pitman of the University of the West of England in Bristol, U.K., and colleagues studied how the bacteria evaded detection by the host. "Genetic analysis indicated that Halo blight was pulling a molecular disappearing act. Upon sensing the bean plant's response, the bacterium kicked out the portion of its genome responsible for making proteins that could be recognized by the plant. This DNA migrated to the cytoplasm, where it formed dormant circular strands… Curiously, the bacteria appear to work just fine without their banished genes, so it's unclear why they haven't dropped them for good." [40]. Here again the reference is to the information carried by the pathogen. The removal of a portion of the genome implies deletion of information from the genetic program. Expressed in terms of information, the results of both the studies question the particulate gene concept.

f) Apart from the non-correspondence of genomes and phenomes, lack of definable physical structure for the gene, non-specificity in gene expression (differential expression by the same gene as well as identical expression by different genes), etc., mentioned above, there are also a plethora of other scientifically valid observations that go against the genome-genetic program equation. It has not been possible to produce life from pure chemicals or culture the dead tissues. If a chemical structure encodes the genetic program, it would have been possible to produce life from it. A virus has either DNA or RNA but yet it is not a free-living organism. Growth and multiplication of the virus particle can occur only if it gets

hooked on to a living cell's DNA.

Notwithstanding any of these evidences, at the instant death occurs, DNA structure and genome in every cell of the body are in tact but still, the organism loses its life. Had genetic program been a property of a chemical structure, the structure would have continued to impart life to the system so long as it remained unchanged. The situation is tantamount to loss of properties of the chemical structure (genome), which is scientifically untenable. If it is the genome that confers life, death would not have occurred to the organism. The loss of 'life properties' of the genome at the time of death of an organism would perhaps form the most compelling evidence against genome-genetic program equivalence [41, 42].

To sum up, it may be stated that the role of DNA is restricted to the synthesis of proteins. This function alone is to be considered as the property of DNA and it is operating at the level of hardware in the living cell. A gene (a piece of DNA strand in the genome) thus shows its property as any other structure (hardware) in the cell does. What constitute a genetic program are the commands and instructions, their sequences and their timings (i.e., which hardware should come into action when) for developmental and post-developmental phases of the organism as well as information such as instincts, etc. These instructions and information which in fact form the software of the organism cannot be ascribed to a chemical structure. The scientific anomalies associated with the concept of genome raise the most important question: is life science on the right track?

3.3 Biology at the crossroads

In an excellent discussion of the present confusion about the gene, Fogle observed: "The reluctance to abandon the molecular gene, and instead, work around problems as they arise, erodes coherence. One may ask when told of a newly discovered molecular gene, "what kind? – one that produces a single product? multiple products? multiple products that have very different functions? functional isoforms? multiple products formed during transcription? or processing? or translation?…Neither the edges of the gene, its relationship to function, nor its biochemistry of expression are constants that can aid the formulation of a finely characterized molecular gene…A molecular gene is a coarse parameter for genomic analysis, poorly suited for the future growth of empirical results" [43].

The controversial particulate gene concept is likely to hit most such fields as molecular biology, biotechnology, genomics and bioinformatics. The results generated through molecular means become suspect and their interpretations meaningless. Since heritable changes are attributed to changes in DNA structure and the explanations are advanced based on this assumption, in the wake of particulate gene concept being questioned, what credibility can we give to genomic data? For instance, we will never be able to determine the gene count in humans or for that matter in any organism because of our inability to identify the particulate gene. We will continue to produce varying gene counts for the same reason. "Don't expect to know anytime soon exactly how many human genes there are. About 60% of our genes exhibit alternative splicing, making the number of protein products close to 100,000,

not a very different number from the more recent estimates… After all, the yeast (*Saccharomyces cerevisiae*) genome has been sequenced since 1996 and the precise number of genes is not yet confirmed. It is also useful to read the *Oxford English Dictionary's* definitions for genome and note the quotation from *Scientific American* Oct. 1970 "The human genome consists of perhaps as many as 10 million genes" [44]. The report of the Invitational DOE Workshop on Genome Informatics held in 1993 in Baltimore MD, pointed out that: "The concept of "gene" is perhaps even more resistant to unambiguous definition now than before the advent of molecular biology. Our inability to produce a single definition for "gene" has no adverse effect upon bench research, [is this true?] but it poses real challenges for the development of federated genome databases" [45]. A tutorial "Ontologies for Molecular Biology Workshop: Semantic Foundations for Molecular Biologies" at the Intelligent Systems for Molecular Biology Conference held in Montreal, noted: "Molecular biology has a communication problem. Many researchers and databases use (at least partially) idiosyncratic terms and concepts for representing biological information. Often, terms and definitions differ between groups, with different groups not infrequently using identical terms with different meanings. The concept 'gene', for example, is used with different semantics by the major international genomic databases" [46]. The situation may well demand that we reexamine how we are organizing data within genome-related databases. "In most or all of these databases, much biological data is attached to these suspect units called genes. Although some aspects of these phenotypes might be associated with different

subsets of alternative products of these genes, the databases might not support the most rigorous parsing of this phenotypic information" [47]. Sydney Brenner, writing in the special *Drosophila* genome issue of *Science* made a similar observation: "Old geneticists knew what they were talking about when they used the term "gene", but it seems to have become corrupted by modern genomics to mean any piece of expressed sequence…" [48].

Besides genome sequencing and bioinformatics, the anomalies and the fluid nature of the gene weaken the evolutionary theory also. It is hoped that major problems in evolutionary biology can be resolved when complete prokaryote and eukaryote genomes are available for comparative analysis [49]. Prof. J.A. Shapiro, a bacterial geneticist at the University of Chicago, U.S.A. remarks that our current knowledge of genetic change is fundamentally at variance with neo-Darwinist postulates. The view of Constant Genome, subject only to random, localized changes at a more or less constant mutation rate, has now changed to the Fluid Genome, subject to episodic, massive and non-random reorganizations capable of producing new functional architectures [50]. Discussing the problems encountered in evolutionary biology, Nevo observes that there are several questions like how much of coding and noncoding genome diversity (the latter comprising more than 95% in eukaryote) affects the twin evolutionary processes of adaptation and speciation, how much of this diversity in coding and particularly in noncoding genomes (junk DNA) contributes to regulation and differential fitness of organisms and is subjected to natural selection, what proportion of genic and nongenic diversity

is maintained in selection, and how much of the diversity in noncoding-DNA is adaptive and regulates gene expression, transcription, translation, recombination, and repair, to be resolved. The adaptive nature of noncoding genome is one of the most intriguing questions in evolutionary genetics [51].

Different rates of sequence evolution for mitochondrial and mammalian nuclear genes were also observed. In addition, different nuclear genes in the same *Drosophila* species evolved at different rates. This may be a disturbing finding for biologists used to thinking of natural selection as acting on the whole phenotype (individual) [52]. Then there is the built-in tendency of the cell to bring about genetic mutation (cell-directed mutagenesis). Elizabeth Pennisi's remarks on this phenomenon is noteworthy: "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….Whether by radically rearranging themselves making use of mobile elements to generate variation, or causing certain stretches of DNA to mutate at high rates, genomes are showing that they can help themselves cope with a changing environment" [53].

We are totally in the dark about the various coding genes and co-players involved in the production of new characters. It remains to be seen how evolutionists will cope with the new scenarios arising from the uncertainty of the particulate gene. The traditional explanations involving mutation of coding DNA followed by natural selection are too simplistic, trivial and inadequate to account for the evolution of new species. With the particulate gene concept becoming increasingly blurred by the day, Darwinism is in a quandary. It appears that the whole gamut of Darwinism needs to be re-examined. At the end of a century of genetic research and phenomenal advancement in molecular biology, we are still in an unenviable situation as far as our knowledge in biology is concerned. We find to our embarrassment that geneticists and molecular biologists do not know what a 'gene' is; evolutionists do not know what a 'species' is; and to top it all, biologists do not know what 'life' is! There is only one reason for all this tragedy – the mistaken identity of the genetic information!

3.4 A century of junk science

How does gene fiasco impact all of us? The picture that emerges from studies in molecular genetics not only questions the particulate nature of the so-called gene but also the assumption that individual gene exists. Since the genome concept is only an extension of the particulate gene concept, it implies that the genetic program of the organism exists in the form of a chemical structure. It appears strange that scientists use such terminologies as transcription, translation, etc., to indicate transfer of genetic information only when protein synthesis is discussed. Protein synthesis is just one of the myriads of biochemical processes taking

place in a living system. Every other biochemical process also has characteristic steps and sequences in which it is performed. Each step involves transfer of information (instructions) in the genetic program of the organism. However, none of these processes is described in terms of information transfer from one molecule to the other. Although conceptualization of protein synthesis as a process involving information transfer between DNA molecules is justifiable, the recognition of the physical gene and hence genome as the 'genetic program' has no basis at all. If the DNA molecule is genetic information, how does it control other biological processes remotely without directly getting involved in the process? Genetic program is the overall genetic information present in the organism which directs every biological activity from the cellular level to the organism level. Apart from its direct involvement in protein synthesis, DNA does not exhibit any extraordinary functional or developmental role and its elevation to the super molecule status of the gene can only be seen as the result of deliberate misinterpretation. This high-handedness of the molecular biologists has caused irreversible damage to the advancement of life science.

Over the past half a century molecular biologists have been taking the whole world for a ride by propagating this misconception of material gene (DNA) as truth. What has been said of Darwinism by Mooto Kimura in the 1980s also holds good for the contemporary gene: "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" [54].

In spite of all the limitations, there is no sign of giving up the particulate gene concept. Craig Holdrege observes: "The gene concept, I believe, is unlikely to be discarded, since it is far too deeply entrenched in the minds of scientists and the public. But we need to realize that the popular usage of the term, which still implicates the gene as the definitive causative agent in biology, simply does not coincide with biological reality…In other words, the gene is not a thing at all, but a way of ordering and interpreting phenomena. This may be surprising to anyone used to thinking about genes as concrete biological substances that make things happen. The gene as a robust "thing" is a figment in the materialist mind, a mind that can only conceive the world as governed by mindless material entities that (somehow) carry out meaningful processes. I do not want to suggest that the concept of the gene has no relation to material happenings. But the gene concept was not, in the first place, derived from engagement in the richness of hereditary phenomena. It was a pre-conceived notion that framed scientists' thinking and action. Experiments were designed with the gene concept in mind, and investigators then interpreted the results in terms of the particulate conception of inheritance they presupposed in the first place…. The gene is an abstraction - a product of a process of isolation, as neurologist Kurt Goldstein would have said - that has guided the development of genetics for over a century. The idea of a fundamental unit of inheritance, the idea of the grand mechanism that determines life, a mechanism that the human mind can fathom and eventually control, has fired the minds of modern geneticists. But the research itself - the

immersion in the phenomena mined from living organisms via experimentation - brings scientists and their concept of the gene to a boundary. It is a boundary one can ignore, as is largely the case in commercialized genetic engineering. It is a boundary that can stimulate scientists to tweak existing models to better fit experimental results. But it is also a boundary that can be felt existentially and become a stimulus for a mental and methodological revolution" [55].

