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Molecular genetic program (genome) contrasted against non-molecular invisible biosoftware in the light of the Quran and the Bible

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ABSTRACT

The current perception of biological information as encoded by a chemical structure (genome) is critically examined. Many features assigned to the genome are violations of chemical fundamentals. Perhaps the most striking one is that a living cell and its dead counterpart are materially identical, *i.e.*, in both of them all the structures including genome are intact. But yet the dead cell does not show any sign of bioactivity. This clearly shows that the genome does not constitute the biological program of an organism (a biocomputer or a biorobot) and is hence not the cause of "life". The molecular gene and genome concepts are therefore wrong and scientifically untenable. On the other hand, the Scriptural revelation of the non-molecular biosoftware (the soul) explains the phenomenon of life in its entirety. The computer model of organism also helps understand the Biblical metaphor "Adam's rib" as chromosome, the biomemory of the cell. The Quran provides ample insight into the phenomenon of human biodiversification. It also reveals the source of biological information required for creating biodiversity in human population. The Scriptural revelation of the invisible non-molecular nature of biosoftware rules out the possibility of creating life from chemical molecules without involving a living cell (or organism) in the process. Claims of creation of "synthetic life" or "synthetic forms of life" employing living cell in the process cannot be accepted as creation of life from non-life as non-molecular biosoftware can be copied from the living cell to the prosthetic cell. Instead of chemically synthesizing a cell from scratch to prove life is a material phenomenon, biologists can as well resort to a more practical and convincing method by restoring life to a dead cell (which carries all the hardware structures including the genome but lacks the biosoftware) by chemical means. The failure of experiments to produce life through purely chemical means or to restore life to a dead cell would in fact invalidate the molecular biological program (genome) concept. More importantly, the failure would confirm the Scriptural revelation of non-particulate nature of the divine biosoftware and the existence of God.

Keywords: Genome; Divine Non-Molecular Biosoftware; Synthetic Life; Computer Model of Organism; The Quran; The Bible; Biosoftware Engineering; Human Biodiversification; Genome Anomalies

1. INTRODUCTION

Over the past six decades following elucidation of the chemical structure of DNA, the genetic research has been centred round the molecular gene and genome concepts. Genome is believed to constitute the genetic program or the 'blue print of life' that is responsible for the biological features and functions of an organism. In other words, "life" is treated as a material phenomenon. In contrast to this, a computer model of organism was proposed earlier in the light of the Quranic revelation of intangible (*ghayb* in Arabic) non-molecular biosoftware (*rooh* or *nafs* of man) to explain the phenomena of life and death, and biological functioning [1,2]. The model is consistent with the non-particulate gene originally proposed by Wilhelm Johannsen in 1909 that agrees well with the Scriptural revelations. This paper addresses the problems associated with the molecular genome bringing to light its inherent weaknesses and also inconsistencies with the fundamentals of chemistry. The relevance of the Quranic and the Biblical revelations about the phenomenon of life is also highlighted in the wake of failure of attempts to create life by chemical means without involving a living cell.

2. ANOMALIES OF THE GENOME CONCEPT

2.1. The Gene is Indefinable

The perception that DNA molecule encodes the biological program has run into serious problems. Although molecular biologists hoped that it would be possible to identify the genes for different attributes of an organism, the gene remained elusive. According to geneticist Peter Portin, "The gene is no longer a fixed point on the chromosome, producing a single messenger RNA. Rather, most eukaryotic 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...." [3]. Other leading scientists like Thomas Fogle and Michel Morange also concede that there is no longer a precise definition of what could count as a gene [4,5]. An important objective of genome projects is the identification of genes. Current estimates of human genes generated from genome sequencing range between 30,000 and 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 [6]. 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." [7].

The objective of genomic research is to ultimately 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 [4].

Instead of generating more evidence in support of the particulate nature of the gene, research in molecular biology is generating evidence to the contrary. 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." [8]. 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 [9].

