A THEORY OF PROGRAMMED ORGANIC EVOLUTION

The creation of biological species except man by God can be thought of as a programmed phenomenon. It can never be a chance phenomenon driven by random mutation and natural selection as suggested by Darwin's theory. There were no gradations either in between any two organisms created by Allah. All of them are perfectly designed ones meeting the requirements of the overall divine scheme of things. On the lines of modern scientific thinking based on the existence of natural biosoftware engineering mechanisms as well as cell-directed mutagenesis, a theory of programmed organic evolution is proposed here.

Natural biosoftware engineering

There are several natural mechanisms and processes occurring in the cell, which can produce tailor-made chromosome compositions (Fig. 1). The ability of the chromosomes to store the biosoftware and the existence of cell-mediated mechanisms for cutting and splicing chromosome sectors and thereby producing different chromosome organizations meet the requirements of a possible cell-directed evolutionary phenomenon.

An important breakthrough in molecular biology is the discovery of various molecular tools and mechanisms available in the cell itself for genetic change. The view that stochastic mutations induced by cosmic radiation, chemicals, etc., are primarily responsible for bringing about genetic mutations is now fast yielding to the view of more extensive, non-random, cell-mediated mechanisms. Several mechanisms and systems capable of re-organizing chromosome and operating in the cell have been recognized. These are in fact biosoftware engineering process carried out in accordance with the biosoftware. A brief account of these natural biosoftware engineering methods is given here. It is to be noted that although the terms 'genetic sequence', 'nucleotide sequence', 'genome sequence' or any other term involving or referring to DNA are retained in this discussion to match the usage in contemporary scientific literature, they should be taken to imply a chromosomal region or a chromosomal sector (not specifically DNA structure) that stores a biomemes (program bits).

a) Genetic recombination: This occurs during meiosis. Through a process of 'crossing over', the segments of non-sister chromatids of a homologous pair of homologous dyads are exchanged. This swapping of portions leads to alteration of genetic information content in the resulting chromosomes. Huge genetic differences observed between siblings are the result of genetic recombination.

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

c) Transposable elements (TEs): The discovery of built-in natural genetic engineering mechanisms dates back to Barbara McClintock's (Nobel laureate) pioneering cytogenetic studies on transposable elements during the late 1940s and early 1950s. These mobile elements offer a powerful tool of cut-and-splice technique in bringing about specific changes and modular organization of genomes as hierarchical systems in the cell. Transposition plays an important role in chromosome rearrangements. Insertion, deletion and inversion occur either as a direct consequence of transposition or by general recombination between two copies of an element present at two locations. Horizontal gene transfer can also occur through transposition. These elements are present in all prokaryotes and eukaryotes.

The proposed process

The concept of programmed organic evolution proposed here does not view the origin of new species as a consequence of random mutations (caused by the action of certain agents external to the cell) occurring in the existing species followed by natural selection. It also does not support the current belief that living things originated from non-living matter as a continuation of inorganic evolution. Instead, the creation of living species has been viewed as the result of execution of the divine Bioprogram. The execution of this program is supposed to have been performed as a cell-directed phenomenon. Based on this rationale, it is possible to look at the process of organic evolution in a quite different light as a programmed phenomenon.

Origin of the primordial biochip

A multicellular biosystem (e.g., a human individual) evolves (develops) through a series of transformations starting from a primordial cell (zygote). The organic evolution might also have got off from a single cell as is generally believed. But, contrary to the current belief, the first cell formed on this planet could not have been an organism or a species but a cell which contained the divine Bioprogram necessary for the evolution of the various species. This first cell containing the Bioprogram may be called as the primordial biochip (PBC). The PBC also compares well with the state of the inorganic universe at the big bang singularity. The universe at time zero (big bang) was a highly condensed mass of zero volume and infinite density. It was that primordial material which carried the program for the evolution of the inorganic world. In other words, in the origins of the inorganic world and organic world (including individual organisms) we find a pattern. Perhaps it is how nature initiates evolution of a system.

