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Research Article

Structural and Functional Stability and Asymmetry Among Organelles and Organs Appears Regulated by The Specific Genes and Stem Cells. II: A Concept of Stem- Genes in Specific Stem Cells

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Abstract

Background

This communication is based on elaboration of the two superb and immortal statements, one by E B Wilson in 1925, "Every individual is a cell or has been a cell" and another by Raspail in 1939: "Omnis cellule e cellule: Cells come from preexisting cells". This is well established that the final product of the fertilization is the Zygote, a single cell in all eukaryotes which is soon covered by an outer protective layer and then starts dividing into many and many cells. It is the stage when clusters of many cells are differentiated as stem cells; some stem cells take over as "specialized stem cells".

Hypothesis: Specific stem cells among several stem cells are probably destined to control many molecular functions of regulating inter-genic and intra-chromosomal events which are directly related with genomic routine as well as evolutionary strategies. These specialized stem cells are typically loaded only with specific stem genes which are never present or can never express even if present, in other categories of stem cells which are fundamentally responsible for morphological, anatomical, structural and functional organization of the specific individuals of a species.

Inference: Even if cells to begin with are multipotent the distribution of genes among differentiating stem cells has to be very selective. Stem cells are of three kinds (stagnant stem cells, mobile or circulating stem cells and Intra-genomic stem cells) but the genes being distributed among these cells have to be very selective and even different. Stem cells regulating intra-chromosomal molecular (natural aberrations, repairing and conservation mechanisms) events have to be absent in other types of stem cells. Stem genes, hypothetically, are chiefly stored as deeply conserved sequences for millions and millions of years among the basic genomes of all eukaryotes. Obviously, revival of these genes may be the explanation of finding some common genes among plants, animals including man. Basic genome is imagined to be those sequences which were randomly distributed among trillions of cells being evolved as "eukaryotes" during the Early Permian. Therefore, Stem –genes are those special genes which are retained for millions of years as deeply conserved DNA sequences (genes) in some exclusive stem cells which may express in various totally unrelated (in terms of evolutionary path) organisms.

Keywords: Concept of stem-genes; Ceaseless replication; Random distribution of DNA sequences ; Basic genomes; Specialized stem cells; Homologous genes.

Introduction

There have been several classical statements pronounced by all time great biologists but two superb and immortal statements, one by E B Wilson in 1925, "Every individual is a cell or has been a cell" and another by Raspail in 1939: "Omnis cellule e cellule: Cells come from preexisting cells" have been immortal and indelible in biology. It is well known since the earliest days of discoveries in biology that the final product of the fertilization is the Zygote, a single cell in all eukaryotes which is soon covered by an outer protective layer and then starts dividing into many and many cells. It is at this stage when clusters of many cells are differentiated as stem cells; some stem cells take over as "specialized stem cells". This basic event is a fundamental truth for embryological stages of plants, animals including man (1-6). This short communication repeats an important question that why and how should certain DNA sequences be found or detected in totally unrelated genomes of a single cell prokaryote to the single cell eukaryote and many multicellular plants, animals (reptiles, birds, many mammals like dogs etc) and seemingly highest evolved "Homo sapiens" the man (7-10). Earlier attempts based on ceaseless multiplication of DNA sequences and their random distribution among evolving and multiplication of trillions and trillions of cells (11- 15) have given only partial answers.

Hereunder is placed a theoretical concept of "stem genes" which are conceived to be very special genes loaded in very selective stem cells exclusively meant for conservation of sequences within genomes. Some of these genes express in all genomes and many are stored as silent or dormant (15), unless provoked by some or the other molecular and chromosomal mechanism (s) (16-23).

Approach and General Observation

The most fascinating and evolutionarily consistent results of regular field and laboratory work since 1970 (onwards) have led to a very indelible result that there are many DNA sequences which are randomly distributed among all kinds of organisms. Several gene sequences have been investigated to be found shared by various organisms like microorganisms, plants, animals including man. All these findings and their significance along with discoveries of many new species have been wrapped in publications (24-33). Some classical examples are presented below along with brief discussion on kinds of organisms examined and known in the relevant literature.