2.2. Phenomenon of Cell-Induced Mutations

Exposure of living organisms to natural radiation is supposed to be the major cause of DNA mutations, which ultimately paves way for evolution of new structures and new species. The annual dose of background radiation received by a human being is 2 to 3 mSv. Whether this too low a dose is sufficient to change a chemical structure is doubtful. Change in cell DNA is invariably attributed to background radiation ignoring the fact that cell itself has the mechanism to bring about that change. Even if the background radiation damages the DNA molecule, how can it make rearrangement of the bases and create new 'viable' DNA molecule is another question that has been overlooked by biologists. Thirdly there is also no explanation as to why no other cell structure is similarly affected by background radiation.

Stephen C. Meyer in an excellent comprehensive review of the evolutionary literature discusses the problems and difficulties in the evolution of novel genetic

information through random mutations [10]. According to Ohno (1996) even a mutation rate of 10^{-9} per base pair per year results in only a 1% change in the sequence of a given section of DNA in 10 million years. Thus, mutational divergence of preexisting genes cannot explain the origin of the Cambrian forms in that time [11].

In 1970 Miroslav Radman discovered that the phenomenon of mutation is cell-directed. He found that bacteria harboured information to make mutations [12]. In 1988 Cairns *et al*. confirmed that genetic mutations are induced from within the cell. They found cell-induced changes of various elements of the lac operon in *Escherichia coli* bacteria [13]. According to Chicural, "…depending on their environmental conditions, bacteria might be able to direct mutations to particular genes….Outraged, a number of evolutionary biologists quickly embarked on their own studies to test the notion" [12]. Clearly biologists do not look beyond the genome. Goodman described the studies conducted by Joshua Lederberg at the University of Wisconsin which showed that mutations for resistance to some antibiotics occurred spontaneously in cells that had never been exposed before to the antibiotics [14]. A recent report of resistance of bacteria to antibiotics further confirms cell-induced mutation [15,16]. Reviewing the works in this area, Pennisi remarked: "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." [17]. As discussed elsewhere [1,2], there are a variety of natural biosoftware engineering mechanisms (e.g., crossing over between chromosome sectors, deletion, duplication of chromosomal sectors, etc.) that can bring about changes in chromosome composition. The discovery of built-in biosoftware engineering mechanisms dates back to Nobel laureate Barbara McClintock's pioneering cytogenetic studies on transposable elements during the late 1940s and early 1950s [18]. These mobile elements offer a versatile cut-and-splice tool in bringing about specific changes in the organization of chromosomes. These are biosoftware-dictated mechanisms to generate new information. Transposition plays an important role in chromosome rearrangements. Insertion, deletion and inversion occur either as a direct consequence of transposition or by general recombination. These elements are present in all prokaryotes and eukaryotes.

Surprisingly, biologists look at these mechanisms as 'errors' and 'mistakes'. These mechanisms are in fact programmed phenomena to produce radically different chromosome compositions and hence semantic (bioinformation) content. They are mechanisms operating in the cell in accordance with the biosoftware of the organism. They are not mistakes or errors. Strictly speaking, a computer cannot make mistakes; its hardware can only carry out instructions as dictated by the software. Same is the case with a cell also. The need to recognize natural biosoftware engineering processes as programmed phenomena is very much reflected in the discovery of cell-induced mutagenesis. All these phenomena are opposed to the particulate biological program concept but they strengthen the view that biosoftware exists in the cell as stored information in non-molecular form. It is because of the existence of biological program independently of any chemical structure, cell-induced DNA mutations occur in response to environmental stimuli. The reports of heritable changes occurring in the organisms including that caused by background radiation are to be viewed in this light.

Development of resistance to pesticides in certain microorganisms [14] and environmental stress-induced changes [13] are examples of environment-induced biomemetic responses. In all these cases the stimuli or signals received from the environment act as switches to trigger specific biomemes into operation. Not all organisms will respond similarly to a given stress or environmental stimulus. An organism reacts to an environmental stimulus in accordance with its biomemome. This would imply that every phenomic change that occurs in an organism is biomemome-directed phenomena from within the cell and not externally induced adaptations as is believed now. These are also instances of abioprogram-bioprogram interactions consistent with the divine control program. The availability of biomemes to respond to special or unusual environmental conditions is natural evidence of God's designing the organism. DNA mutations have to be seen as hardware changes required for the execution of the newly activated biosoftware package in the organism.