The development of the particulate gene concept is not a success story but a case of manipulation of science to suit the materialist agenda. By projecting an exaggerated role for DNA in the scheme of life, molecular biologists have been trying to boost the overall image of secular science. The gambling has not paid off as expected but has cost us dearly. It created a large body of junk science. Ever since the discovery of the double helical structure of DNA, this molecule has assumed an iconic significance in biology. It has been dubbed as the molecule of the century, blue print of life and what not! The discoverers of DNA structure and a couple of others were also honoured by awarding Nobel Prize – all this to send the (wrong) message to the lay world that the mystery of the phenomenon called life has been unfolded. Ironically though, it is when the scientific community is celebrating the 50th anniversary of the discovery of the "blueprint of life", the biologists are realising their blunder. Molecular biolgists now think that gene expression is regulated by noncoding-DNA. With this unexpected turn of events, the long-ignored junk DNA is whirled into genetic limelight. Before long, the biologists will face the same problem with the noncoding-DNA as they faced with the coding-DNA.

They will ask the same question: what is triggering the noncoding-DNA into action? It will not come as surprise if more and more organelles and extranuclear structures of the cell are tagged on to the genetic bandwagon in a bid to explain the genetic program. But all these attempts will only repeat the cycle of failure. In spite of that, it still appears unlikely that biologists will ever give up the concept of particulate gene.

Recognition of junk DNA's functional role, to say the least, is tantamount to rewriting biology in general and genetics in particular. During the last half century or so, genetics has been coding-DNA, and coding-DNA has been genetics. The entry of noncoding-DNA into the province of gene would require overhauling of all our ideas about genetics that have been 'firmly' established in our minds and taught in the classrooms for generations. Already we have hundreds of explanations and glossaries generated by the particulate gene concept which while adding to the confusion also increase the volume of junk science. Over the years, hundreds of books have been written about genes and genomes, and thousands of research papers have been published implicating only coding-DNA in heredity. The scientific literature and databases so built have now turned out to be trash, a waste of effort, money and time. Looking back, one sees that what passed as genetics all these years has been 'scientific nonsense'. The fact that "the concept of gene has been changing so fast that most print resources (and some online) are out of date" [56] is something unprecedented in science. However, the writing on the wall is clear – particulate gene will not leave the textbooks, science curricula, and research programmes too soon

in spite of its non-currency and irrelevance. That is also a cause for concern. Sadly, it is the third world that is destined to pay the price for all the scientific vandalism and where junk science will stay for many years to come!

The magnitude of the impact of the new developments in genetic science is inestimable as it would not only influence the thinking in several disciplines of biology but also it would put the overall credibility of science in balance. Darwinism (or its modern variant 'synthetic theory') will have to face yet another handicap; it has to now explain how mutation of coding-DNA and the regulatory noncoding-DNA takes place simultaneously to bring about new changes in the phenotype. This might turn to be the death blow to the already reeling theory of evolution. The evolutionists have to do every explanation all over again in the light of these new developments. More over, the results of the human genome project and several such studies in other species have all become useless. A more arduous task of revising science curricula lies before us. Revamping genetic research is also on the cards. All these and more are reflected in the words of Gibbs, a senior writer in *Scientific American*: "This year biologists celebrated the 50th anniversary of the discovery of the double helix, and the Human Genome Project announced its completion of a "final draft" of the DNA sequence for *Homo sapiens*. Scientists have clearly mastered DNA in the lab. Yet as they compare the DNA of distantly related species and look more closely at how chromosomes function in living cells, they are increasingly noticing effects that current theories cannot explain. Journals and

conferences have been buzzing with new evidence that contradicts conventional notions that genes, those sections of DNA that encode proteins, are the sole mainspring of heredity and the complete blueprint for all life….It will take years, perhaps decades, to construct a detailed theory that explains how DNA, RNA and the epigenetic machinery all fit into an interlocking, self-regulating system. But there is no longer any doubt that a new theory is needed to replace the central dogma that has been the foundation of molecular genetics and biotechnology since the 1950s" [57].

References

1. Watson, J. 1973. *The Molecular Biology of the Gene*, third edition. Menlo Park, California: The Benjamin/Cummings Publ. Co.
2. Pearson, H. 2003. DNA: Beyond the double helix. *Nature* 421: 310-312.
3. Craig Holdrege. 2005. The Gene: A Needed Revolution. *In Context* No.14 (Fall, 2005, pp. 14-17). http://natureinstitute.org/pub/ic/ic14/gene.htm Accessed 9-1-2006.
4. Singer, M. and Berg. P. 1991. *Genes and Genomes: A Changing Perspective*. Mill Valley: University Science Books, p. 622.
5. Portin, P. 1993. The Concept of the Gene: Short History and Present Status, *The Quarterly Review of Biology* vol. 68, pp. 173-223.
6. Burian, R. M. 1985. On Conceptual Change in Biology: The Case of the Gene. *In* Depew, D. J. and B. H. Weber (Eds.) *Evolution at a Crossroads: The New Biology and the New*

Philosophy of Science, Cambridge: MIT Press, pp. 21-42.

7. Fogle, T. 2000. The dissolution of protein coding genes in molecular biology. *In* Peter Beurton, Raphael Falk, and Hans-Jörg Rheinberger, *The Concept of the Gene in Development and Evolution. Historical and Epistemological Perspectives.* Cambridge University Press, Cambridge, pp. 3-25.
8. Morange, M. 2000. The developmental gene concept: History and limits. *In* Peter Beurton, Raphael Falk, and Hans-Jörg Rheinberger (eds.), *The Concept of the Gene in Development and Evolution. Historical and Epistemological Perspectives.* Cambridge University Press, Cambridge, pp.193-215.
9. Eddy, S.R. 2001. Non-coding RNA genes and the modern RNA world. *Nature Reviews Genetics* 2(12): 919-929.
10. Judson, H. F. 2001. Talking about the genome. *Nature* 409: 769, 15 Feb. 2001; cited from: Gene definitions. http://www.genomicglossaries.com/content/gene_def.asp Accessed 8 October 2005.
11. Falk, R. 2000. The gene – a concept in tension. *In* Peter Beurton, Raphael Falk, and Hans-Jörg Rheinberger (eds.), *The Concept of the Gene in Development and Evolution. Historical and Epistemological Perspectives.* Cambridge University Press, Cambridge, pp. 317-348.
12. Kitcher, P. 1982. Genes. *British Journal for the Philosophy of Science* 33:337-359.
13. Gros, F. 1991. *Les secrets du gène. Nouvelle édition revue et augmeentée*, Editions Odile Jacob, Paris.

14. Morange, M. 1998. *La part des gènes.* Odile Jacob, Paris.
15. Keller, E. F. 2002. *The Century of the Gene.* Harvard University Press. http:/www.scienceandreligionbookstore.org/book_details.asp?book_id=1231 Accessed 11-6-2005.
16. Hardison RC (2003) Comparative Genomics. *PLoS Biol* 1(2): e58.
17. Gelbart, William. 1998. Databases in Genomic Research. *Science* 282:659-661. Cited from: Gene definitions. http://www.genomicglossaries.com/content/gene_def.asp Accessed 8 October 2005.
18. East, E. M. 1929 The concept of the gene. *Proceedings of the International Congress of Plant Sciences, Ithaca New York, August 16–23, 1926,* vol. 1. Menasha, WI: George Banta Publishing Co. pp. 889–895.
19. Jacob, F. 1976. *The Logic of Life. Vanguard,* New York.
20. Nelkin, D. and Lindee, M.S. 1995. *The DNA Mystique: The Gene as a Cultural Icon*. Freeman, New York.
21. Raff, R.A. and Kaufman, T.C. 1983. *Embryos, Genes and Evolution*. Macmillan, New York.
22. Wells, J. 2001. Homology in Biology: A Problem for Naturalistic Science. By Jonathan Wells, Dept. of Molecular and Cell Biology, Univ. of California, Berkely, California, USA; HYPERLINK "http://www.trueorigin.org/homology. asp" http://www.trueorigin.org/homology.asp dated 24/11/2001.
23. Blaxter, M. 2003. Two worms are better than one. *Nature* 426:395-396.
24. Stein, L. *et al*., 2003. *PLoS Biol.* 1:166-192.
25. Foster J, Ganatra M, Kamal I, Ware J, Makarova K, et al.

(2005) The *Wolbachia* Genome of *Brugia malayi:* Endosymbiont Evolution within a Human Pathogenic Nematode. *PLoS Biol* 3(4): e121.

26. Gibbs, W.W. 2003. The unseen genome: Gems among the junk. *Scientific American*, 289(5):46-53, November 2003 issue.
27. Epigenetics By: Andrew Hughes. http://cnx.org/content/m11532/latest/ Accessed 26-2-2006.
28. Hall, B. 1992. *Evolutionary Developmental Biology*. Chapman & Hall, London.
29. Goodwin, B.C. 1985. What are the causes of morphogenesis? *Bioessays* 3: 32-36.
30. Nijhout, H. F. 1990. Metaphores and the role of genes in development. *Bioessays* 12: 441-446.
31. Evans, J.D. and Wheeler, D.E. 1999. Differential gene expression between developing queens and workers in the honeybee, *Apis mellifera*. *Proc. Natl. Acad. Sci. USA*. 96:5575-5580.
32. Legname, G. *et al.* 2004. *Science* 305:673-676; cited from: Helen Pelcher. 2004. Lab-made prions trigger mad cow symptoms. *Nature News*, 29 July 2004; doi:10.1038/news040726-11.
33. Beisson, J. and Sonneborn, T.M. 1965. Cytoplasmic inheritance of the organization of the cell cortex in *Paramecium aurelia*. *Proc. Natl. Acad. Sci. USA.* 53: 275-282.
34. Meyer, P. Gene silencing in plants. doi:10.1038/npg.els.002022.
35. Epigenetics. http://www.wellcome.ac.uk/en/genome/thegenome/hg02b002.html Accessed 26-2-2006.

36. Epigenetics by Chaya Venkat. http://clltopics.org/CellBio/Epigenetics.htm Accessed 26-2-2006.

37. Epigenetics By: Andrew Hughes. http://cnx.org/content/m11532/latest/ Accessed 26-2-2006.

38. http://www.hopkinsmedicine.org/press/2002/November/epigenetics.htm Accessed 26-2-2006.

39. Voss, T.S. *et al*. 2006. A *var* gene promoter controls allelic exclusion of virulence genes in *Plasmodium falciparum* malaria. *Nature* 439 (7079), doi:10.1038/nature04407.

40. Amy R. Coombs. 2005. Out, Out Damn Gene! *Science*NOW Daily News, 19 December 2005.

41. Wahid, P.A. 1998. *The Divine Expert System*, Centre for Studies on Science, MAAS, Aligarh, India.

42. Wahid, P.A. 2003. Definitions of life, death, genetic program and soul based on the Quran and computer concept of the universe. *J. Islamic Sci.* 18(1-2):137-147.