Woese [1] proposed the concept of the 'universal ancestor' to look at the rooting of the evolutionary tree. It was a genetic annealing model to develop a picture of the universal ancestor. The ancestor according to this model could not have been a particular organism, a single organismal lineage. It was communal, a loosely knit, diverse conglomeration of primitive cells that evolved as a unit, and it eventually developed to a stage where it broke into several distinct communities, which in turn became the three primary lines of descent. The primary lines, however, were not conventional lineages. Each represented a progressive consolidation of the corresponding community into a smaller number of more complex cell types, which ultimately developed into the ancestor(s) of that organismal domain. The universal ancestor is not an entity, not a thing. It is a process characteristic of a particular evolutionary stage. Woese [2] advanced a theory of evolution of cellular organization based on the dynamic of horizontal gene transfer. According to him, horizontal gene transfer is one of the important keys to understand cellular evolution. If a cell was simple and highly modular in organization, horizontal gene transfer would play a stronger role in its evolution than otherwise and the cellular evolution would have been driven in the main by horizontal gene transfer at its beginnings. The universal tree has no root in the classical sense. The root is actually a Darwinian Threshold, the first point at which we can begin to give tree representation to the organismal evolutionary course. A certain 'symmetry of descent' is inherent in the classical view that is totally lacking here, because the root is not classical root, the sister lineages resulting from the earliest branchings are in no sense 'sisters'. They differ in fundamental ways. He proposed a framework for conceptualizing cellular evolution involving evolution of translation process in an RNA-world populated by what he called 'supramolecular aggregates' (higher-order architectures designed around nucleic acid componentry) and a variety of other stages and conditions ultimately producing not one but three distinctly different cell types from which the extant life on the earth had descended.

The functional areas in which key developments have occurred before the formation of Last Universal Ancestor include exploitation of available chemical energy sources, uptake and extrusion of small molecules as needed in general metabolism, biosynthesis of unavailable intermediate chemicals, synthesis of specific and detailed structures for nucleic acids and proteins, regulation of macromolecular synthesis, synchronization of DNA synthesis and cell division with the growth of cytoplasm, establishment of cell shape and cell division and development of 'preplanned' responses to environment challenges. In addition, there are many thousands of enzymatic reactions that must have been perfected or perfected enough to be functional for growth and survival of the individuals in the period from the First Cell to the Last Universal Ancestor [3]. This is a long list of highly complicated and complex processes and mechanisms that are thought to be necessary to originate the Ancestor. Given that these are all what is required for the origin of the Ancestor, do our wisdom and logic permit us to believe that these things can occur by chance in the required chronology. Further how will new mechanisms and processes arise by chance?

Molecular evolutionists gave the name LUCA (last universal common ancestor) for the common ancestor of all life [4]. Despite the wealth of genomic data, LUCA has remained elusive. Whether it is a simple or a complex one is not yet understood. Genome sequencing has given hope to find out the answers to many such questions, and the general thinking is that LUCA may be a pool of genes shared by a host of primitive organisms [5]. 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 University in Orsay [5]. 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 concept comes very close to the requirement and role of the PBC in the proposed theory of programmed evolution. The theory of programmed evolution does not assume that the primordial cell formed at the beginning of life is an organism (i.e., the first species) as assumed in the Darwinian model. The LUCA, however, differs from the PBC in an important aspect namely, the latter has a program to guide the evolution of millions of microbioprograms (or species) without the need of chance mutation and natural selection. The PBC is defined here as a cell consisting of chromosomes that store the Bioprogram, and other necessary organelles (hardware components) to execute the Bioprogram. 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 evolution (development) of a human individual in the mother's womb. The PBC with a built-in program as the driving force can explain the phenomenon of evolution of species consistent with natural evidence. As against *chance* implied in Darwinian models, the theory of programmed evolution views the origin of PBC as a pre-determined, directed synthesis. A probable sequence of events that might have led to the production of the PBC is discussed here.

The Quran tells us that Allah created every living thing from water.

"…We made from water every living thing. Will they not then believe?"

(Q. 21:30)