Discussion

Stem cells

The stem cells are innately undifferentiated cells located in the meristems of plants are totipotent cells equipped with re-

generative powers that facilitate plant growth and production of new organs throughout lifetime. Two distinct areas of stem cell, the apical meristem and the lateral meristem are recognized on the basis of prevalence. These cells (34-37) serve as the origin of plant vitality by providing a steady supply of precursor cells to form differentiated tissues and organs in plants. Additionally, stem cells are clonogenic cells that are capable of differentiation into multiple mature cell types (multipotency), and simultaneously replenishing stem cell pool (self-renewal), which allows them to sustain tissue development and maintenance. Theoretically stem cells are of three types : stagnant stem cells, mobile or circulating stem cells and Intragenomic stem cells. (I) Stagnant cells are those stem cells which are localized at a fixed locus within a specific tissue. For example, the stem cells in a leaf, root or stem tissue are localized in the meristematic region; in leaf tissue always within the marginal tissue. These stem cells are characterized by unique ability to create all differentiated cell types and the ability to self-renewal (so that the number of stem cells is maintained). Plant stem cells never undergo aging process but immortally give rise to new specialized and unspecialized cells, and possess the molecular potential to grow into any organ, tissue, or cell in the plant body. These stagnant stem cells are helpful in framing structural as well as functional stability among different organs

(II) Circulating stem cells: These are mobile adult stem cells with specific gene expression profiling, as well as enhanced mitochondrial remodeling which might be helping in restoring the conservative intricacies of genomic evolution.

Genomes conserve Genes for millions and millions of years. One of the most fascinating results of modern DNA technologies and revolutionary developments on molecular genetics have proved that there are many DNA sequences which are randomly distributed among all kinds of organisms. Several gene sequences have been investigated to be found shared by various organisms (26,38-46) like microorganisms, plants, animals including man..Some classical examples are presented below. Infact by all technical approaches have confirmed that genes were randomly distributed among evolving cells in too Early phase of PreCambrian (44, 46-49)

An alga

A significant observation concerns a single cell alga (Figure.1A) Chlamydomonas (44). Chlamydomonas reinhardtii is a unicellular green alga whose lineage diverged from land plants over 1 (one) billion years ago. Analyses of the Chlamydomonas genome (Merchant et al, 2007) advance our understanding of the ancestral eukaryotic cell and reveal previously unknown genes associated with photosynthetic and flagellar functions. Many Chlamydomonas genes can be traced to the green plant or plant-animal common ancestor

by comparative genomic analyses. It is a model system for studying chloroplast-based photosynthesis, as well as the structure, assembly, and function of eukaryotic flagella (cilia), which were inherited from the common ancestor of plants and animals but lost in land plants (except in some forms of gametes). Specifically, many *Chlamydomonas* and angiosperm genes are derived from ancestral green plant genes, including those associated with photosynthesis and plastid function; these are also present in *Ostreococcus* spp. and the moss *Physcomitrella patens*). Genes shared by *Chlamydomonas* and animals are derived from the last plant-animal common ancestor and many of these have been lost in angiosperms.

Bryophytes (Liverworts Figure. 1 B & C)

The classical observations based on most modern and sophisticated experimentations have confirmed that the liverwort *Marchantia polymorpha* Y chromosome has the same MSY sequences which are typical of human Y chromosomes (26-29; 49-50). Finally, Japanese molecular biologists also confirmed that human Y chromosome sequences (MNS) are definitely present in a liverwort *Marchantia polymorpha* genome.