43. Fogle, T. 2000. The dissolution of protein coding genes in molecular biology. *In* Peter Beurton, Raphael Falk, and Hans-Jörg Rheinberger, *The Concept of the Gene in Development and Evolution. Historical and Epistemological Perspectives.* Cambridge University Press, Cambridge, pp. 3-25.

44. Gelbart, W. 1998. Databases in Genomic Research. *Science* 282:659-661. Cited from: Gene definitions. http://www.genomicglossaries.com/content/gene_def.asp Accessed 8 October 2005.

45. http://www.genomicglossaries.com/content/gene_def.asp Accessed 8 October 2005.

46. http://www.ornl.gov/hgmis/publicat/miscpubs/bioinfo/infrep2.html ; cited from: Gene definitions. http://www.genomicglossaries.com/content/gene_def.asp Accessed 8 October 2005.

47. http://www-lbit.iro.umontreal.ca/ISMB98/anglais/ontology.html ; cited from: Gene definitions.http:www.genomicglossaries.com/content/gene_def.asp Accessed 8 October 2005.

48. Brenner, S. 2000. The end of the beginning. *Science* 287 (5451): 2173, Mar. 24, 2000 Cited from: Gene definitions. http://www.genomicglossaries.com/content/gene_def.asp Accessed 8 October 2005.

49. Karlin,s., Campbell, A.M. and Mrazek, J. 1998. *Annu. Rev. Genet.* 32:185-225; cited from: Nevo, E. 2001. Evolution of genome-phenome diversity under environmental stress. *Proc. Natl. Acad. Sci. USA* 98(11):6233-6240.

50. Shapiro, J.A. 1997. A third way. *Boston Review* 22(1):32-33.].

51. Nevo, E. 2001. Evolution of genome-phenome diversity under environmental stress. *Proc. Natl. Acad. Sci. USA* 98(11):6233-6240.

52. Grantham, R.L. Codon usage in molecular evolution. doi: 10.1038/npg.els.0001806.

53. Pennisi, E. 1998. How the genome readies itself for evolution. *Science* 281(5380):1131-1134.

54. Kimura, M. 1983. *The Neutral Theory of Molecular Evolution.* Cambridge University Press, p.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, University of Chicago Press, 1994.

55. Craig Holdrege. 2005. The Gene: A Needed Revolution. *In Context* No.14 (Fall, 2005, pp. 14-17). http://natureinstitute.org/pub/ic/ic14/gene.htm Accessed 9-1-2006.
56. Brenner, S. 2000. The end of the beginning. *Science* 287 (5451): 2173, Mar. 24, 2000 Cited from: Gene definitions. http://www.genomicglossaries.com/content/gene_def.asp Accessed 8 October 2005.
57. Gibbs, W.W. 2003. The unseen genome: Gems among the junk. *Scientific American*, 289(5):46-53, November 2003 issue.

4 THE PHENOMENON OF LIFE

How to define 'life' is a sweeping question that affects whole branches of biology, biochemistry and genetics. Carol Cleland opines that it is a mistake to try to define 'life' [1]. Nevertheless, life has been described, but not defined, in terms of the properties or attributes of a living being as given below.

a) "Living things tend to be complex and highly organized. They have the ability to take in energy from the environment and transform it for growth and reproduction. Organisms tend toward homeostasis: an equilibrium of parameters that define their environment. Living creatures respond, and their stimulation fosters a reaction-like motion, recoil, and in advanced forms, learning. Life is reproductive, as some kind of copying is needed for evolution to take hold through a population's mutations and natural selection. To grow and develop, living creatures need foremost to be consumers, since growth includes changing biomass, creating new individuals and the shedding of waste. To qualify as a living thing, a creature must meet some variation for all these criteria. For example a crystal can grow, reach equilibrium, and even move in response to stimuli, but lacks what commonly would be thought of as a biological nervous system" [1].

b) Five basic characteristics are used to describe life namely, evidence of growth and replication, evidence of purposeful energy transfer, response to stimuli, self-preservation, and significant difference from the surrounding environment, although difficulties are faced in its implementation [2].

c) "Living beings are systems that have three simultaneous features: they are self-supported, they reproduce themselves and they evolve through interaction with the environment" [3].

d) "Life is a chemical system able to replicate itself through autocatalysis and to make mistakes that gradually increase the efficiency of the autocatalysis" [3].

e) "Living beings are protein-made bodies formed by one or more cells that communicate with the environment through information transfer carried out by electric impulses or chemical substances, and capable of morphological evolution and metabolism, growth and reproduction" [3].

f) "Life is a self-sustained chemical system capable of undergoing Darwinian evolution" [4].

g) "The property or quality that distinguishes living organisms from dead organisms and inanimate matter, manifested in functions such as metabolism, growth, reproduction, and response to stimuli or adaptation to the environment originating from within the organism" [5].

None of the above definitions characterizes the phenomenon of life but only indicates its manifestations. All the experiments hitherto conducted on the origin of life show that life can arise only from life. Chemists have been able to make complex organic molecules such as proteins, amino acids, DNA, RNA and other complex building blocks of life in the laboratory but no one has been able to synthesize a cell or put together simple structures such as mitochondria or choloroplasts from its constituents [6]. According to Cleland and Chyba, "there is no broadly accepted definition of 'life'. Suggested definitions face

problems, often in the form of robust counter-examples. Here we use insights from physiological investigations into the language to argue that defining 'life' currently poses a dilemma analogous to that faced by those hoping to define 'water' before the existence of molecular theory. In the absence of an analogous theory of the nature of living systems, interminable controversy over the definition of life is inescapable" [7]. Added to that Darwin, while formulating his theory of origin of species, was conspicuously silent about definition and origin of life.

The lack of knowledge of the true nature of life has undoubtedly disabled us to understand what a species is. The problem of defining 'species' has been recognized since Linnean time. The term 'species' means different things to different people and it will continue to be so in the future also as there is no indication of a meaningful concept in sight. This leads to a very complicated situation in the field of evolutionary biology because species is the unit of evolution.

There are many definitions for species. Some of these are: 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. [8]. It is an irony that biologists have not been successful in advancing a unifying concept of species as yet. But then Darwin himself did not know what a 'species' was, when he talked about how they evolved! The situation is very much similar to that of the gene. The geneticists and molecular biologists do not know what

the gene is when they talk about it. Darwin comments about species in *The Origin of Species* thus:

a) "… 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 fluctuating forms. The term variety, again, in comparison with mere individual differences, is also applied arbitrarily, and for mere convenience sake" [9, p. 46; emphasis added].

b) "No one definition has as yet satisfied all naturalists; yet every naturalist knows *vaguely* what he means when he speaks of a species" [9, p. 39; emphasis added].

c) "Certainly *no clear line of demarcation has as yet been drawn between species and sub-species* that is, the form which in the opinion of some naturalists come very near to, but do not quite arrive at the rank of species; species also is a vague form, or again, between sub-species and well marked varieties, or between lesser varieties and individual differences" [9, p. 45; emphasis added].

It is important to note that the so-called genealogy of a species changes depending on how it is identified and described. As already discussed, comparison of genome is plagued by the uncertainty of the material gene. This would mean that phylogeny based on molecular methods is also vague. Further the lack of satisfactory genome-phenome correspondence also makes identification of species highly subjective. All these indicate that the ill-defined species can make Darwinism-based evolutionary theories ridiculous because depending on the method adopted,

the placement of a species on the evolutionary tree can change. As rightly pointed out by Graybeal, to try and divide all organisms into 'species' using one of today's concepts, is misguided because the important characteristics used to define species, interbreeding and descent, are only variably attained by groups of individuals which one might call species [10].

4.1 Origin of life

The concepts of molecular gene and genome (genetic program) imply a chemical origin of life. In other words life originated from non-life. According to Davies and Joyce, "there is nothing in physics that says that matter has got to become living. I think the question has been sidestepped for a hundred years by chemists who think in terms of the "recipe" - that you can make life by mixing a bit of this and a bit of that and stirring. But from the point of view of the physicist, what's important about life is not the "stuff", it's the information processing…. Saying that we form all the molecules that we find in our body from chemistry is as ridiculous as saying that we took all the components of a watch and they all fell in a heap and made a watch and it suddenly started ticking. I'm not arguing for creationism here - what creationists fail to realize is that nobody in their right mind is suggesting that life in all its complexity would form in one great leap. But we do have to find a path from physics and chemistry into life" [11]. The view reflects a psychological bias for favouring the material foundation of life, at the same time an inner feeling that it is not.

There are essentially two theories (better called hypotheses) about the origin of life namely, spontaneous origin of life on the earth from primitive self-replicating macromolecules

acted upon by natural selection, and extraterrestrial origin (panspermia) through meteor, comet borne from elsewhere in universe [5].

Spontaneous origin: Several theories have been advanced to explain the origin of life; the most popular being 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 [12]. 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 [12]. 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 [12].

All attempts to assemble an integrated scheme of physicochemical processes have significant weaknesses [13]. 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 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 [13]. 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 [14]. Mineral-catalyzed reactions, followed by a series of fractionations, would offer the most plausible route to RNA [15, 16].

According to Smith *et al*. [17], 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 [1]. Francis Crick (Nobel laureate) once wrote: "An honest man, armed with all the knowledge available to us now, could only state that in some sense, the origin of life appears

at the moment to be almost a miracle, so many are the conditions which would have had to have been satisfied to get it going" [18]. In spite of that evolutionists maintain that life originated accidentally from inanimate matter.

Panspermia theory: The idea that life originated on its own on this planet in continuation of the inorganic evolution received a jolt when, in 1973, Francis Crick and L. Orgel proposed a new theory called the "directed panspermia" [19]. 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) [20]. Nevertheless, there has been no evidence whatsoever to suggest that there is life anywhere else in this universe except on the planet earth.

Much of what is reported about origin of life in scientific literature is purely conjectural. The theories of terrestrial origin of life, which are rooted in the idea of primordial soup, are products of thought experiments. Practically no effort has been made to

explain the origin of biological information in the prebiotic environment that is vital for the biological evolution. Instead, life is still supposed to have originated from non-life.

4.2 Organism as information processor

Biology provides the most sophisticated organization of matter, often spanning more than 24 orders of magnitude from component molecules (0.1 attograms) to entire organism (100 kilograms) [21]. According to Rothemund *et al.*: "This organization is information-based: DNA sequences refined by evolution encode both the components and the processes that guide their development into an organism – the developmental program. For a language to describe this carefully orchestrated organization, it is tempting to turn to computer science, where the concepts of programming languages, data structures, and algorithms are used to specify complex organization of information and behavior" [21]. Using two-dimensional self-assembly of DNA tiles, they reported the molecular realization of a cellular automaton, a fabrication of a fractal pattern – a Sierpinski triangle. Although imperfect, it was claimed that the growth of Sierpinski triangles demonstrated all the necessary mechanisms for the molecular implementation of arbitrary cellular automata. This shows that engineered DNA self-assembly can be treated as a Turing-universal biomolecular system, capable of implementing any desired algorithm for computation or construction tasks [21].