This is one aspect (or perhaps the only one) of the origin of living beings in which there is consensus among biologists and which agrees with the Quran. 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 [6]. The most crucial step in the formation of the PBC may be the creation of chromosome, which by virtue of its chemical structure acquires the property of information storage in accordance with the Abioprogram. The creation of the first memory device in the prebiotic aqueous environment is to be seen as a landmark event in the history of life on this planet. The divine Bioprogram can now be installed in that memory device leading to biogenesis (the birth of life) in the non-living world. With the installation of the divine bioprogram, the ambient chemical environment got switched over to biotic (biological) environment. Initially, the program would have directed bioprocesses utilizing the chemical compounds in the prebiotic soup leading to the production of hardware components (cellular structures) and ultimately organizing them in the form of a cell, the first biochip, which may be called the Primordial Biochip (PBC). The PBC so formed would have the hardware components necessary to execute the Bioprogram. 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. Recent discovery of nanobes in ancient Australian sandstone by scientists at the University of Queensland, indicated that the structures were as small as 20 nm across and looked like fungi. These nanobes seemed to have the enzymatic and genetic material considered essential for life. Nanobes are now seen virtually everywhere [7]. The PBC would have been a cell with minimal hardware components (cellular structures) to store the Bioprogram and also to execute it. The execution of the Bioprogram carried in the PBC led to the programmed evolution of living organisms.

The development of a human individual from the zygote (as already discussed) illustrates how the program contained in that cell is executed with the help cellular hardware to ultimately produce a natural computer biosystem, the adult. In other words, different kinds of tissues (groups of homogenous cells) were produced through the operation of a biomemome (bioprogram at the level of individual) carried in the starting biochip, the zygote. It is therefore reasonable to assume that the Bioprogram carried in the PBC is such that its execution will produce a large number of cells with different microbioprograms (bioprogram at the level of the species). In that programmed evolutionary process, several biosoftware engineering mechanisms would have played key roles. The evolutionary process is supposed here as essentially a programmed phenomenon to differentiate the Bioprogram into as many microbioprograms (species) as specified in it. Software engineering mechanisms and systems like mobile elements and enzymes would have come into operation to perform a wide range of tasks like cutting and splicing of chromosomal sectors, shuffling of the sectors, replication, deletion and copying of the sectors with remarkably high fidelity to ultimately accomplish the mission. All these cellular functions are program-directed phenomena carried out with extreme specificity and accuracy. These processes might have been triggered into operation in the sequences and time schedules specified in the Bioprogram to ultimately produce a large number of cells each with a different but viable microbioprogram carried in its chromosomes.

The origin of PBC has more significance than what the traditional theories of evolution give to the origin of the first organism or to the LUCA. Although the evolutionists treat organic evolution as a continuation of inorganic evolution, the phenomenon has never been thought of as a landmark changeover event from chemical principles to biological (information) principles. It is to be acknowledged that biological principles are fundamentally different from chemical principles and that genetic information was not available in nature prior to the installation of the divine biosoftware. With the installation of the bioprogram in the PBC, transition from non-life to life took place.

Evolution of the microbioprograms

A microbioprogram is bioprogram at the species level. We may now examine the probable pathways through which the PBC could have produced millions of microbioprograms each representing a species (Fig. 2). The execution of the bioprogram carried in the PBC may be supposed to have occurred through a *phylogenetic biosoftware differentiation* (PBD) mechanism involving such processes as cutting and splicing of chromosome sectors (program bits), their replication, shuffling and rearrangement of sectors to form new chromosome architectures and finally reallocation of the chromosomes to biochips (cells) carrying viable microbioprograms. The process of PBD may be defined as the programmed synthesis of microbioprograms during which the Bioprogram stored in the PBC undergoes step-by-step differentiation leading to the production of as many microbioprograms as specified in the Bioprogram. Physically this would appear as a process during which the chromosomes carried in the PBC underwent cutting and splicing, deletion, translocation, recombination, replication, etc. (natural software engineering processes), in specified sequential steps ultimately leading to the production of cells each with a microbioprogram carried in specific number of chromosomes. Each of these end cells carries the microbioprogram of a species.