An important discovery has been again brought to light by Li et al.,(53) regarding the plant hornwort, *Anthoceros* (Figure.1C). According to them the hornwort *Anthoceros* (bryophyte), centromeres may not be characterized by a higher

repeat density compared to other parts of the genome. In *Anthoceros agrestis* Bonn, tandem repeats with a unit size over 30bp gave rise to only very short arrays, and these repeats do not show a clear spatial clustering. While gene density does fluctuate along the scaffolds, extensive regions with low gene density typical for centromeric regions of vascular plants were missing. Also, Li et al., did not identify stretches of scaffolds having an elevated repeat content, other than the putative telomeric regions. Since the *Anthoceros* genomes lack repeat-dense centromeres as well as whole-genome duplication, the genus becomes of superlative importance from both morphological as well as evolutionary (54) point of view. Several genes have been found which are known to be involved in angiosperm meristem and stomatal function and these are also conserved in *Anthoceros*.

These genes get regulated during sporophyte development, suggesting possible homologies at the genetic level. Li et al. have also found genes involved in cyanobacterial symbiosis and they report that LCIB, a *Chlamydomonas* CCM gene, is present in hornworts but absent in other plant lineages, implying a possible conserved role in CCM function. This is an established fact known for centuries that both theoretically and practically closely related species differ in genetic make-up and related morphological and functional traits. This is remarkable that modern DNA technology based approaches are discovering such unique variations even at specific gene levels.