To biologists, an organism is a bundle of chemical atoms and molecules. Arthur D. Lander, Chair of the Department of Developmental and Cell Biology and Director of the Center for

Complex Biological Systems at the University of California at Irvine, observes: "As a group, molecular biologists shy away from teleological matters, perhaps because early attitudes in molecular biology were shaped by physicists and chemists. Even geneticists rigorously define function not in terms of the useful things a gene does, but by what happens when the gene is altered. Molecular biology and molecular genetics might continue to dodge teleological issues…. Mechanistic information about how a multitude of genes and gene products act and interact is now being gathered so rapidly that our inability to synthesize such information into a coherent whole is becoming more and more frustrating. Gene regulation, intracellular signaling pathways, metabolic networks, developmental programs – the current information deluge is revealing these systems to be so complex that molecular biologists are forced to wrestle with an overtly teleological question: What purpose does all this complexity serve?" [22]. Scientists often seem to invoke the term 'emergence' to find explanation to an otherwise unexplainable phenomenon. This term is used to explain any new properties (properties that are absent from the constituents of the system) that arise when a system exceeds a certain level of size or complexity. It is a concept often summed up by the phrase that "the whole is greater than the sum of its parts," and it is a key concept in the burgeoning field of complexity science. Life is often cited as a classic example of an emergent phenomenon: "no atoms of my body are living, yet I am living" [23].

In the words of Davies: "All organisms are information processors: they store a genetic database and replicate

it….Biological molecules serve two distinct roles: (i) specialized chemicals, (ii) informational molecules. This reflects the underlying dualism of phenotype/genotype. Using the analogy of computing, chemistry corresponds to hardware, information to software. A full understanding of the origin and function of life requires the elucidation of both the hardware and software aspects. Studies of biogenesis have tended to focus on chemistry (i.e., hardware), by attempting to discover a chemical pathway from non-life to life" [24]. 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 [25]. 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) [26, 27].

4.3 Is life an intangible phenomenon?

The current perception of genetic program is inextricably woven into the idea of material gene. Adherence to the wrong notion that genetic information is constituted by physical material has virtually taken biology to a blind alley. Phenomena of 'life' and 'species' have defied definition on account of this. Chemical principles which explain the nature and behaviour of non-living matter are distorted to explain living things also. Thus a chemical structure that carries a particular chemical information is assumed to contain biological information also when it resides inside a living cell and only chemical information when it lies outside the living

cell. This perception is absurd because it does not explain in the first place the source of biological information and secondly how a chemical structure (e.g., DNA) can behave differently depending on its place of occurrence. Concept of particulate gene thus led to the belief that life originated from inanimate matter.

Peter Beurton, Raphael Falk and Hans-Jörg Rheinsberger discuss at length the contemporary gene scenario: "The more molecular biologists learn about genes, the less sure they seem to become of what a gene really is. Knowledge about the structure and functioning of genes abounds, but also, the gene has become *curiously intangible*. Now it seems that a cell's enzymes are capable of actively manipulating DNA to do this or that. A genome consists largely of semistable genetic elements that may be rearranged or even moved around in the genome thus modifying the information content of DNA. Bits of DNA may be induced to share in the coding for different functional units in response to the organism's environment. All this makes a gene's demarcation largely dependent on the cell's regulatory apparatus. Rather than ultimate factors, genes begin to look like hardly definable temporary products of a cell's physiology. Often they have become amorphous entities of unclear existence ready to vanish into the genomic or developmental background at any time" [28, emphasis added]. Paul Griffiths and Eva Neumann-Held state: "[In the molecular gene concept] 'gene' denotes the recurring process that leads to the *temporally and spatially regulated expression* of a particular polypeptide product. The gene is identified not with these DNA sequences alone but rather with a process in

whose context these sequences take on a definite meaning" [29, emphasis added]. These two statements are particularly noteworthy because they give a hint of the intangible nature of the gene *whose expression is temporally and spacially regulated.* Keller's argument of an integrated genetic program in place of individual genes [30] appears to be more realistic. All these observations indirectly support the view that the genetic program is the intangible software, and the DNA, a hardware component in the biological machinery. The notion of individual particulate genes should be dispensed with and the whole genetic program must be seen as coherent integrated software that drives all the biological activities and the one which is responsible for all the features of an organism. This proposal goes well with Johannsen's original concept of non-particulate gene [31].

There are two options before us; one is to continue research ignoring the failure of century-long research efforts to identify and characterize the gene and at the same time assuming that there is gene, the gene is discrete, and it is of material nature. Going by the past experience, this will only help to generate more spurious explanations and worsen the situation. The second option is to discard the particulate gene concept *in toto* realizing the gene fiasco as the wake-up call for an inevitable change in our view about the genetic program. It directs us to treat biological information as intangible software stored in the living cell. This option would certainly be hard on the scientific community to whom anything intangible is irrational and superstitious. But this is a false notion to be corrected. It is the scientists' view that the universe is

completely corporeal and material that is irrational and nonfactual. There are several intangible non-physical phenomena in nature; for example, human consciousness, information storage in computer memory, to cite but a few. Instead of attempting to explain the non-material phenomena in abstract physical terms, scientists must accept such phenomena as entities beyond human perception and visibility. Basically a computer system consists of software and hardware components. In the computer jargon, the term 'software' describes the programs. A program is a set of instructions written in a suitable language in the proper sequence and is loaded into the memory of the computer for executing the task intended for. The software is thus the *unseen* component, which drives the computer to perform the task specified in it. The term 'hardware' describes all the visible components of a computer. The programs, data and information we store in the storage devices exist in the computer not in a perceptible form but in an intangible form. This is a proof of existence of intangible phenomenon in nature. An organism is also a (natural) computer system. Suppose that a computer machine was sent to the earth by some aliens before the advent of our computer technology. At that time we would not have the slightest inkling of what software was. Suppose that our scientists started studying the alien computer to elucidate its functional mechanism. In all probability they would not have discovered the intangible software stored in the memory devices of the computer. Instead they would have thought that the storage material itself encoded information. A similar thing is happening in the science of genetics now. With the arrival of the molecular gene concept; DNA (a biological hardware component) has been

mistaken for the genetic information (software). The biological role of DNA in protein synthesis is presently misconstrued as the genetic role. It is hard to understand how protein building machinery can be considered as the hereditary material as life is not just protein synthesis. Why then biologists took this strange view of characterizing the DNA as the molecule of life? It is something difficult to fathom. Perhaps because any assumption other than a material-based one is unthinkable in science in view of the likely divine underpinnings associated with it. As one definition of science states, it is "the study of the material universe or physical reality in order to understand it" [32] which is not only presumptuous but is also a pre-emptive one to rule out the intangible from the purview of science even if such phenomena exist in nature. The basic hypotheses of materialist philosophy are: first, all reality is essentially a material reality; second, no supernatural or immaterial reality can exist; and third, all organic life arises from and returns to inorganic matter [33]. The main disagreement of materialists is over the mind-brain problem, which has been the focus of the twentieth century materialist debate. The materialist philosophy rests on assumptions that are ultimately *meta*scientific, though never meta*physical* in the Aristotelian sense. That is, the assumptions of materialism reached *beyond* empirical science, though never beyond *physical reality*. Nature has no beginning or end. It is an eternal, self-generating and self-sustaining material fact without any sort of barrier or limit zoning it off from a nonmaterial, non-physical, or supernatural type of being. The only foundational being there was, was material being, and some kind of natural substance underlay all visible phenomena. These assumptions imply lack of

any governance or management of the universe by any sort of transcendental intelligence, and therefore materialism is implicitly atheistic. Materialism has always viewed atheism as merely a necessary consequence of its premises and not as a philosophically important end in itself. Supernatural gods, spiritual deities, or immaterial moralizers could obviously not be taken seriously, or for that matter even imagined to exist, in the materialist hypothesis [33]. Even mind has been viewed as material in the sense that: "if all matter were to be removed from the world, nothing would remain – no minds…." [34].

The materialists may argue on the basis of the hypothesis of property dualism that software in a computer has physical existence as it is stored on a medium. Property dualism holds that nonphysical *substances* or things do not exist, but that there are nonphysical *properties* of physical matter. For the property dualist, only physical substances exist, but these physical 'things' can have physical or nonphysical properties. Consciousness, it is argued, is a nonphysical property of the brain because it doesn't have properties commonly associated with physical phenomena (e.g. mass, shape, size, density, electric charge, temperature, position in space, etc.) [33]. But then the software (information) does not form the intrinsic property of the medium, because it can be removed from the medium without affecting the property of the physical medium on which it is stored. It is like our thoughts. Thoughts are created in human brain; and the brain has physical existence. Materialists may therefore argue that thoughts can also be explained on the basis of property dualism. The argument of

property dualism is not averse to characterization of an intangible phenomenon. Intangible phenomenon only means that it cannot be perceived by human senses or detected by man-made instruments. The recognition of the independent existence of biological information (i.e., it is not constituted by a chemical structure) is essential for explaining the phenomenon of life and evolution of biological species. This rationale calls for a revolutionary change in our perception of the genetic program (biological information) and the phenomenon of life. All the structures in the cell together constitute the hardware. The functioning of cell structures including DNA must be seen as executing the genetic program (the software) by the hardware. The continued failure of the particulate gene concept to account for the biological organization and system functioning does not justify defending it any longer. Genetic program must be viewed from a different angle, as the software of the biological system which exists in an intangible form in the cell independently of the material hardware. It is in this context, a religio-scientific dialogue between science and the Quran assumes a do-or-die significance and relevance.

References

1. Life's working definition: does it work? http://www.astrobio.net/news/article428.html Accessed April 6, 2005.
2. http://web.mit.edu/12.000/www/finalpresentation/science/life.html Accessed November 13, 2001.
3. Newton magazine (Italian version) June 2001 issue, in a report entitled "Segnali di Vita Aliena" (Signs of Alien Life); cited from: http://www.lifeinuniverse. org/noflash/lifedefinition-04-

01.html. Accessed November 13, 2001.

4. Joyce, G.F. 1994. *Origins of Life:The Central Concepts*, eds. Deamer, D.W. and Fleischaker, G.R. Jones & Bartlett, Boston, pp. xi-xii. cited from: Chyba, C.F. and Philips, C.B. 2001. Possible ecosystems and search for life on Europa. *Proc. Natl. Acad. Sci. USA* 98:801-804.
5. http://www.answers.com/topic/life Accessed 10-1-2006.
6. Bhandari, N. 1998. Life beyond earth. *Curr. Sci*. 75:991-994.
7. Cleland, C.E. abd Chyba, C.F. 2002. Defining life. *Origins of life and evolution of the biosphere* 32(4): 387-393.
8. EEOB 208: Process of Evolution. http://www.tulane.edu/~eeob/Courses/Heins/ Evolution/lecture6.html Tulane University, New Orleans, Louisiana. Accessed November 22, 2004.
9. Darwin, C. 1859. *The Origin of Species*. Bantam Books, New York (1999).
10. Graybeal, A. 1995. Naming species. *Syst. Biol*. 44:237-250. cited from Inskipp, T., Lindsey, N. and Duckworth, W. 1996. *An Annotated Checklist of the Birds of the Oriental Region*. Oriental Bird Club, Bedfordshire, U.K. pp. 3-6.
11. Davies, P. and Joyce, H. Life as we don't know it. [http://plus.maths.org/issue36/features/davies/ Accessed 21-12-05.
12. Wachtershauser, G. 1994. Life in a ligand sphere. *Proc. Natl. Acad. Sci. USA* 91:4283-4287.
13. Smith, J.V. 1998. Biochemical evolution I. Polymerization on internal, organophilic, silica surfaces of dealuminated zeolites and feldspars. *Proc. Natl. Acad. Sci. USA* 95:3370-3375.
14. Gilbert, W. 1986. *Nature* (London) 319:618; cited from Sowerby, *et al.* 2001. *Proc. Natl. Acad. Sci. USA* 98:820-822.