Taking the cue from the evolution of a human individual from the zygote, we may visualise the whole process of creating millions of microbioprograms as follows. The PBC might have undergone division initiating the biological evolution. During division, the program might have been differentiated and partitioned into as many number of mother cells as stipulated in the Bioprogram. The number of mother cells produced (or the number of cell divisions occurred) depends on the number of evolutionary lineages (domains of life) to be created. Taking the universal tree of life, i.e., the modern phylogenetic classification based on 16S ribosomal RNA data (16S rRNA), as the basis, three domains namely, Bacteria, Archaea (microbes living in extreme environments) and Eukarya (or sometimes termed Eukaryota) [8] may be considered to form the three lineages for which separate mother cells are produced from the PBC. The three kingdoms – animals, plants and fungi – are just three of about a dozen extant major branches of the eukaryote domain [9]. The universal tree of life represents the evolutionary relationships among all cellular life forms (thereby excluding viruses). However, the evolutionary relationships among these three groups, and even the status of the Archaea, are still hotly debated among evolutionary biologists [10]. Nevertheless, for convenience in illustration of PBD, the mother cells that form from the PBC during the initial software differentiation process may be treated on the lines of this categorization. Each mother cell might have undergone further differentiation of the software in successive steps along different courses in accordance with the program representing the domain concerned. For example, the Eukarya mother cell, following PBD, produces daughter cells representing each kingdom in that domain. Further differentiation of the mother cell representing each kingdom might have, in turn, directed the evolution of microbioprograms of species in the kingdom concerned. For example, the plant mother cell or the plant mother chip (PMC) carried the program to direct the evolution of the species of the plant kingdom and the animal mother cell or the animal mother chip (AMC) carried the program to direct the evolution of species of the animal kingdom, and so on (Fig. 2). It may be noted that human species is not included among the species created through programmed evolution as the Quran informs us that man was created in Allah's abode.

Physically, the PBD may be visualized as follows. A mother cell undergoes shuffling of chromosomal sectors through cutting and splicing, replication and reorganisation of the chromosomes in ways specified by the program and repeated cleavage to produce something like a morula, a ball of cells. In this way, the chromosomes (memory that stores the Bioprogram) in the mother cell were restructured, grouped and allocated to different cells. Each of these daughter cells separates from the cluster to become the starting cell for the evolution of the species in a phylum. This would mean that a daughter cell had the software package necessary for the evolution of all the species under a phylum. The daughter cells might have undergone further differentiation of software through the same processes as in the previous stage, perhaps on different time schedules as stipulated in the program. This stage may be referred to as the embryonic stage of the bioworld. The PBD led to the production of end cells, each of which represented a species under the phylum. An end cell is a full-fledged cell with all the hardware components (cellular structures) required for the development of an individual of the species. The end cell might have undergone further software differentiation and division producing daughter cells representing sexual dimorphs, polymorphs, castes, etc., depending on the species. These daughter cells formed the ‘zygotes’ for the growth and development of the first individuals of the various species via process of development through differentiation. The term ‘phylum’ is used here to denote a group of organisms and not the taxonomic species under a phylum. If the stages of programmed organic evolution and ontogenetic development of an individual from zygote are compared, each tissue of the human individual may be likened to an end cell (i.e., species) of the programmed organic evolution and each intermediate cell that represented a blastomere of the ontogenetic development that led to the development of an organ of the body may be likened to a phylum of the programmed organic evolution. Thus the tissues and end cells, the products of ontogenetic development and programmed organic evolution respectively, represent stable stages.

The end cells produced by the animal mother cell might have been in the form of eggs while those originated from the other mother cells might have been in the form of single cells, spores, seeds, etc. Whatever the form in which they emerged, these cells might have been dispersed over the water and land areas by natural processes resulting in the widespread distribution of the species on the earth. In fact, for all practical purposes, the evolution of species is complete with the creation of the end cells (microbioprograms). The ontogenetic development of individuals from the end cells representing species might have been programmed to take place on different time schedules. This is reflected in the sequence and chronology of appearance of the various species in the fossil record. Depending on the species, sexually dimorphic, polymorphic, asexual and other forms of individuals would have developed from the end cells, which through further reproduction increased their population and perpetuated their species. It may be noted that programmed evolution does not require intermediate stages to create a fully designed, perfect organism. It is creation in one go through a programmed evolutionary process. Therefore the theory is consistent with the natural evidence of lack of transitional forms in the fossil record.

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

a) A divine software ‘Bioprogram’ (the source of biological information on this planet) is supposed to be the driving force behind the organic evolution.
b) The origin of species is viewed as the creation of diverse software packages (microbioprograms) from original single software, the Bioprogram, through a process of software differentiation.
c) The organisms that developed from the microbioprograms are in perfect form and required no intermediate forms.
d) Programmed evolution does not assume a common ancestor for all the species.
e) Programmed evolution is a deterministic phenomenon with a purpose and a goal identical to a task performed by a computer.