Results obtained in several other studies can also be explained the same way. For instance, the observations made by Grant and Grant of the changes in beak size of Darwin's finches (bird species) [19] can be explained as a case of cell-induced genetic change and not as evolution caused by random mutation by some external mutagen. They studied two predominant species namely, *Geospiza fortis* (medium ground finch) and *G. scandens* (cactus finch). The main food items of the birds were

seeds, flowers, etc. The former had a bigger beak and could crack larger and harder seeds whereas the latter had a smaller beak and hence was more efficient in handling smaller seeds. Their results indicated that mean body size and beak shape were significantly different in both species at the end of a thirty-year experimental period. The changes in beak size occurred depending on the kind of seeds available to them in a changing environment influenced by drought etc. The environmental changes acted as switches to bring specific biomemes into operation and as a result beak size altered to suit the new environment. The other examples often cited as "evolution in action" are also products of cell-directed mutations and not random mutations. These include changes in mouth sizes of mud snails of the genus *Hydrobia* that eat diatoms (diatoms are protected by a hard silicate shell and the size of the snail mouth determines what size diatoms it can eat), changes in wingspan in bird-eating hawks and eagles of the family Accipitridae to enable them to carry their prey, changes in mouth sizes of desert seed-eating rodents of the families Cricetidae and Heteromyiidae, and changes in mouthparts in Cichlid fishes [20]. The variations in morphological characters observed in these organisms cannot be considered as random phenomena but are cell-directed changes to counter specific environmental stress experienced by the organism concerned.

There are many kinds of DNA repairs. Rosenfeld gives a detailed account of the self-healing strategies of the master molecule. 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 [21]. 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. DNA repair is a true reflection of the existence of the biological program independent of the DNA structure. All these documented evidences confirm that DNA mutation is not a random phenomenon but is biosoftware-directed hardware change.

2.3. Lack of Genome-Phenome Correspondence

Studies at the molecular level fail to demonstrate the expected correspondence between genome and phenotype. The most spectacular example of this is the morphological dissimilarity between human being and chimpanzee 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 identical phenotypic characters in human and chimp in terms of anatomy, physiology, development and other biological features. In fact there is none! A chimp is not even 0.1% human being nor a human being 0.1% chimp. 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.

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. *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]. "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 [24].

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 the bee species *Apis mellifera* revealed that numerous genes appeared to be differentially expressed between the two castes [25]. 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 natural existence of similar genomes exhibiting dissimilar phenotypes. The absence of genome-phenome relationship is very much evident from these studies. It implies that genome does not constitute the biological program. All these cases indicate the independent existence of biosoftware as non-molecular information stored on the chromosome.

3. GENOME IS CHEMICALLY UNTENABLE

Several non-chemical features have been attributed to the material genome. Some of the obvious departures from the chemical fundamentals are given below.

3.1. Junk DNA

It has been observed that an overwhelming 95% of DNA consists of non-coding DNA in eukaryotes and about 5% is constituted by the coding-DNA (or the genes). The non-coding DNA (ncDNA) is referred to as "junk DNA". Though structurally comparable to coding DNA, surprisingly, the so-called junk DNA does not encode similar biological information (or vice versa).

3.2. Genome Can Change its Own Structure

Another surprising feature of the genome is that DNA is the only molecule in nature that can undergo self-alteration. How is it possible for a chemical structure to encode information for its own change? For example, in human being with the formation of the zygote, the biological program comes into operation. The zygote undergoes ontogenetic development; then the individual passes through adult stage and old age, and ultimately dies. It is a continuous process like the operation of an integrated computer program. During ontogenetic development, the genome produces not only tissues with diverse functions but also undergoes itself changes in its structure as is evident from the recent discovery of variations in the genomes of different tissues [26]. Prior to this discovery (in 2009) it was believed that the genomes of the body cells, irrespective of the tissues to which they belong, were all identical. That view is also a violation of chemical fundamentals as it implies that a given chemical structure can show different properties—in this case, differences in the information encoded by identical genomes in different tissues. The discovery of variable genomes in different tissues also brings up another issue as to how such differences arise in the daughter cells as a result of successive mitotic divisions of the same parent cell—the zygote.