Chlamydomonas sp

Marchantia polymorpha male plant

Anthoceros sp

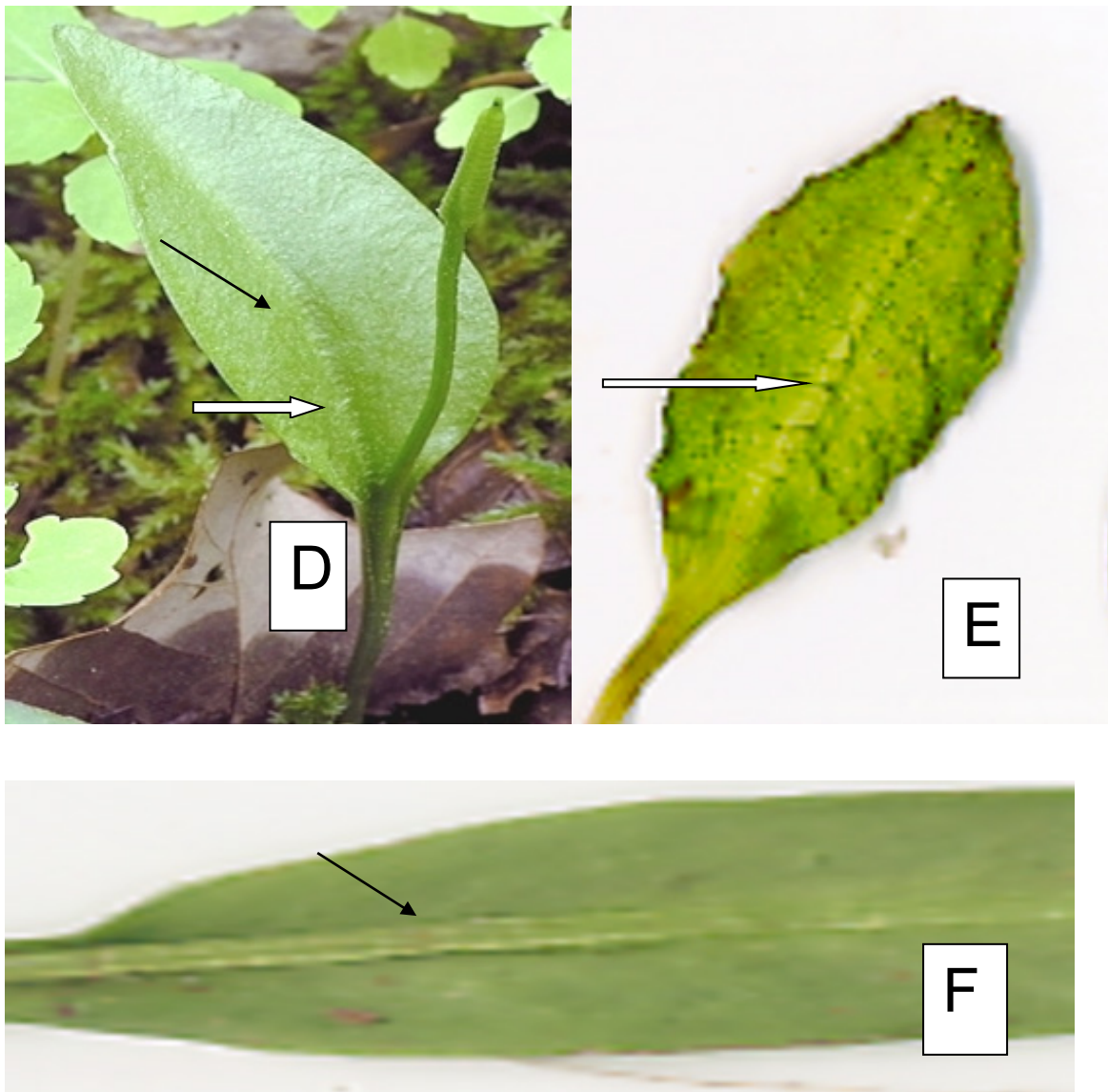


Figure 1. A Alga Chlamydomonas; B. & C; Liverworts Marchantia & Anthoceros; D- A plant of *Goswamia glossii* ; not the stripped mid vein ; also arrowed on very thick mid veins in E & F. See text for significance.

Pteridophytes

Recently a unique evolutionary feat of whole-genome duplication in ferns-one at the base of 'core leptosporangiates' and another one specific to *Azolla* .(one of the aquatic ferns; Figure 2 D).One duplication is fern-specific gene that has been identified, which confers high insect resistance. This gene seems to have been derived from bacteria through horizontal gene transfer See,,Rev: Goswami, 2022). Aquatic fern genus *Azolla* is exactly the same as was millions of years ago and is one of the finest examples of possessing symbiont blue green alga *Anabaena azollae*. Ferns are the closest sister group to all seed plants.

Goswamia (Ophioglossaceae; Figure. ! D-F)

A large number of publications have discovered that the plants possessing several hitherto unknown traits observed in some plants of erstwhile called old genus *Ophioglossum* L are actually the natural variants of newly evolved species of the genus *Goswamia*. Based on a consistent record of many totally unknown features including highly elevated thick mid veins with some stripped mid veins in a few (Figure. 1 D-F) trophophylls (leaves) of the same plant; these plants are named as *Goswamia glossii* Goswami et al . The naming of the species has based on many resemblances with some leaves of *Glossopteris* genus (see 32-34). Several trophophylls (leaves) possess small pockets on the veins contain-

ing spores thus informing about the possibility of forming primitive sporangia. This feature has never been recorded or known in a living plant.

Ophioglossums (Ophioglossaceae)

Kuo et al (39-40) have recently informed that Ophioglossaceae genome exhibits intracellular gene transfer (IGT) and horizontal gene transfer (HGT). This enables ferns to possess an evolutionary significance of this genetic mechanism in plants which otherwise is known in angiosperms. So far angiosperm-to-fern HGTs have been discovered only in Ophioglossaceae by Davis et al., in 2005 (Referred from Kuo et al). Robison et al. (21) have detected MORFFO genes in many fern plastomes which have also been discovered in Ophioglossaceae plastomes. Kuo et al. have also recovered mitochondrial MORFFO genes in Ophioglossaceae. Ophioglossaceae genome shows elevated substitution rates in organellar genomes and a trend toward AT-rich and smaller plastomes.

This is being understood that evolutionary rate heterogeneity and AT-biased codon usages in this fern lineage are likely associated with gene expression levels. Interestingly, HGT (or IGT-like) sequences occur in the mitogenomes of sub-families Mankyuoideae, Helminthostachyoideae, and Botrychioideae.