Although the existence of natural genetic engineering systems and mechanisms, and the possibilities of genetic rearrangements and evolution of new genotypes are known, the process of evolution employing such engineering systems has not been conceptualized. These mechanisms are recognized here as “biosoftware engineering processes”. The number of steps indicated in the biosoftware differentiation process discussed above is purely arbitrary and is only intended to explain the process in a broad sense. The number of steps through which the differentiation process might have taken place would be as specified in the program. Only through a process like PBD, biodiversity of very high magnitude as observed in nature can be created. Darwinian factors of spontaneous mutation and natural selection are too inadequate to explain the origin of organisms even if we accept such factors do operate in nature.

Sudden appearance of new species punctuated by long periods of stasis (Punctuated Equilibrium) can be explained by the proposed theory of programmed evolution. According to Douglas Futuyma, a prominent evolutionary biologist, “Organisms either appeared fully developed or they did not. If they did not, they must have developed from preexisting species by some process of modification. If they did appear in a fully developed state, they must indeed have been created by some omnipotent intelligence” [11]. The proposed theory of programmed evolution supports the latter. Almost all groups at all taxonomic levels first appear in the fossil record as ‘type’ forms, and then ‘explode’ into a large number of diverse lineages with a mix of related but not identical potentials for adaptive morphological change [12, 13, 14]. This pattern is suggestive of partitioning of a very large common genetic package with a large number of alternate morphological potentials. But no known mechanism is so far available for generating such information-dense primordial source. According to Grasse, evolving species acquire a new store of genetic information through “a phenomenon whose equivalent cannot be seen in the creatures living at the present time (either because it is not there or because we are unable to see it)” [15]. These observations are fully consistent with the proposed theory of programmed evolution because it recognizes the existence of the divine bioprogram (the source of biological information) as the driving force behind the evolution of species.

Insofar as chromosomes form the storage device of the cell (biochip) and the bioprogram is stored in parts (program bits) in different sectors of the chromosomes of the PBC, microbioprograms specific to different species can be created by generating the required sectors through natural software engineering mechanisms and assembling and reorganising them into viable sets of instructions in a programmed manner. In this way ‘new’ genetic package can be produced. This aspect is the most important and unique feature of the theory of programmed evolution as it describes the original source of genetic information and how ‘new’ genetic information can be generated from this source. The current scientific theories are silent about the source of genetic information.

The theory of programmed evolution allows great flexibility in time scales required for the evolution of the biological species. Although the time schedules stipulated by the divine Bioprogram for various stages of software differentiation cannot be reasoned out, the rapidity with which the chromosomal changes, cutting and splicing of chromosome sectors and cell division occur in nature is very much indicative of the speed with which the organic evolution up to the stage of creating the end cells (microbioprograms of the various species) would have occurred. The ontogenetic development of the end cells might have occurred subsequently over a long period and in the sequence specified in the bioprogram. The sequences and spacing (time intervals) observed in the appearance of the species in the fossil record are a reflection of this programmed phenomenon.