15. Boyce, G.E. and Orgel, L.E. 1993. *The RNA World*, eds. Gesteland, R.F. and Atkins, J.F. Cold Spring Harbor Lab. Press, Plainview, NY, pp. 1-25.
16. Parsons, I., Lee, M.R. and Smith, J.V. 1998. Biochemical evolution II: Origin of life in tubular microstructures on weathered feldspar surfaces. *Proc. Natl. Acad. Sci. USA* 95:15173-15176.
17. Smith, J.V., Arnold, F.P., Jr., Parsons, I. and Lee, M.R. 1999. Biochemical evolution III: Polymerization on organophilic, silica-rich surfaces, crystal-chemical modeling, formation of first cells, and biological clues. *Proc. Natl. Acad. Sci. USA* 96:3479-3485.
18. Crick, F. 1981. *Life Itself: Its Origin and Nature.* New York: Simon & Schuster, p. 88.
19. Crick, F.H.C. and Orgel, L.E. 1973. Directed panspermia. *Icarus* 19:341.
20. http://www.iscid.org/encyclopedia/panspermia Accessed June 7, 2004.
21. Rothemund PWK, Papadakis N, Winfree E (2004) Algorithmic Self-Assembly of DNA Sierpinski Triangles. *PLoS Biol* 2(12): e424.
22. Lander, A.D. 2004. A Calculus of Purpose. *PLoS Biol* 2(6): e164.
23. Morowitz, H.J. 2002. *The Emergence of Everything.* Oxford: Oxford University Press.
24. Davies, P.C.W. 2004. Does quantum mechanics play a non-trivial role in life? *BioSystems* 78:69–79.
25. Alberts, B., Bray, D., Lewis, J., Raff, M., Roberts, K. and Watson, J. D. 1994. *Molecular Biology of the Cell*, 3rd edn. Garland, New York.

26. Bray, D. 1990. Intracellular signaling as a parallel distributed process. *J. Theoret. Biol.* 143:215-231.

27. Gerhart, J. and Kirschner, M. 1997. *Cells, Embryos and Evolution: Toward a Cellular and Developmental Understanding of Phenotypic Variation and Evolutionary Adaptabiltiy.* Blackwell Science, Malden, Mass.

28. Beurton, Peter, J., Raphael Falk and Hans-Jörg Rheinsberger (Eds.) (2000). "Introduction," in *The Concept of the Gene in Development and Evolution*. Cambridge: Cambridge University Press, pp. ix-xiv.

29. Griffiths, Paul E. and Eva M. Neumann-Held (1999). "The Many Faces of the Gene," *BioScience* vol. 49, pp. 656-662.

30. Keller, E. F. 2002. *The Century of the Gene.* Harvard University Press. http://www.scienceandreligionbookstore.org/book_details.asp?book id=1231 Accessed 11-6-2005.

31. Johannsen, W. 1911. The genotype conception of heredity. *The American Naturalist* 45, 129-159.

32. http://www.biology-online.org/dictionary/science Accessed 20-12-05.

33. Richard C. Vitzthum. Philosophical Materialism. http://www.infidels.org/ library/modern/richardvitzthum/materialism.html Accessed 9-2-2005.

34. Jaegwon Kim "The Mind-Body Problem" in *The Oxford Companion to Philosophy* edited by Ted Honderich, p. 579; cited from: Richard C. Vitzthum. Philosophical Materialism. http://www.infidels.org/library/modern/richard_vitzthum/materialism.html Accessed 9-2-2005.

5 THE DIVINE UNIVERSAL SOFTWARE – THE SOURCE OF INFORMATION

The growing body of evidence discussed in the preceding sections warrants a re-look at the concept of genetic program. The work of Gilad *et al*. [1] shows that it is the similarities and differences in gene expression rather than genes themselves that are more important in defining species. Commenting on this work, Pennisi wrote: "On a genetic level, humans and apes are nearly identical, sharing between 96% and 99% of their DNA. So what makes us so different? … it comes down to where, when, and how vigorously these genes are expressed" [2]. The genetic program has to be redefined in terms of non-particulate software and the current particulate concept has to be done away with. The functioning of genome can be explained if it is treated as a hardware component of the cell executing the task under the direction of a software.

The need for independent existence of chemical information and biological (genetic) information in nature is not recognized in science. Although scientists acknowledge the presence of genetic information, they do not acknowledge the presence of chemical information. As a result, no one asks questions like why a hydrogen molecule behaves as it does or why water (H_2O) is a fire extinguisher when its constituents hydrogen and oxygen are highly inflammable? We know that atoms, molecules and substances have characteristic chemical structures and it is the structure of a substance that determines its properties. This leads to another question: how did they acquire their

structures? Did they decide their own structures and properties? These questions can be answered only if we accept the existence of chemical information. Nature is an information-laden system. It has both chemical and biological information distinctly different from each other.

The Quran distinguishes the nature of living and non-living components of the universe clearly. Based on the Quran and natural evidence, a computer model of the universe was proposed to understand the functioning of the universe [3, 4]. According to this concept, the origin of natural laws, properties of matter in relation to chemical structure, evolution and functioning of the physical universe and biological organisms, their interactions, modes of communication and interconnectivity, etc., can be traced to the existence of a divine software for the universe which may be referred to as the divine master program (DMP).

> ***"Allah does blot out (delete) or confirm (retain) what He pleases: with Him is the Mother of the Book."***
>
> ***(Q. 13:39)***
>
> ***"Nay, this is a Glorious Quran, (inscribed) in a Tablet Preserved."*** ***(Q. 85:21-22)***

The "Mother of the Book" (*Ummul kitab*) and "Tablet Preserved" (*Lohul mahfooz*) mentioned in the above verses may be referring to the divine knowledgebase which contains all kinds of software including the DMP. The DMP may be visualised as having composed of three subprograms namely, the Abioprogram, the Bioprogram and the Control Program. The Abioprogram (the source of chemical information) governs abiogenesis (origin of the inanimate world) and the characteristic properties of the inanimate

components while the Bioprogram (the source of biological information) governs biogenesis (origin of species) and the characteristic properties of the living matter. The Control Program is responsible for the co-ordination and control of the whole universe during its genesis as well as in the post-developmental stage. For a clear idea of the biological information, the origin of chemical information is also to be understood.

5.1 The Abioprogram (Chemical information)

The Quran tells us:

> ***"So He completed them as seven skies…and inspired in each sky its duty and command…"*** ***(Q. 41:12)***
>
> ***"And among His signs is this, that sky and earth stand by His command…"*** ***(Q. 30:25)***

These messages indicate that the divine instructions are immanent in the system itself. The mode of behaviour and functioning of the component systems of the universe are, therefore, governed by these programs (the commands mentioned in the Quran) coded in their structures. Each substance has an intrinsic chemical structure. This, in turn, confers specific properties to that material. We now know 118 elements [5] with one or more atomic species for each of them. An atomic species characterized by its nuclear constituents is called a nuclide. Each nuclide has a certain structure, which determines its physical and chemical properties. These nuclides can combine in numerous combinations obeying certain specific rules to produce a wide variety of substances each with a specific structure and properties of its own. How does this happen? Are the elements (or nuclides) intelligent entities to invent and decide their structures, properties and rules by themselves? This is one of

the most fundamental aspects of the working of the universe. The first task of science is, therefore, to explain the origin of chemical information. Unfortunately, the issue does not figure in the agenda of science and hence, it has not been addressed so far. The rules that govern the formation of chemical structures (non-living forms) as well as acquiring properties by them may be attributed to the existence of divine Abioprogram. A substance may be therefore conceived as an embodiment of information in a coded form. The Abioprogram immanent in various forms of energy/matter can therefore be explained in terms of a structure-code concept. Considering the atom as the basic unit of matter, the concept may be illustrated as follows. We may assume that the structure signifies a code 'written' in a special language like the symbolic language used in computer machines. This code (semantic content) is deciphered in terms of the Abioprogram and the structure derives its properties. The Quranic message that God's commands are built into the universal components (Q. 41:12) can be explained in this way. Thus the Abioprogram determines and confers the properties to inanimate matter, which forms the raw material for the hardware components (including the hardware of living systems). Structure at the level of a molecule (substance) is defined here as the totality of the nuclide composition and arrangement of the atoms. In the structure-code concept, the nuclides form the alphabets and along with their arrangement, as in a word, through bonding, etc., the code is deciphered in terms of its properties (Table 5.1). A set of alphabets can carry meaning only if it has affiliation with a language. The meaning of a word depends on its alphabetic composition as well as the order in which they are

Table 5.1 Illustration of the mechanism of acquiring the characteristic properties by inanimate matter based on the Abioprogram-based structure-code concept

Building block	**Unit**	**Software**	**Task**
Alphabet	Word	English	Meaning
Element	Molecule	Abioprogram	Properties

(Source: Wahid, P.A. 2006. *The Computer Universe – A Scientific Rendering of the Holy Quran.* Adam Publishers, New Delhi)

arranged. Two words may be different in their alphabetic composition or in their arrangements. For instance, English words 'nest' and 'sent' have the same alphabets but different arrangements whereas the words 'take' and 'buy' are different in their alphabetic composition. Likewise, different chemical structures are formed based on the composition and arrangement of the atoms of the elements. The structures of n-butane and iso-butane have the same elements and same number of atoms with the chemical formula of C_4H_{10}; but the arrangement of the atoms is different in the two substances. These two structures correspond to English words 'nest' and 'sent'. The chemical structures of water (H_2O) and benzene (C_6H_6) are different in their elemental (alphabet) composition. They are comparable with English words 'take' and 'buy'. By this analogy, the mechanism of how chemical structures (substances) derive their properties based on the Abioprogram can be explained. Periodicity in the properties of elements which provide the basis for their classification (Periodic Table) and also for the prediction of properties of a hitherto

unknown element; specificity in the change of properties of a substance with a change in structure, etc., are clearly the clauses of the Abioprogram operating at different levels of structural hierarchy. Please see Wahid [4] for a detailed discussion. The chemical structure may be thus likened to a kind of algorithm conforming to the Abioprogram. The universe is therefore nothing but information dispersed in space. The Abioprogram is the source of chemical principles pervading the whole universe.