However, these foreign mitochondrial genes seem to be pseudogenized or functionally redundant for host plants. Notably, the origins of these mitochondrial HGTs can be traced

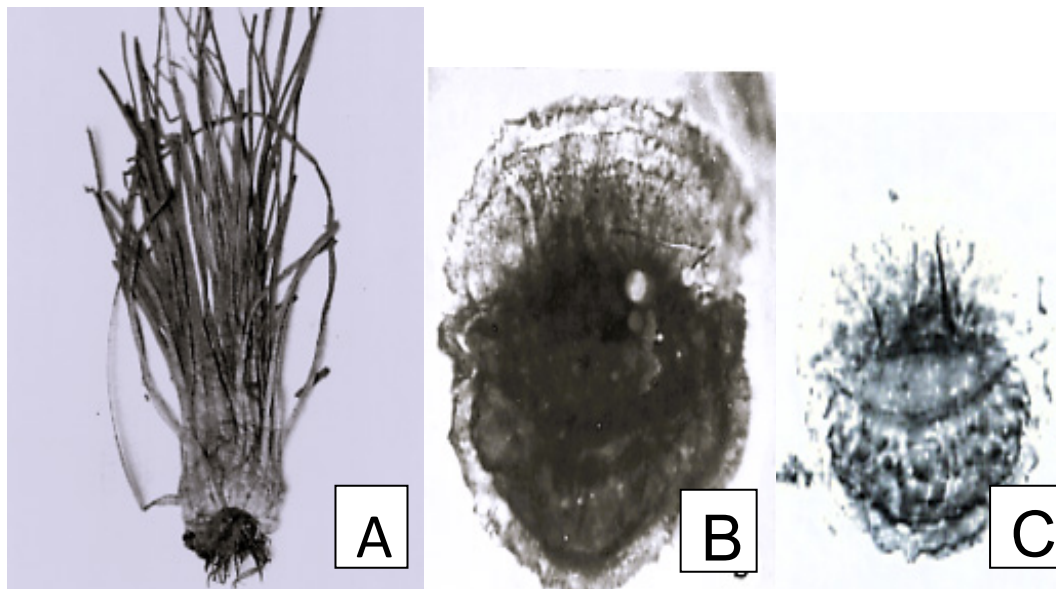
to different vascular plant lineages, and ferns and root-parasitic angiosperms.

Isoetes L

Palingenetically, the genus *Isoetes* L, an extant, mainly aquatic heterosporous lycopod, is one of the rarest plant genus which represents geologically longest journey of series of reductions initiated by the giant lycopods (measuring up to 15 meters in Palaeozoic) to the present day small herbaceous forms (6 cms to 45 cms). Surprisingly, *Isoetes* plants exhibit exact anatomy, spore structures and many other morphological features suggesting as if, DNA sequences from giant and larger ancestors (24, 29, 55) have been encapsulated within the genome of this small aquatic lycophyte. There are a large number of features among spores of *Isoetes* *pantii* which develop in the heterosporangium (heterosporous sporangia) resembling fossil lycopods. Also molecular genetic studies have revealed a few DNA sequences within the genome of *Isoetes* *pantii* resembling a few sequences of human Y chromosome (56).

Gymnosperm

Ginkgo biloba is a classical genus with only one surviving species whose early geological history speaks of 16 species; all of them became extinct except *G. biloba*. Genomic DNA sequences available on Data base were blasted with some human genes and many genes have shown concordance ranging from 60-80% (