The theory of programmed organic evolution based on the bioprogram (biosoftware) differentiation and its reorganisation into viable sets of millions of microbioprograms predicts extensive mixing of chromosomal regions and the possibility of finding identical program bits in the microbioprograms of the species. Physically these program bits will be represented by identical chromosomal sectors, which store them. Since DNA is part of the chromosomal material, the existence of identical sequences in the genomes of different species is a reflection of the existence of identical chromosomal sectors in them. This can be taken as a confirmatory proof of the occurrence of PBD during evolution. Studies relating to molecular evolution provide considerable evidence of chromosome rearrangement, shuffling, reorganisation, etc., during the evolution of species. These findings serve as a window to the mechanism of PBD that was in operation during programmed evolution of species. Little wonder that Philippe and Forterre [16] found the phylogenies as highly confusing due to the combining effects of gene duplication, gene loss, lateral gene transfer, etc. Experimental evidence for the occurrence of PBD can also be obtained from several published reports on comparison of genome sequences. Wide variations are observed in karyotypes (number, size and shape of chromosomes in a somatic cell) of organisms. Comparison of karyotypes within and between species reveals that the differences are due to chromosome rearrangements. These rearrangements had played a major role in organic evolution [17]. There is undoubtedly a correlation between the rates of speciation and chromosome rearrangement [18]. Chen *et al.* [19] described the evolution of antifreeze glycoprotein (AFGP) gene in an Antarctic fish from a gene encoding a pancreatic trypsinogen. Freezing resistance in this fish is due to blood serum glycoproteins that lowered their freezing temperature below that of the subzero sea surrounding them. Commenting on their work, Logsdon and Doolittle observed that the relationship of the two genes was not simply one of duplication and divergence, co-option/recruitment or exon shuffling, but the novel portion of the AFGP gene (encoding ice-binding function) derives from the recruitment and iteration of a small region spanning the boundary between the first intron and second exon of the trypsinogen gene [20]. Regulation of physiological functions with approximate daily periodicity (circadian rhythms) is a characteristic feature of eukaryotes. Among the prokaryotes, cyanobacteria only possess circadian rhythmicity. It is controlled by a cluster of three *kai* genes. Dvornyk *et al*. reported that the prokaryotic circadian pacemakers had evolved through multiple lateral transfers and gene duplications and losses [21]. Cases of genes in the same phylogenetic clade occurring in different chromosomal regions and genes belonging to distantly related phylogenetic clades occurring very closely in a chromosomal region are quite common [22]. These observations were explained as the result of several chromosomal rearrangements occurred at the regions of these genes and the shuffling of genes (physically chromosomal regions) contained in different genomic clusters. In another study, Pevzner and Tesler [23] found large number of rearrangements and extensive reuse of breakpoints from the same short fragile regions in mammalian evolution. Multigene families occur in animals and plants. Some multigene families arise by concerted evolution, a process that generates new genes by interlocus recombination or gene conversion. There is also evidence that other multigene families such as immunoglobulin (Ig) genes (genes associated with the immune system in mammals) can also be created by repeated gene duplication in the evolutionary history of the organisms [9, 24]. All these findings add strength to the operation of PBD during organic evolution.

Several studies had provided evidence for cell-directed mutagenesis (see section 5.5), which can be considered as program-directed phenomena implying that the cell itself can decide the type of mutation to take place. It is reminded here that the term 'mutation' in the proposed theory means a change in software package brought about by a change in chromosome sector(s), which carries a program bit. Transposable elements present in the cells have enormous mutagenic potential. Deletions, insertions, frameshifts, inversions, duplications and translocations have all been observed as consequences of transposition events. The time-scale on which transposable element-induced mutation events can take place is unrivalled by any other natural mutagenic agency. So if mutations are the raw material of the origin of all species, then transposable elements must be involved in the origin of most if not all species [25]. These observations provide ample evidence for the existence of necessary structures and commands within the cell itself to execute mutation (change in chromosomal sectors) operations.

The so-called co-evolution, parallel evolution, convergent evolution, etc., of Darwinian origin, are nothing but events resulting from programmed timing and scheduling of development of individuals from the end cells representing various species. They are not a product of random process or chance event.

References

[1] Woese, C. 1998. The universal ancestor. *Proc. Natl. Acad. Sci. USA.* 95:6854-6859.

[2] Woese, C.R. 2002. On the evolution of cells. *Proc. Natl. Acad. Sci. USA* 99(13):8742-8747.

[3] Koch, A.L. "Bacterial origins" doi: 10.1038/npg.els.0000445.

[4] Lazcano, A. and Forterre, P.J. 1999. *J. Mol. Evol.* 49:411-412. Taken from [17].

[5] Whitfield, J. 2004. Born in a watery commune. *Nature* 427:674-676, News feature.

[6] 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.

[7] Leslie Mullen. 2003. Life from scratch? Astrobiology Magazine, Nov 4, 2003 issue.

[8] Koch, A.L. "Bacterial origins" doi: 10.1038/npg.els.0000445.

[9] Ayala, F.J. and Fitch, W.M. 1997. Genetics and the origin of species: An introduction. *Proc. Natl. Acad. Sci. USA* 94:7691-7697.

[10] Brown, J. R., Universal Tree of Life, http://www.els.net/els/public/search/ search_public.asp.