5.2 The Bioprogram (Biological information)

The biological systems (organisms) are not governed by the Abioprogram although the structure and properties of chemical atoms and molecules that make up their hardware are governed by it. One of the inherent defects of the theories of biogenesis and evolution of biodiversity is their inability to account for the origin of biological information. Although the need for biological information has been long recognized, its existence is wrongly conceived as physical. Biological complexity is distinguished by being *information-based* complexity, and a fundamental challenge to science is to provide an account of how this unique information content and processing machinery of life came into existence [6].

The problem with modern science is that it does not distinguish chemical information from biological information. A chemical structure encodes (information) only the chemical information responsible for the physical and chemical properties. Thus DNA structure encodes chemical information which confers to it the characteristic physical and chemical properties. The physical and chemical properties which the genome exhibits outside the cell are its innate properties derived from the Abioprogram. It

will not show any 'life (biological) properties' because the structure does not encode any biological information. This is also true of any other chemical structure (organelles) residing in the cell. A chemical structure cannot encode biological information because its semantic content is specified by the Abioprogram (the source of chemical information). Ignorance or non-recognition of this vital characteristic of a chemical structure is the underlying cause of the confusion associated with the role of genome in the living system. As any other structure in the cell, genome is also a hardware component. This distinction will help explain why the particulate gene does not constitute the genetic information. Recognition of independent existence of chemical and biological information would help understand the nature of the so-called non-living and living components.

The Quran provides a clear idea of the nature of biological information while mentioning the process of creation of the first individual of *Homo sapiens*, Adam. Allah created Adam by breathing into a clay model of human being (Q. 6:2; 15:26) from His *ruh* (Q. 15:28-29; 17:85). The word *ruh* mentioned in the Quran may be considered as the general term for the divine biological software, the Bioprogram, and breathing of *ruh* as the process of installing the software in the clay model. In this way, the inanimate clay model was brought to life. The Quranic messages on the process of creation by Allah have been discussed in detail elsewhere based on the computer concept of the universe [3, 4].

5.3 Organism as natural biocomputer

An organism is a natural computer biosystem (NCB) whose development and functioning are determined by the divine

software, Bioprogram. The diverse forms of life originated on this planet through programmed evolution. The programmed evolution is the generation of small packages from the Bioprogram supposedly through a process of *phylogenetic software differentiation*. Each of these packages, called microbioprogram, forms the software (genetic program) of a species. The microbioprogram is thus the Bioprogram at the level of species. For details see Wahid [3, 4, 7, 8]. 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 components. Since the hardware components (chemical 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 microbioprogram 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. Based on this reasoning, a species may be defined as the phenotypes that can be produced from a microbioprogram.

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) 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 property of a chemical structure (e.g., magnetic property) for storing information. In the same way, the chromosomes derive the property of information storage from their chemical structure in conformity with the Abioprogram. 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).* The biomemory (chromosome) is assumed to have been organised in sectors, i.e., a group of bytes. Each sector stores part of the program (a few instructions or a program bit required for a given task), enabling the system processor to read from any sector as required. For example, each biochemical event has its own specified steps and sequences. These steps in the right sequence form a "program bit" in the microbioprogram of the species. A storage sector in the chromosome represents a "program bit" [3, 4, 7, 8].

The analogy may be illustrated with the help of examples drawn from computer technology and biological processes. A simple C program to input two numbers and print their sum is given below.

```
# include <stdio.h>
# include <conio.h>
        void main ( )
                {
                 int n1,n2,n3;
                 clrscr();
                 printf("Enter first number   :    ");
                 scanf(" %d ", &n1);
                 printf (Enter second number  :   ");
                 scanf ("%d", &n2);
                 n3=n1+n2;
                 printf("\n\n Sum= %d", n3);
                 getch();
                }
```

This program shows the important features of a computer program. Firstly it is a set of clear-cut instructions to the computer to do the task of adding two numbers and print the result. Secondly these instructions are given in certain sequences. The order in which the instructions are to be carried out is equally important as the instructions themselves. Therefore each instruction has a specified order in which it should be executed. If the sequence is changed the computer will not be able to do the job properly or it will fail totally. These features are also reflected in all the biochemical and biological processes and functions. Consider the following example

of a biochemical process – the citric acid cycle.

The citric acid cycle constitutes an important set of reactions in carbohydrate metabolism. The cycle produces two carbon dioxide molecules. This general oxidation reaction is accompanied by the loss of hydrogen and electrons at four specific places. These oxidations are connected to the electron transport chain where many ATP are produced.

Step-1: Synthesis of citric acid

Acetyl CoA and oxaloacetic acid condense to form citric acid. The acetyl group CH_3COO is transferred from CoA to oxaloacetic acid at the ketone carbon, which is then changed to an alcohol. The enzyme citric acid synthetase catalyzes this reaction.

Step-2: Synthesis of isocitric acid

Isomerization of the position of the -OH group on citric acid takes place in two steps. The first step is a dehydration of an alcohol to make an alkene. Next a hydration reaction of an alkene occurs to make an alcohol. These reactions are catalyzed by aconitase. The net effect is to move the -OH group from C-3 to C-2, which is isocitric acid.

Step-3: Oxidation

In this first oxidation reaction an alcohol is converted to a ketone and 2 hydrogens and 2 electrons are transferred to NAD^+ to $NADH + H^+$. The reaction marks the first entry point into the electron transport chain. The reaction is catalyzed by isocitrate dehydrogenase and the product, oxalosuccinic acid, remains attached to the isocitrate dehydrogenase for the next step.

Step-4: Decarboxylation

In this first decarboxylation reaction catalyzed by isocitrate

dehydrogenase, a carbon group is lost as carbon dioxide and alpha-ketoglutaric acid, a 5-carbon compound, is produced.

Step-5: Oxidation, decarboxylation and synthesis of thiol ester

This complex oxidative decarboxylation is catalyzed by alpha-ketoglutarate dehydrogenase complex. The reaction is non-reversible and prevents the cycle from operating in the reverse direction. In this second oxidation reaction an alcohol is converted to a ketone and 2 hydrogens and 2 electrons are transferred to NAD^+ to NADH + H^+. The reaction is another entry point into the electron transport chain. This is the second decarboxylation reaction where a carbon group is lost as carbon dioxide. The remaining 4 carbon group is attached to the CoA through a thiol ester high energy bond. The final product is succinyl CoA.

Step-6: Synthesis of ATP

Catalyzed by succinyl CoA, the hydrolysis of the thioester bond takes place with the formation of succinic acid and ATP. First guanosine triphosphate is formed which is coupled with the ADP to make ATP.

Step-7: Oxidation

This reaction catalyzed by succinate dehydrogenase results in the removal of the hydrogens from saturated alkyl carbons to form fumaric acid, an alkene, and 2 ATP. The hydrogen acceptor is the coenzyme FAD.

Step-8: Formation of an alcohol

In this hydration reaction catalyzed by fumarase, an alkene is converted to an alcohol.

Step-9: Oxidation

In the final reaction of the citric acid cycle catalyzed by malate

dehydrogenase, an alcohol is oxidized to a ketone to make oxaloacetic acid. The coenzyme NAD+ causes the transfer of two hydrogens and 2 electrons to NADH + H^+. This is the final entry point into the electron transport chain.

Take another mechanism, working of an organ, say ear. Hearing, one of the five senses, is a complex process of picking up sound and decoding it into a meaningful perception. The human ear is fully equipped to do that job. The mechanism of hearing may be visualized in broad five steps.

Step-1:

The pinna, the ear which we see outside, collects the sound vibrations and funnels them into the ear canal. It enables us to determine the direction and source of sound.

Step-2:

As sound waves strike the eardrum, it starts vibrating. The sound wave is thus converted into mechanical vibration.

Step-3:

The vibration of eardrum sets the three small bones in the middle ear in motion.

Step-4:

This forces the cochlea's (inner ear) fluids move. The fluids stimulate the tiny hair cells which respond to specific sound frequencies. The hair cells change the mechanical energy from the

movement into nerve impulses (electric pulses).

Step-5:

The nerve impulses are transmitted by the cochlear portion of the acoustic nerve to the brain where they are interpreted as sound.

All the biochemical processes and biological activities show clearly defined steps and sequences in which they take place. Although we describe them in terms of reactants and products, they reflect the implementation of instructions specified in the 'program bits' of the process concerned. The microbioprogram of a species may be supposed as a having composed of a large number of 'program bits' required for the execution of all kinds of biological activities. These 'program bits' might have been stored in various sectors on the chromosomes. For carrying out a biological function, the cell would need the instructions from different sectors. The chemical structures including DNA take orders and act like hardware to perform the task. The biological reactions and processes are therefore manifestations of the execution of the program. In the case of a sexually reproducing organism, from the moment of formation of the zygote, the execution of the microbioprogram is on and continues till death of the organism. It is this program that determines which hardware should come into action when. Thus we find an orchestrated response to the commands occurs from the sub-cellular (molecular) through cellular (organelles), tissue, and organ to the level of the organism. This is the unequivocal proof of the existence of the divine Bioprogram in living beings. These programs are intangible and hence any attempt to characterize them in physical form (e.g.,

DNA) will end up in failure. This would explain the cause of the utter failure of the particulate gene concept.

If genome is the genetic program of an organism, molecular biologists must be able to demonstrate the synthesis of life from pure chemicals; but they are not. Alternatively, a much simpler approach can also be tried to confirm whether genome is genetic program, by bringing a dead cell to life. At the time of death, the cell has all the structures of a living cell. Bringing the dead cell back to life has also not been demonstrated. In fact, there is no indication so far that life can originate from non-life.

5.4 Definitions of life and death

The problem of defining life and death can be effectively solved if these phenomena are explained in the light of the Quranic messages. As already mentioned, the *ruh* mentioned in the Quran may be considered as the general term to indicate the Bioprogram or the biological information. Besides this, at several places the Quran uses the term *nafs* specifically to denote a human individual (i.e., the biological system with software) or the human software alone depending on the context (Q. 3:30; 6:93). Therefore *nafs* may be considered as the microbioprogram of human individual. At the time of death, the *nafs* of the individual is removed (Q. 6:93).

"….At death, the Angels stretch forth their hands (saying)

"Yield up your nafs…" ***(Q. 6:93)***

Death can therefore be defined as the removal of the software from the body. In effect, the microbioprogram is 'deleted' from the body. *A dead body is thus comparable to a computer*

without software. The system has been deprived of its software and hence in spite of the existence of all the hardware components (including genome), the body is incapable of sustaining its biological functions. *The phenomenon of life can be therefore defined as the manifestation of the execution of the microbioprogram*. The testability of this argument lies in at least two predictions: a) life will never be produced in the laboratory from pure chemicals or from dead matter; it can only be copied from a living thing to another, b) the phenomenon of death will remain unexplained in science so long as a chemical structure (e.g., DNA) is considered as the genetic program [3, 4, 7, 8].