3.3. Dead Cell Genome Does Not Encode Biological Information

A fundamental feature of chemical molecule is that it cannot but exhibit the properties assigned by its structure. The genome is an exception to this rule also. Going by the present concept of particulate genetic program, a cell carrying the genome should invariably show the life properties. However a dead cell with its genome remaining intact fails to exhibit "life" clearly indicating the genome does not encode the biological program. If not, how can a molecule lose the information encoded by its structure? All these issues are chemically inexplicable. The gene and genome concepts are therefore fundamentally wrong.

3.4. Other Odd Features

Although there are certain criteria to identify the genes, their application has not been straightforward. Besides, issues like overlap, alternative splicing, and pseudogenes are also involved. "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." [27].

The variation observed in the use of triplet codes among organisms is another issue. Like the pseudogene this aspect is against chemical fundamentals and remains 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 [28]. The 'genome hypothesis' which tries to explain the variation in codon use states that codon use is spe-

cies-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 [29]. 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 [28].

4. DIVINE NON-MOLECULAR BIOSOFTWARE

The invisible (*ghayb* in Arabic) nature of human biosoftware was discussed in detail in an earlier paper [2]. "Breathing of *rooh*" into a clay model to create man (Adam) mentioned in the Quran (Q. 15:26-29) and "breathing of life" mentioned in the Bible (Genesis 2:7) refer to one and the same event – installation of divine non-molecular biosoftware in a clay model of man. Upon installation of the *rooh* (the term *nafs* is also used in the Quran) in that non-living clay model, it sprang to life much like a lifeless computer springs to "life" when software is installed. Thus the *rooh* or "breath of life", which is non-physical, is the divine biosoftware (bioprogram or the soul) of human species. Based on that, the phenomenon of life has been defined and explained as the manifestation of the execution of the divine biosoftware. The Quran further informs us that it is the removal (or in computer parlance, 'deletion') of the *nafs* (biosoftware of human being) that causes death (Q. 6:93). In other words, a dead body is like a computer without software [2].

As in the case of man-made computer program, the non-molecular biosoftware needs a physical medium for its storage. The storage device is the chromosome. This can be deduced from the Quranic and Biblical revelations. The Quran states that it was from the *nafs* (biosoftware) of Adam, woman (Eve) was created (Q. 7:189). The Bible further says that it is from Adam's rib, Eve was created. The "rib" mentioned in the Bible may be taken as metaphor to mean X chromosome of Adam for the obvious reason that chromosome was unknown to the people of Prophet Moses's time [30]. Ribs are the only part of human body that morphologically resemble the chromosome. As two arms of a chromosome are joined on either side of the centromere, two ribs are joined on either side of a vertebra (**Figure 1**). Of the two sex chromosomes (X and Y), Adam's rib must be referring to the X chromosome because XX combination determines femaleness. Further, the arms of the X chromosome are more nearly equal in length than those of the Y chromosome. This characteristic of X chromosome makes it more comparable with the ribs on either side of a vertebra. Since the Bible mentions only one rib, the biomeme for femaleness might be located on one of the arms of X chromosome. The analogy of rib used in the Bible for chromosome is revelation of the biosoftware storage medium. The Scriptural account of creation of Eve from Adam also reveals the karyotypes of Adam and Eve. If we designate karyotype of Adam as 22 $(\text{autosomes})_A + (XY)_A$, where subscript A denotes Adam, the karyotype of Eve will be 22 $(\text{autosomes})_A + (XX)_A$.

4.1. Human Biodiversification

4.1.1. Source of Bioinformation

Biodiversity is in reality phenotypic manifestation of diverse biosoftware. How new information arises in human beings for creating variability in the population is still not understood. The Quran is the only source which provides information on this subject. The Quran reveals that human species was created from a single biosoftware (*nafs*). "O mankind! Fear your Lord who created you from a single *nafs* and from that, He created its mate, and from them both, He (created and) spread plenty of men and women…." (Q. 4:1). The *nafs* (biosoftware) mentioned here is the *rooh* which created Adam (Q. 15:26-29) as discussed elsewhere [2]. The Quran further reveals: "O mankind! Indeed we created you from a male and a female and made you into divisions (civilizations, nations, cultures, etc.) and tribes that you may know each other…." (Q. 49:13). "And among His signs is the creation of the skies and the earth, and the variations in your languages and your colours. Verily in that are signs for those with knowledge." (Q. 30:22). These revelations imply Adam's *nafs* is the microbioprogram (*i.e.*, bioprogram at the species level) of the human species. It serves as the common biomeme pool to create phenotypic diversity in human species in time and space. The process of human biodiversification is therefore a