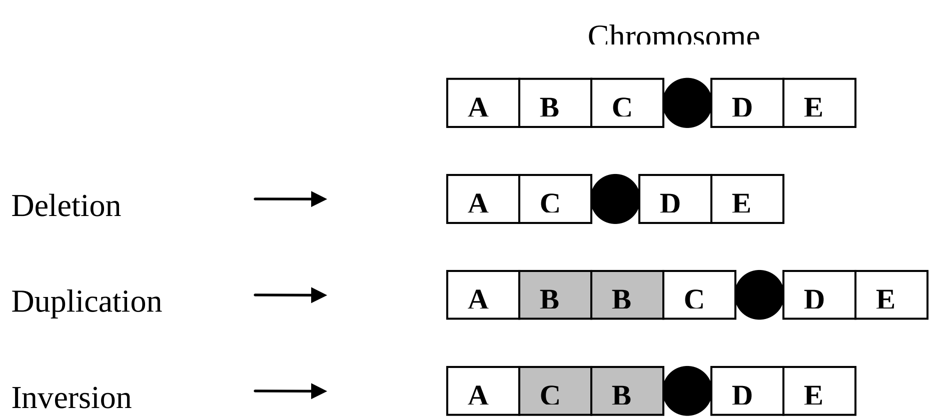
[11] Futuyma, D.J. 1983. Science on Trial, New York: Pantheon Books p. 197; Cited at: http://www.harunyahya.com/20evolution01.html. Accessed November 14, 2002.

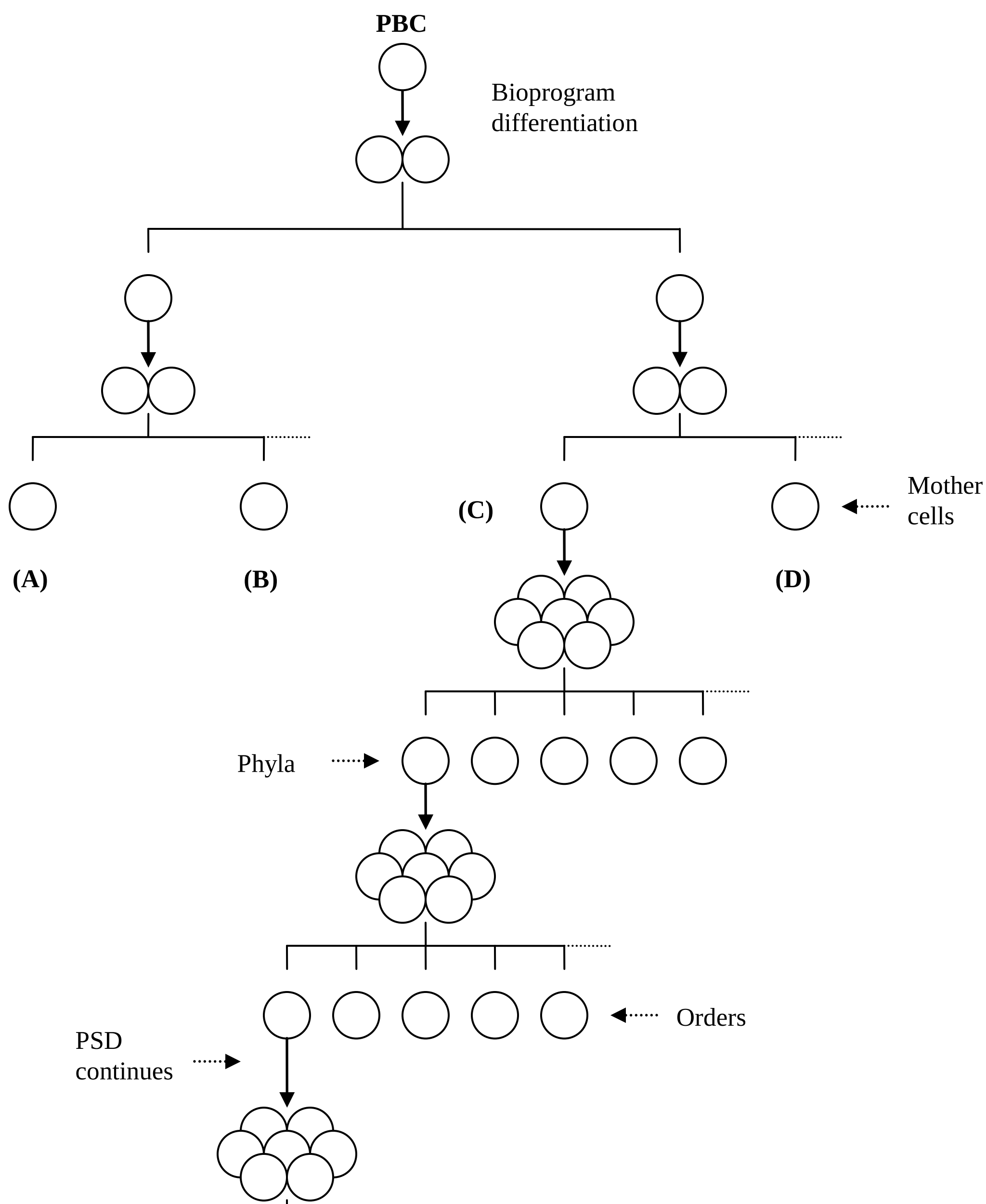
[12] Carroll, R.L. 1988. Vertebrate Paleontology and Evolution. W. H. Freeman and Company, New York. Taken from: Wilcox, D.L. 1992. A blindfolded watchmaker: The arrival of the fittest. *In* Darwinism: Science or Philosophy, Chapter 13. *Proc. Symp. Darwinism:Scientific Inference or Philosophical Preference?* eds. J. Buell and V. Herne, Foundation for Thought and Ethics, Texas.