5.5 The defining moment of the bioworld

Biological information which governs the functioning of an organism (living system) is different from chemical information which governs the structure and properties of chemical substances (non-living things). Meyer made a thorough examination of the problem of the origination of organismal form from the point of view of the origin of the information that is necessary to generate morphological novelty [9]. The Cambrian explosion is the classical example. The "Cambrian explosion" refers to the geologically sudden appearance of many new animal body plans about 530 million years ago. At this time, at least nineteen, and perhaps as many as thirty-five phyla of forty total made their first appearance on earth within a narrow five- to ten-million-year window of geologic time. Many new subphyla, between 32 and 48 of 56 total, and classes of animals also arose at this time with representatives of these new higher taxa manifesting significant morphological innovations. The Cambrian explosion thus marked

a major episode of morphogenesis in which many new and disparate organismal forms arose in a geologically brief period of time [9, 10]. If one assumes that the Cambrian explosion took place within a relatively narrow 5-10 million year window, explaining the origin of the information necessary to produce new proteins, for example, becomes more acute in part because mutation rates would not have been sufficient to generate the number of changes in the genome necessary to build the new proteins for more complex Cambrian animals [11]. Even if one allows several hundred million years for the origin of the metazoan, significant probabilistic and other difficulties remain with the neo-Darwinian explanation of the origin of form and information [9]. All the theories of life now doing rounds have flopped miserably because of the wrong perception of the biological information. The biologists should give up the chase for life on the chemical trail. The Quran reveals to us the true nature of life. It exists as intangible non-particulate phenomenon – the *ruh*.

The Quranic revelation (Q. 6:2; 15:26, 28-29; 17:85) of creation of Adam by breathing *ruh* into a clay model of man may be examined further. This expression is metaphorical to indicate that the clay model (non-living) of the human being sprang to life with the installation of the software (the Bioprogram) clearly suggesting that life is not an intrinsic property of chemical substance (clay model). But the chemical structure acquired life following the installation of the biological software. An analogous situation may be found in the example of our computer machines. The computer is a non-living (chemical) structure but when a software is installed, it comes to (artificial) life. The probable pathway of

origin of life on this planet may be constructed on the lines suggested by these Quranic messages with the support of scientific expectations. A detailed discussion of these aspects may be found elsewhere [3, 4, 7, 8]; only important points are touched upon here.

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 cell containing the Bioprogram may be called the primordial biochip (PBC). Ohno proposed the existence of a hypothetical ancestral form that possessed virtually all the genetic information necessary to produce the new body plans of the Cambrian animals. He asserts that this ancestor and its "pananimalian genome" might have arisen several hundred million years before the Cambrian explosion. On this view, each of the different Cambrian animals would have possessed virtually identical genomes, albeit with considerable latent and unexpressed capacity in the case of each individual form [11]. While this proposal might help explain the origin of the Cambrian animal forms by reference to preexisting genetic information, it does not solve, but instead merely displaces, the problem of the origin of the genetic information necessary to produce these new forms [9].

Woese proposed the concept of "the universal ancestor" to look at the rooting of the evolutionary tree [12]. 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 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 gave the name LUCA (last universal common ancestor) for the common ancestor of all life [13]. Despite the wealth of genomic data, LUCA has remained elusive. Whether it is a simple or a complex one is not yet understood. The general thinking is that LUCA may be a pool of genes shared by a host of 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 [14]. Obviously, LUCA is a misfit in the Darwinian model, but the fact that LUCA is looked upon as a more likely take-off point for the organic evolution is a disturbing signal to the supporters of Darwinism.

The LUCA comes very close to the proposed concept of PBC. 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 *ruh* (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 womb. The PBC with built-in program as the driving force can explain the phenomenon of evolution of species consistent with natural evidence. The Quran 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 Quran. …*We made from water every living thing. Will they not then believe?* (Q. 21:30). 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 impossible [15].

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 hot-spring 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 [16]. Nanobes discovered in ancient Australian sandstone by scientists at the University of Queensland were as small as 20 nm across and looked like fungi [17]. These nanobes seemed to have the enzymatic and genetic material considered essential for life. Nanobes are now seen virtually everywhere [16]. The PBC may be likened to a nanobe

with minimal hardware components (cell structures) to store the Bioprogram and also to execute it.

The essential pre-requisite for the beginning of life prior to the appearance of the first cell, PBC, would be the formation of a chemical structure in an aqueous milieu, which is capable of storing the biological information. This structure may be either chromosome or more likely a clay particle. The latter is considered because of the Quranic revelation of 'breathing of *ruh* (the biological information) into clay' (Q. 6:2; 15:26, 28-29; 17:85) as well as the scientific indication of the probable role of clay in the origin of life in the prebiotic environment [4]. Thus a clay substratum might have served as the storage device for the installation of the divine Bioprogram (*ruh*) in the first instance (Fig. 5.1). The installation of the Bioprogram in the clay material

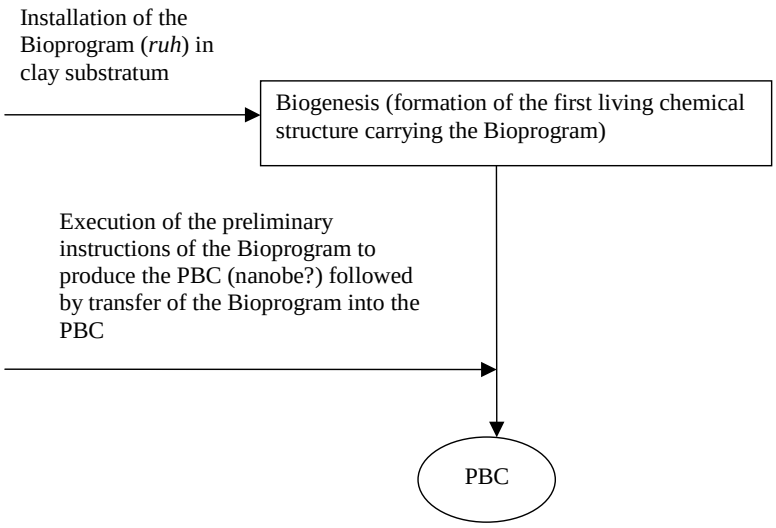

Fig. 5.1. Proposed pathway of biogenesis in an aqueous milieu on the earth from a religio-scientific perspective. PBC – Primordial biochip

would have initiated execution of the preliminary instructions in the Bioprogram to produce from the prebiotic soup rich in minerals and carbon compounds, the necessary organelles particularly chromosomes for the final storage of the Bioprogram (via transfer from the clay particle), and organize them in the form of a minimal cell such as nanobe. This first cell may be called the PBC. Thus the formation of the PBC itself can be thought of as the result of execution of the Bioprogram. The installation of the divine biological software into the first memory device (clay) would have been effected *in situ* through transmission of *ruh* by Allah through an Angel as similar process has been mentioned in the Quran in another context. For instance, Virgin Mary conceived Jesus Chrisrt (A.S.) by such a process. As the Quran put it:

> ***"…We sent to her Our ruh and he appeared before her as a man in all respects ...He said: I am only a messenger from your Lord to gift a holy son to you." (Q. 19:17-19)***

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 on the earth is the cause, and manifestation of life is the result.

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. The arrival of the Bioprogram is the landmark changeover event from chemical principles to biological (genetic) principles. This is the defining moment of the bioworld. It is to be realized that biological principles are fundamentally different from chemical principles and that genetic information was not available

on the earth prior to the installation of the divine Bioprogram. The transition from non-life to life took place with the installation of the biological software. The notion that life originated from non-life is therefore baseless. Life did not jump-start from non-life based on chemical principles through a hypothetical emergent phenomenon; it started only when the biological information (the divine software Bioprogram) was made available on the earth by Allah. It could be from this Bioprogram, multitudes of species were created through programmed evolution. A theory of programmed evolution based on *phylogenetic software differentiation* during which the Bioprogram differentiated into mini packages was discussed elsewhere [4, 8]. Each of these mini packages called *microbioprogram* (genetic program) represented a species.

References

1. Gilad, Y. et al. 2006. *Nature* 440, 242–245.
2. Pennisi, E. 2006. It's the Expression, Stupid. *Science*NOW Daily News. 8 March 2006.
3. Wahid, P.A. 1998. *The Divine Expert System*, Centre for Studies on Science, MAAS, Aligarh, India.
4. Wahid, P.A. 2006. *The Computer Universe – A scientific Rendering of the Holy Quran.* Adam Publishers, New Delhi.
5. http://www.webelements.com/ Accessed 28-1-2006.
6. Davies, P.C.W., 2003. *The Origin of Life*. Penguin, London (Previous title: *The Fifth Miracle*. Penguin, London and Simon & Schuster, New York, 1998.
7. Wahid, P.A. 2003. Definitions of life, death, genetic program and soul based on the Quran and computer concept of the universe. *J. Islamic Sci.* 18(1-2):137-147.

8. Wahid, P.A. 2005. Origin of genetic information and evolution of biological species. *Islam and Science* 3(1):7-42.
9. Meyer, S.C. 2004. The origin of biological information and the higher taxonomic categories. *Proc. Biol. Soc. Washington* 117(2):213-239.
10. Meyer *et al*. 2003. DNA and the origin of life: information, specification and explanation. pp. 223-285, *In* J. A. Campbell and S. C. Meyer, eds., *Darwinism, Design and Public Education*. Michigan State University Press, Lansing, Michigan.
11. Ohno, S. 1996. The notion of the Cambrian pananimalia genome. *Proc. Natl. Acad. Sci. USA* 93:8475-8478.
12. Woese, C. 1998. The universal ancestor. *Proc. Natl. Acad. Sci. USA*. 95:6854-6859.
13. Lazcano, A. and Forterre, P.J. 1999. *J. Mol. Evol*. 49:411-412.
14. Whitfield, J. 2004. Born in a watery commune. *Nature* 427:674-676, News feature.
15. Wallace, A.R. 1907. *Is Mars Habitable? A Critical Examination of Professor Percival Lowell's Book "Mars and Its Canals" with an Alternative Explanation.* Macmillan, London.
16. Leslie Mullen. 2003. Life from scratch? *Astrobiology Magazine*, Nov 4, 2003 issue.
17. Uwins, P.J.R., Webb, R.I., Taylor, A. P. 1998. Novel nano-organisms from Australian sandstones. *American Mineralogist* 83:1541-1550.

6 FUTURE PROSPECTS

Presently scientific community looks at the phenomena of life and non-life from the chemical angle in terms of material entities. Consequently, chemical structures are believed to be responsible for both these phenomena. This assumption has to go in the first place. Recognition of independent nature of the two phenomena, i.e., non-life based on chemical information and life based on biological information, would lead to the right perception of the universal components and their mode of functioning. Molecular biology and genetics need a radical mutation to recognize this truth. Molecular tools applied in genetic manipulations of the organisms must be treated as nothing but interventions at the hardware level and not at the software level. Technology based on manipulation of particulate gene (DNA) or other cellular structures can only be considered as hardware-related technology and may be more appropriately called 'biohardware technology'. It is not 'biosoftware technology'. The extent of biological change that can be brought about by mutation of hardware is very limited. While this realization will take the sheen off the much-hyped potential of genetic engineering tools, it would also expose the hollowness of the fears over cloning, stem cell research, etc., and exaggerated bioethical concerns over the outcome of genetic engineering initiatives. Currently, biotech products such as genetically modified (GM) plants and animals, clones, etc., are considered as the result of manipulation of the biological software. It gives the impression that molecular biologists and geneticists are tampering with the very basis of life. This perception has sent

grossly wrong, panic-creating messages to the people. There is a feeling among the public that meddling with cellular DNA can lead to the production of bizarre creatures and monsters. If we realize that genome does not constitute the software and it is only a hardware component, much of the apprehension about molecular interventions in organisms can be removed. From our experience of computer technology, it is obvious that the chance for producing a radically different viable output through manipulation of hardware is insignificantly small. This is also the case with biological organisms. Most of the mutations are either lethal or undesirable because of this. The production of a new viable output by the computer requires intervention at the software level. Successful development of biotechnologies employing genetic engineering in agriculture, medicine, and other fields is extremely rare as all the interventions at present are hardware-related.