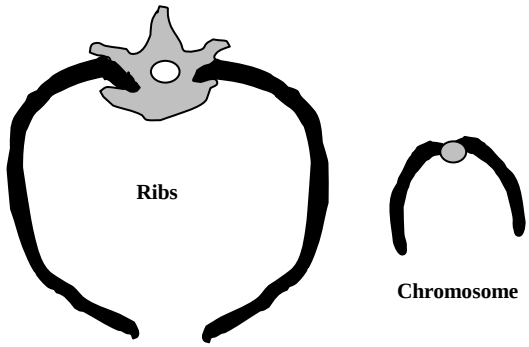

Figure 1. Morphological semblance between human ribs and chromosome.

programmed phenomenon through which God creates diverse individuals, communities with different colours, languages, etc., at different times and in different geographical regions.

Human biodiversity is manifested in biological attributes including mental prowess. Some of the readily observable variations include morphological (e.g., body shape and size, height, bone structure, obesity), gender, race, ethnicity, physical abilities, color (e.g., skin, eyes and hair), blood type, temperament, cultural differences, mental abilities (e.g., intelligence, aptitude, likes and dislikes, etc.), language, food preferences, etc. With wide-ranging characters, skills and talents, human biodiversity profile is unwieldy and overwhelming to say the least. No two individuals including the so-called monozygotic twins are identical. *Homo sapiens* is the only species whose members can be identified by face as well as by other phenotypic characters because of the variability. Each human being is unique, unprecedented and unrepeated in time and space. Such is the magnitude of variation existing in human race. And the source of biological information responsible for this scale of biodiversity is Adam's *nafs*, the divine microbioprogram of *Homo sapiens*. The Quran also informs us that longevity of a human individual is also biosoftware-controlled. "And Allah created you from dust (or clay); then from a sperm-drop; then He made you mates. And no female conceives or delivers without His knowledge. No man is granted extension of life nor is his lifespan shortened except in accordance with (what is given) in a record. All that is easy for Allah." (Q. 35:11).

4.1.2. Phenomenon of Human Biodiversification

As biosoftware is non-particulate and is stored on the chromosomes as biomemetic sectors [2], changes in biological information can be brought about via shuffling and mixing of the biomemetic sectors on the chromosomes. Appropriate natural biosoftware engineering mechanism comes into operation during gametogenesis (gamete formation through meiosis followed by mitosis) to produce gametes carrying biomemes as specified in the biosoftware. A particularly notable phenomenon in this context is the "crossing over" taking place during meiosis during which the segments of non-sister chromatids of a homologous pair of homologous dyads are exchanged. This swapping of portions leads to alteration of biomemetic content of the resulting chromosomes. Huge biomemetic differences observed between siblings are the result of this crossover. The exchange is not carried out in random fashion as is believed now; it is a programmed function executed in accordance with the biosoftware of the individual to prepare the next generation biomememomes (biosoftware of individuals). If it were a random process, most of the resulting gametes would have been infertile. This implies that the programmed "crossing over" produces diversity in human population along a specified timeline and based on specific distribution pattern. The origin of diverse ethnic groups, races, cultures, linguistic groups, etc. at different times of human history and their distribution in different geographic locations on the earth can be explained as consequence of this programmed biodiversification.

Besides crossing over, another mechanism that controls the human biodiversification may be the fertilization phenomenon as can be inferred from the Quranic verse 13:8: "Allah knows what every female (womb) bears, by how much the wombs fall short (in number) or exceed. Every thing is in accordance with a calculated measure (due proportion) with Him." It is very clear that the whole process of creation of human individuals involving gametogenesis, fertilization in the female womb, infertility and fecundity, and phenotype determination is according to God's program. In support of these revelations we find that the fertilization of female egg with male sperm is a highly controlled phenomenon. As a general rule, we find only one sperm out of the millions in the ejaculate fertilizes the egg. Scores of sperms are produced in the human semen perhaps to provide options for wide-ranging situations. According to biochemist Jerry Hedrick, "Sperms have the opportunity to interact with many other kinds of cells in the female. How egg and sperm recognize one another is a fundamental question in reproductive biology." [31]. It is also surprising how a sperm evades fusion with another sperm. Further once fertilized by a sperm, the zygote (fertilized egg) is inaccessible to another sperm. Evidently there is a mechanism to guide a particular sperm to fertilize a particular egg (**Figure 2**).