[13] MacFadden, B.J. and Hulbert, R.C. 1988. Explosive speciation at the base of the adaptive radiation of Miocene grazing horses. *Nature* 336:466-468. Cited in: Wilcox, D.L. 1992. A blindfolded watchmaker: The arrival of the fittest. *In* Darwinism: Science or Philosophy, Chapter 13. *Proc. Symp. Darwinism:Scientific Inference or Philosophical Preference?* eds. J. Buell and V. Herne, Foundation for Thought and Ethics, Texas.

[14] Larson, A. 1989. The relation between speciation and morphological evolution. *In* Speciation and Its Consequences. Eds. D. Otte and J.A. Endler. Sunderland, MA: Sinauer. P. 575-598. Cited in: Wilcox, D.L. 1992. A blindfolded watchmaker: The arrival of the fittest. *In* Darwinism:

Science or Philosophy, Chapter 13. *Proc. Symp. Darwinism:Scientific Inference or Philosophical Preference?* eds. J. Buell and V. Herne, Foundation for Thought and Ethics, Texas.
[15] Grasse, P.P. 1973. L'Evolution de Vivant – published in English entitled "The Evolution of Living Organisms (1977) – Cited in: Johnson, P.E. 1994. Darwin's rules of reasoning. In Darwinism: Science or Philosophy. (eds.) J. Buell and V. Hearn, Foundation for Thought and Ethics, Richardson, U.S.A.
[16] Philippe, H. and Forterre, P. 1999. The rooting of the universal tree of life is not reliable. *J. Mol. Evol.* 49:509-523.
[17] Burt, D.W. Chromosome rearrangement in evolution. doi:10.1038/npg.els.0001500.
[18] King, M. 1993. Species Evolution: The Role of Chromosome Change. Cambridge: Cambridge University Press.
[19] Chen, L., DeVries, A.L. and Chang, C.-H.C. 1997. *Proc. Natl. Acad. Sci. USA.* 94:3811-3816.
[20] Logsdon, Jr., J.M. and Doolittle, W.F. 1997. Origin of antifreeze protein genes: A cool tale in molecular evolution. *Proc. Natl. Acad. Sci. USA.* 94:3485-3487.
[21] Dvornyk, V. Vinogradova, O. and Nevo, E. 2003. Origin and evolution of circadian clock genes in prokaryotes. Proc. Natl. Acad. Sci. USA. 100(5):2495-2500.
[22] Niimura, Y. and Nei, M. 2003. Evolution of olfactory receptor genes in the human genome. *Proc. Natl. Acad. Sci. USA.* 100(2):12235-12240.
[23] Pevzner, P. and Tesler, G. 2003. Human and mouse genomic sequences reveal extensive breakpoint reuse in mammalian evolution. *Proc. Natl. Acad. Sci. USA.* 100(3):7672-7677.
[24] Nie, M., Gu, X. and Sitnikova, T. 1997. *Proc. Natl. Acad. Sci. USA* 94:7799-7806.
[25] Becker, H.A. and Lonnig, W.E. "Transposons: Eukaryotic". doi:10.1038/npg.els.0000592.





PBC
Bioprogram
differentiation
Mother
cells
(C)
(A)
(B)
(D)
Phyla
Orders
PSD
continues

Fig. 2. Proposed phylogenetic biosoftware differentiation (PSD) pathway for the synthesis of microbioprograms (representing species excepting man) from the non-physical divine bioprogram.