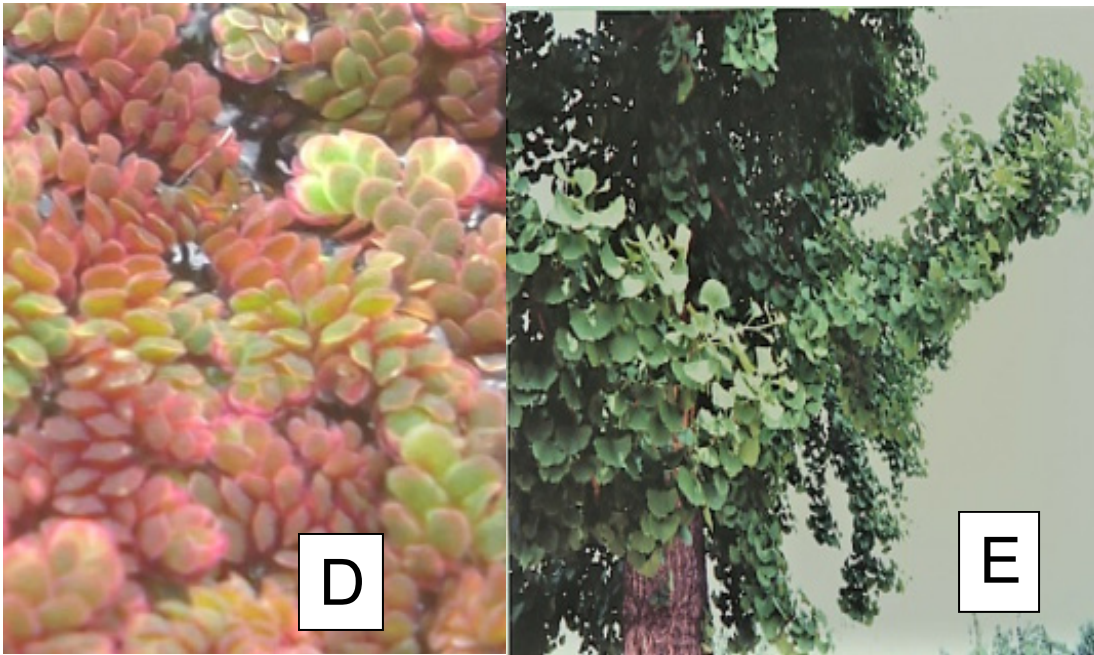


Figure 2. A. *Isoetes pantii* an aquatic lycopod; B & C Megaspores from heterosporangium of *Isoetes pantii* resembling some fossil genera of Paleozoic era; D Water fern *Azolla* E. The classical gymnosperm tree *Ginkgo biloba*. All these plants have some DNA sequences resembling a few genes of human genome. (Figures are published with the copyright of the author)

Genomes Trigger Strategies for Survival: Ecological Genetics

Ever since the life forms evolved on the earth some or the other small or big or even disastrous geological events and natural turmoils (volcanoes, glaciers etc) have been influencing the decline as well as the rise of populations.

Palingenetically, we have been, and will be able to understand the flora and fauna of past geological times only on the availability of excellently preserved fossils. The breakdown or partitioning and or gradual alterations in the habitats often results in decline of populations because the reproductive performance and survival becomes challenged in various ways. Biologically, each and every species must reproduce to survive and survive to reproduce (Goswami, 1990). Evolutionary strategies have offered many approaches (eg. asexual types; sexual) for reproduction but not all plants or animals can exercise such an option. So when the environmental stresses are beyond tolerance and the species is gradually losing capability of reproduction or also the offspring have threats for survival, the genera or species facing such adverse situations ultimately decline in distribution. The most classically popular example is about the total vanishing of giant reptiles, the Dinosaurs. The earth was gradually cooling down affecting sex glands which lowered reproductive performance. Also, smaller rodents had evolved by then, which were actively enjoying feasting on the large sized eggs with rich yolk; an excellent food for their survival. During this geo-

logical period, (in Jurassic) smaller plants and grass lands were becoming more widely distributed offering support to rodents and small animals. The raining of many asteroids during this time further ruined the population of larger animals. We now today have only surviving genome-wise relatives, the crocodile, exhibiting almost the same gene sequences as we could ascertain from fossils of giant reptiles. So, total disappearance of those moving giants has been due to many factors out of which biological factors cannot be ignored

Some Animals

Invertebrates

The recently described 890-million-year-old sponge fossil illuminates the early evolutionary path to the emergence of animal sentience. A sentient animal is aware of feelings and sensations due to the activity of a nervous system. Indirect markers suggest that the foundations of sentience originated hundreds of millions of years before the Cambrian. If the first neuron was a sensory cell, the presence of epithelial "neural stem cells" in ancient Porifera may have been the ancestral state of the nerve cell that appeared in Eumetazoa. In addition, sponges have neurotransmitters, such as glutamate and GABA, and other molecular markers. If the 890-million-

year-old fossil is identified as a sponge, the emergence of the building blocks of sentience among animals began much earlier than previously thought.