Spermatozoa normally encounter the egg at the fertilization site (in the Fallopian tube) within 24 hours after ovulation. A considerable fraction of the spermatozoa ejaculated into the female reproductive tract remains motionless in storage sites until ovulation, when the spermatozoa resume maximal motility and reach the fertilization site within minutes. Although the nature of the signal for sperm movement is not known, a study conducted by Ralt *et al.* suggests that attraction of spermatozoa to a factor(s) released from the egg may be a key event in the fertilization process and may give insight into the mechanism underlying early egg-sperm communication [32]. In other words, which sperm must fuse with which ovum is determined by the biodiversification software. This is what Allah says in the Quran: "It is He who shapes you in the womb as He likes. There is no God but Him—the Mighty, the Wise." (Q. 3:6). It is evident from these Quranic messages that it is God who decides the biosoftware and hence phenotype of every

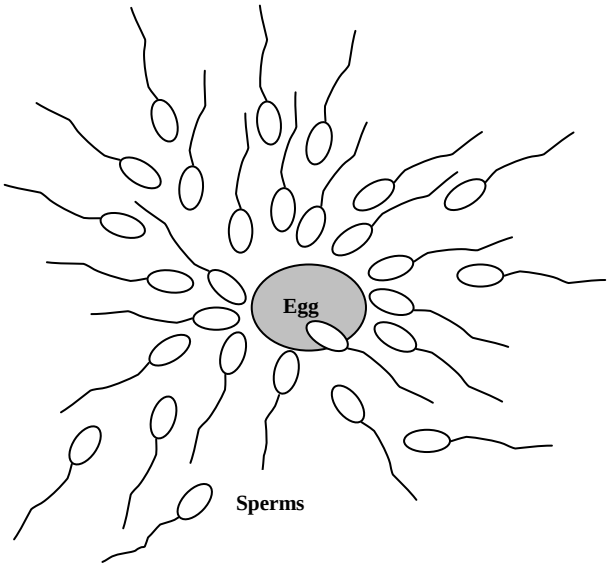

Figure 2. Fertilization of human female egg. Note: Diagram shows a swarm of sperms surrounding the egg. Only one sperm from among the millions present will be able to enter the egg and fuse with it.

individual.

It may also be deduced from these revelations that every one of us is carrying biomemes of hitherto unexpressed human potential for transmission to the next generation. It is one's biomemome that determines the biomemes to be expressed by the individual during his/her life and the biomemes to be generated in the gametes through biosoftware engineering processes for transmission to the next generation. The presence of unexpressed biomemes in one's biomemome makes him a 'biomemetic vector' (**Figure 3**) in the sense that he carries unexpressed biomemetic information for transmission to future generations [1].

The Quranic revelations are a clear indication of the programmed biodiversification process in human beings. Each human being represents a link in the biodiversification chain and carries a specific set of biomemetic instructions transmitted down to him through programmed diversification of the original *nafs* of Adam. The process preserves the continuity of a common bioinformation pool. It is not possible to say whether *Homo sapiens* has attained yet the maximum potentials physically and mentally. What we observe now is the scale of human biodiversity created so far. The biodiversification process will go on till the end of the world bringing about all the variability specified in the microbioprogram of human species (*i.e.*, Adam's *nafs*) at prescribed times and in prescribed geographic locations.