Consider, for example, gene therapy. Employing an engineered protein called a zinc finger nuclease, a new technology for repairing or altering a cell's existing genes is emerging. The protein latches onto a specific gene and snips its DNA. The cell then heals the broken strand using copies of a replacement gene supplied to it. Although the technique appears to hold promise in gene therapy, like other gene-therapy strategies, the use of zinc finger nucleases poses serious safety questions [1]. Modification of a cell's gene is preferred to simple insertion of a new gene into a cell's genome as the new gene may not function in the same way as the one it is meant to replace. This is because the introduced gene usually lands in a random location, far from the promoters and other noncoding regions that control the natural gene.

Consequently, the cell makes too much or too little of the added gene's protein product. The random location of the gene also leads to serious side effects. Scientists have also tried to exploit one of the cell's natural repair mechanisms to edit genes, but with limited success. When a chromosome is damaged, cellular enzymes can restore it through a process called homologous recombination in which a corresponding strand of DNA from the cell's other copy of the chromosome is used as a template. The very low rate of repair achieved by this technique is too low to be useful. Another gene-repair technique, chimeraplasty, has not proven to be easily reproduced. Gene repair via homologous recombination employing zinc fingers has also been tried. The strategy is to attach zinc fingers to enzymes called endonucleases that make double strand breaks in DNA. The zinc finger nucleases can alter specific genes in a cell's chromosomes and can also be used to repair a mutation in the gene. Although a lot of hope is attached to this technique, safety issues remain particularly because it can create double strand breaks at DNA sequences other than the target gene [1].

We also find that scientists' hit or miss trials employing molecular tools are not yielding any horrific or weird products of the kind we fear. Further, most of the DNA (hardware) mutations are lethal. We must accept the fact that Allah is the source of our knowledge and all our research has limits set by Allah. Advancement of science and technology takes place according to the scheme of the Creator. That is to say, the growth of our knowledge is limited to the extent Allah wants us to know.

"….Of knowledge it is only a little that is communicated to you (oh men!)." ***(Q. 17:85)***

If something unexpected happens, it can only be due to the wish of Allah and not because of the unethical excursion of scientists into the realm of life. Bioethical concerns expressed by different sections of the society also do not carry weight. This is particularly relevant to stem cell research, and the so-called cloning of animals and man.

A clone is literally the genetically identical facsimile of an individual. Such a copy does not exist on the earth for any individual. There is variability among all 'clones' irrespective of whether they are man-made or naturally occurring. For instance, the 'identical twins' (monozygotic twins) produced from the two cells originating from the division of a zygote are not genetically identical. Since 'identical twins' (which by scientific expectation must be cent percent true-to-type or clones) are not identical to each other, it can be safely concluded that genetically identical clones do not exist in nature. It is the notion that genome constitutes the genetic program that created all the confusion. We make a lot of noise over bioethics and other issues associated with cloning. There is also a lot of media hype and debates on these issues. In reality, however, there is absolutely no cause for concern, as we cannot produce animals or human beings more identical than the naturally occurring 'identical twins'. All these are non-issues but became issues following the false claims of cloning animals. The scientific claim of having produced clones of animals (e.g., sheep Dolly) is false. Dolly was created by fusing the nucleus of an adult mammary gland cell to a sheep egg from which the nucleus was removed. Creation of Dolly only demonstrated that from a differentiated cell, an adult could be produced but not that a clone could be

produced. Dolly was not a clone of its donor parent. We have not so far produced identical copies of any animal or a human being. The methods we currently use for cloning animals (e.g., nuclear transplant) cannot produce offspring that is genetically anywhere near to the naturally produced 'identical twins'. Nature's method of producing 'identical twins' is the limit of sophistication of the cloning technique, i.e., development of two individuals from two cells resulted from the division of a single cell, the zygote. Even that method does not produce clones. The stem cell controversy centres around research on both adult and embryonic stem cells. Being undifferentiated, these cells have the ability to self-renew indefinitely and differentiate into cells with specialized functions. Apart from offering considerable opportunities for developing medical therapies for debilitating diseases, stem cell research also addresses fundamental questions of biology. Research on human embryonic stem cells has become controversial due to the diverse views held in our society about the moral and legal status of the early embryo. The apprehensions about genetic modifications, stem cell research, etc., stem from our ignorance or deliberate refusal to admit that it is Almighty Allah who gives us knowledge. The entire gamut of these issues is under the control of omnipotent Allah. Neither can man prevent any undesirable discovery from happening nor can he predict any desirable to happen in the future. All these depend on Allah's scheme for this world.

There were instances of failure of theories in the past. Steady state cosmology which was engineered to question the big bang theory (as it implies a creator for the universe) is a classic

example. The ongoing controversy over the theory of evolution is another example. To this list is to be added now the particulate gene concept. This is perhaps the most opportune time to set aside the differences between the religious and scientific communities and prepare ground for religio-scientific dialogue to unravel the mystery of life. Already more than six decades into the particulate concept and every passing day making the concept more confusing, there is no justification to hold on to it any more. Life can be defined and understood only in conjunction with the Quran. The gene fiasco is a wake-up call to humanity in general and to the scientific community in particular to remind the existence of the Creator.

References

1. Kaiser, J. 2005. Gene therapy: putting the fingers on gene repair. *Science* 310 (5756):1894 – 1896. DOI: 10.1126/science.310.5756.1894.

7 CONCLUSIONS

Genome is not the whole story of an organism from the point of view of heredity, development and its moment-to-moment existence. Although biologists cannot deny this fact, their reluctance to seek an alternate explanation for life from outside of material phenomenon literally creates a stumbling block for the advancement of science along the right track. Consequently, biology is 'advancing' in the wrong direction. All the research so far conducted and being conducted in life sciences treat the particulate gene as the sole entity responsible for life properties exhibited by an organism. It is now being recognized that noncoding DNA also has significant genetic role. Even if the total genome is supposed as encoding the genetic information, it will not improve the quality of our information. The inadequacies and limitations of the particulate gene must be taken as sufficient ground for re-examination of this century-old belief. Biologists must be prepared to review the situation and look at the phenomenon of life from whatever alternative angle possible. The recognition of organism as *natural computer biosystem* (NCB) assumes paramount importance in this context. A revolutionary feature of this concept is that it treats the organism as a system made of hardware and software components. It distinguishes chemical information (the divine Abioprogram) from genetic (biological) information (the divine Bioprogram). The chemical structures encode chemical information and life is not derived from chemical information. Life is the manifestation of the execution of microbioprogram (the Bioprogram at the species level) stored in the memory device of

the cell. The cell is a biochip. It has storage device (chromosomes), clock, and other hardware. All the chemical structures (including DNA) in the cell constitute hardware and microbioprogram (genetic program) is the invisible component – the software. The software determines the attributes of the species and potential of each attribute which get translated in terms of the phenotype. The environment influences the phenotype within the range (potential) permitted by the software. All cellular activities, processes and functions carried out by an organism are dictated and governed by the program and not one of them is 'error' or 'mistake' for the simple fact that a cell can function only as it is programmed. Conceptualization of an organism on these lines provides a radically new option to look at the biological system. Implied in this concept is the assumption that software (microbioprogram) is not encoded in any chemical structures; but it is stored in the storage medium (chromosome) of the cell. The microbioprogram exists in the cell as the software of the computer exists in its memory disks. The nature of life and organism based on the computer model is summarized below.

- The molecular gene concept is wrong. Material gene does not exist.
- There are no individual genes but only an integrated genetic program – the software.
- The ever-increasing confusion about gene and our inability to define or describe gene must be taken as proof of its nonexistence.

- An organism can be best treated as a natural computer biosystem with characteristic hardware and software.

- The chemical information and genetic (biological) information are distinctly different and have independent existence. Whereas chemical information (the divine Abioprogram) is coded in the chemical structure, biological information (the divine Bioprogram) is stored in the cell memory devices probably in chromosomes.

- Genetic information is not coded in the DNA structure or in any other structure in the cell. DNA is a hardware component like any other chemical structure.

- Microbioprogram is Bioprogram at the level of the organism. It stipulates which hardware component should come into operation when. It is these instructions that form the software of the organism.

- Ontogenetic development is the result of execution of specific instructions for the development of the individual. The organic body with its multifarious and multifaceted structures from molecular level to organs and systems capable of a range of functions from the level of the cell to the level of the organism are produced through execution of the development instructions in the software by the hardware.

- Biological (housekeeping) functions are carried out by the hardware concerned in accordance with the

microbioprogram.

- Instincts exhibited by the organisms are in accordance with the instructions carried in the microbioprogram of the organism.

- The so-called 'adaptive mutations' (or hypermutations) are alterations in hardware (e.g., changes in DNA) carried out by the cell in accordance with the microbioprogram in response to the signals received from the environment. It is a biological software-based strategy to enable the organism to meet a special situation. Such changes in hardware would occur only if the microbioprogram of the organism has the required instructions. Cell-directed mutagenesis in response to environmental stresses observed in certain organisms to alter the DNA sequences (hardware component) is a reflection of this strategy.

- There are also cases where alteration of hardware or production of new hardware is not required to tide over an environmental challenge; in such cases the organism behaves as directed by the program. All the environmentally induced behaviour such as phototropism in plants can be included in this category.

- The limitations and inadequacies of the particulate gene and genome concepts in explaining life processes and hereditary mechanisms will become more and more evident with advancement in molecular biology, bioinformatics, genetics and allied fields. Although much

hope is laid on these areas for technology generation through genetic manipulations, the efforts in this line will prove disappointing as the interventions are confined to the biohardware level and not biosoftware level. For that reason, the future of these disciplines as technology generators appears to be bleak.

- The bioethical concerns and fears expressed over the outcome of hit or miss genetic interventions in various organisms are rather overblown and ill-founded.

- Life science is replete with concepts and glossaries necessitated by the molecular gene concept. In the NCB concept all such explanations are redundant and unnecessary.

It is high time we realized that genetic science is founded on wrong principles. Basing genetic science on DNA (molecular gene) is the fundamental mistake made by biologists. There is no physical or material gene and that is precisely the reason why we are unable to define and locate the 'gene' on the genome. Studies in this line also generate several blind alleys and anomalies for which scientists strive to find still misleading explanations. All these add to the already existing junk. Concepts of epigenetics, introns, exons, coding DNA, noncoding DNA and a variety of others are created thus. The situation demands us to give up the chemical trail and turn to the holy Quran for guidance to understand the phenomenon of life.