Do Parrots Differ with Other Birds?

In general, birds have 10-12 pairs of normal or macrochromosomes and 30 to 40 microchromosomes but some parrot species have only $2n=48$ chromosomes. Quite surprisingly, some monk parakeets have quite large sex chromosome (unlike too small often seen in birds) and recent finds indicate that the chromosome 11 was added (fused) to the ZW chromosome of all parrots and chromosome 25 was additionally added to sex chromosomes in monk parakeets (Rev. Goswami, 32) the evolutionary mechanisms display unique and fundamentally identical mechanisms of loss and gain in chromosome segments, chromatin insertions and deletions, rearrangements of chromosomes assisted by fission and fusion (aberrations), as well as triggering loss and gain of genes. Very interestingly, the transposable sequences have been authorized evolutionarily to support or influence such drastic alterations within genomes. Also several evolutionary (57-59) mechanisms also go on enriching various genomes during evolutionary phases

Human Genome

There have been a large number of masterly publications by David Page and his colleagues (57). Few decades ago a "Line finger gene" was reported on the human Y chromosome which was considered to be identical with T.D.F. of Y-linked testis determining factor responsible for initiating male development. The identification of this gene, now called ZFY, was hunted for its presence in other animals. Quite interestingly, Sindair, Page and their co-workers have reported that marsupial sequences most closely related to ZFY are on autosomes, not on the Y chromosome as expected. Several of the genes conserved on the X chromosome in all eutherians are located on autosomes in marsupials. The probe for Duchenne muscular dystrophy gene which is near ZFX in humans hybridizes to chromosome 5 in wallabies. There is a hypothesis that in humans, both ZFX and ZFY could be required for testis formation. Genes hybridizing to a ZFY probe have also been detected in other vertebrate groups to be housed in autosomes. This is true of reptiles with a chromosomal sex determination mechanism (reptiles with Z and W chromosomes).

Consistent with this phenomenon of dispersion of identical gene sequences in different chromosomes at different levels of evolutionary strategies I had advanced the concept of ceaseless replication of DNA which explained that since the time when DNA molecule got an abode within the primitive stages of cellular evolution the DNA molecule has been replicating and replicating. This unstoppable phenomenon must have resulted in distribution and incorporation of same and

different DNA stretches which were randomly housed in the frame of evolving eukaryotic chromosomes. To begin with, all chromosomes were "autosomes" unless the sex controlling genes were specifically localized later in evolutionary phases, on a specific chromosome.

Why concept of Stem-genes ?.

This is intriguing that many genes with the same sequence have different functions in different organisms; in some organisms these are present but deeply conserved, not as active genes and in some of the organisms these sequences have exactly the same functions. Chromosomes also store relic sequences and there ought to be very selective mechanisms which might be confined to highly selective and exclusive stem cells with very specific genes to be retained and get deeply conserved within the respective genomes (hence named as Intragenomic stem cells with stem-genes). The most scintillating and evolutionarily famous is the small quillwort aquatic lycopod ISOETES L which is the example of reduction series (58) from giant lycopods (10-15 meters tall trees) of the Paleozoic era yet retains and exhibits all major anatomical and typical reproductive (Figure. 2 A, B, C) features, obviously due to revitalizing of conserved relic genes (13, 24,29).

Contributions of Nakamura, Merchant and Li with their colleagues (26,44, 53) are another testimony to the Stem-gene concept. Additionally, genes exert rare variation on gene expression across tissues and organs thereby many new characteristics may appear in a population. (60). Molecular mechanisms like DNA methylation, heterochromatinization (20, 61) etc. may also be responsible for variations.

Therefore, Stem –genes are those special genes which are retained for millions of years as deeply conserved DNA sequences (genes) in some exclusive stem cells of Basic eukaryote genomes which may express in various totally unrelated (in terms of evolutionary path) organisms be even Chlamydomonas Yeast or Anthoceros and the man.

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