5. CREATION OF LIFE FROM NON-LIFE

From the foregoing, it is obvious that molecular biosoftware

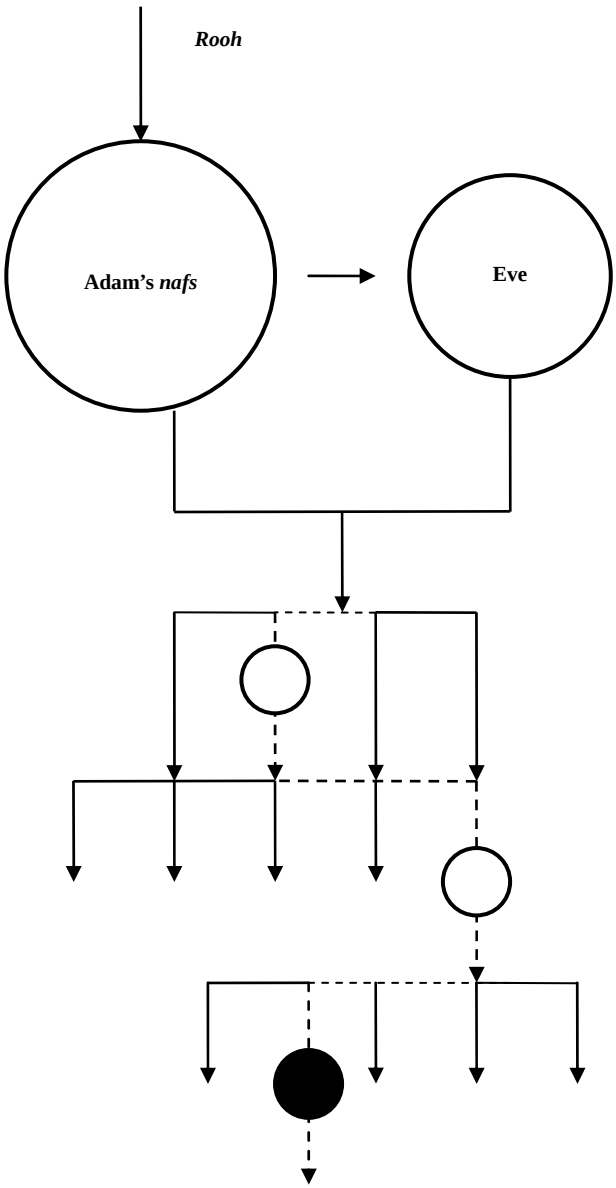

Figure 3. Illustration of programmed human biodiversification from a common biomeme pool (Adam's *nafs*). Note: A hypothetical biomemetic pathway of a biomeme is shown in the diagram by dashed line. Filled circle represents the individual in whom the biomeme is expressed. Unfilled circles represent vectors of the biomeme along the germ line. Downward arrows indicate diverse lineages. Racial, ethnic, linguistic, geographic, cultural and other types of phenomic diversity may be supposed to have been created in this way.

(genome) concept has several inexplicable anomalies and chemically untenable features. In contrast, Scriptural revelation of non-molecular biological information enables us to explain the phenomenon of life including human biodiversification comprehensively. Biologists are unable to explain "life" and "death" because the molecular gene and genome concepts adopted by them are

wrong. In other words, life is not a material phenomenon. Non-recognition of this truth leads biologists to try out synthesizing "life" from non-life. To create 'life", biologists start from scratch by synthesizing genome, chromosome, or a cell through artificial means using chemical molecules. Synthesis of these should in no way involve the use of living cell since it is likely that the non-molecular biosoftware of the living cell can be copied to the material or the cell being synthesized. The problem can be however approached from a totally different angle. Instead of creating synthetic cell without involving a living organism (which of course is impossible), a dead cell can be considered as equivalent to a prosthetic cell. It can be used as the starting material for the creation of life. The dead cell provides all the hardware configuration of a cell (genome, cytoplasm and other cell structures including cell wall) except life (biosoftware). That is to say, it is materially identical to a living cell. Biologists only have to restore life to it by chemical means without employing a living cell to prove that life is a material phenomenon and it originated from the combination of chemical molecules in the primitive environment. It may be noted in this context that the Scriptural revelation of non-material nature of bioinformation is a falsifiable proposition in the true scientific tradition. The failure to create a living cell through chemical synthesis without using a living cell or to restore life to a dead cell in fact invalidates the molecular biological program (genome) concept confirming instead the validity of the Scriptural revelation of the non-molecular invisible nature of the biosoftware and the existence of God.

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