

Ceaseless Replication and Random Distribution of DNA Sequences during Early Phases of Evolution is Responsible for Unrelated-Homologies

Hit Kishore Goswami*

Department of Genetics, Bhopal University, Bhopal, Madhya Pradesh, India

Abstract

Resemblance of certain DNA stretches from the genomes of geologically very old (4000 million years and more) and evolutionarily very important plants, with some sequences prevalent within the human genome may be due to the fact that these DNA sequences might have been prevalent in biota before bifurcation of plant and animal cells during pre-Cambrian period. The evolution of DNA molecule and its inherent tendency to go on replicating within primitive and evolving cells during the earliest phases of biological evolution must have been installed within (cells) and this mechanism can be referred as “in built-genetic clock”. This inherent tendency with architectural ease of the DNA molecule (double helix loaded with bases of template origins) should be considered as one of the fundamental characteristics of ceaseless multiplication and random distribution of DNA sequences among evolving and multiplying cells thereby increasing not only the millions and millions copies of cells but also, enriching inherent genome of those cells by adding DNA stretches to the parent genome. This hypothesis of random distribution of DNA sequences among evolving organisms was propounded more than a decade ago by the present author on the basis of Southern studies on the plant taxon, *Isoetes pantii* Goswami and Arya. This hypothesis has also been confirmed by the search for homologies by blasting gene bank data (public data base; <http://www.ncbi.nlm.nih.gov/>) and homology search with some sequenced DNA stretches from *Isoetes* (a descendent from giant pteridophytes of Carboniferous) and a gymnosperm genus *Ginkgo* (genome alive since Triassic, 200 million yrs. ago). DNA stretches from 15 genes exhibit a good proportion of concordance but a *Ginkgo* gene, L23107, nuclear encoding chloroplast a/b binding protein mRNA complete cds remarkably shows 89% base pairs identity/homology in a row to a human gene locus cDNA clone image: 5194336. We have also found 13 genes in *Ginkgo* which do not show any homologous DNA stretches on blasting with the human genome. Many other publications have also found specific plant sex chromosomal segments exactly in concordance with human Y chromosome MSY sequences. Lastly, the animal genus *Platypus* which should be called “Amalgamated-gene pool” is a glaring example which possesses many common genes and thereby exhibits features common to several categories of organisms. Certainly, we can explain as to why hundreds of gene sequences have been uniquely found conserved in variety of organisms, plants, animals including man (*Homo sapiens*). Obviously, this could have been possible only when “ceaselessly multiplying and random distribution of DNA sequences would have been operative during earliest phases of evolution. Hence, this is plausible to opine that 50-75% DNA sequences are fundamentally identical to basic sequences in all organisms which were tailored during early phases of cellular evolution and which were randomly distributed among then-newly evolving cell populations.

Keywords: DNA hypothesis; DNA stretches; Evolutionary genetics; Plant-human DNA homology; Evolutionary bioinformatics; Pre-cambrian DNA homology; Evolutionary significance; Palaeozoic lineage

Introduction

William Bateson in 1902 defined genetics as “the science of inheritance and variation” By and large; this is a comprehensive statement in few words only. Inheritance means passing and expression of specific traits or hereditary units or genes from generation to generation and variation means the differences; differences we know, could be due to genic combinations thus resulting variable phenotype or may be due to environmental interactions. Environmental factors could be internal factor within the individual (s), or may be external or may be both. But this is certain that exactly same traits or genes or DNA sequences being passed on for millions of generations have to be the major part of evolutionary genomes and their timely expression as traits or characters must be based on evolutionary extractions from the Basic Gene Pool. So, though denied by many, but now there are many evidences that there may be many genes among some plants which are shared by animals including man.

During past few years we have emphasized [1-3] that finds of homologous DNA stretches in closely or distantly related species do not always account for common evolutionary heritage. We have evidences to hypothesize that DNA stretches might have randomly distributed in all primitive gene pools which went on ceaselessly multiplying in

the earliest phases of evolution nearly during departure era of plant-animal systems (pre Cambrian; 4500 million years ago). These most primitive sequences must have been randomly distributed on repeated multiplications in millions of evolving genomes and duplicated also at several times in many groups of organisms [4,5]. Since there are hundreds of examples of finding conserved DNA sequences in variety of organisms, both related or widely separated from the evolutionary path, we can presume that DNA stretches have been blindly conserved in variety of organisms, the best evidence coming from comparison of genomic DNA stretches from an aquatic weed *Isoetes pantii*, whose ancestors in Palaeozoic were giant trees with that of many other plant species and also with, totally unrelated on the evolutionary track, the *Homo sapiens* [1,6]. We have found many loci in human genome in concurrence with the plant *Isoetes*-DNA stretches after blasting by

*Corresponding author: Hit Kishore Goswami, Retired From Department of Genetics, Bhopal University, 24, Kaushalnagar, PO Misrod, Bhopal, Madhya Pradesh, India, Tel: +07552807950; E-mail: hitkishoreg@gmail.com

Received April 13, 2018; Accepted April 28, 2018; Published May 05, 2018

Citation: Goswami HK (2018) Ceaseless Replication and Random Distribution of DNA Sequences during Early Phases of Evolution is Responsible for Unrelated-Homologies. J Genet Genom 2: 117.

Copyright: © 2018 Goswami HK. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Gapped blast and PSI-blast techniques advanced [6,7]. At this time we had planned to investigate and study comparative genomics of those plants which are too old geologically, at least surviving since Palaeozoic and are represented by copies of DNA stretches multiplying, mutating, and or recombining and are conserved in the modern extant genera/species. Since, events of bisecting of basic gene pool struck too early in the evolution of primitive plant and primitive animal cells there by enabling erection of plant and animal cells. A large number of DNA sequences are being reported to have been conserved in various divergent animal phyla, many of the genes retaining the same function [8-10] in humans.

Since appearance of traits and performance of all basic functions are exclusively under control of many genes, Table 1 presents some of those functions and characteristics which are common to all living organisms with mentioning particular emphasis on eukaryotes. Then there are also a large number of genes (DNA sequences) known to have strict homology among organisms but for quite different functions. For example, in *Drosophila melanogaster* patched mutations are known to cause faulty winged veins and the human version of this PTC gene results in defective ribs as well as skin cancer. This gene is mapped on the long arm of human chromosome 9, very near the site where genetic linkage studies have shown the presence of gene for basal cell nevus syndrome. Another such example where a normal gene in fruit fly causes cancer in other organisms is wnt1 gene which in fruit fly, functions as wingless gene, while it causes mammary tumour in human on becoming overactive. Also a human GLI gene which was discovered as an oncogene in a rare human brain tumour is now known to be the counterpart of the Cubitus interruptus gene of the fly [11].

We have strong evidences to assume that conserved sequences can be found in diversified and apparently unrelated phyla but the functions performed in that organism by that very gene need not be the same. Lately, this is becoming clear that humans, other mammals and probably other organisms might also have their own versions of genes found in many organisms, for example, vertebrate homologues of hh and PTC have been identified in mice, chicken and Zebra fish. In humans these genes have important roles in organizing many tissues including neural tube, skeleton, limbs, craniofacial structures and skin. Many genetic variants are known to affect phenotypes but the same functional variant can have a different effect on the phenotype in different individuals of the same species [12] or in totally different and unrelated genera and species [1,5,13]. Obviously, understanding the impact of genetic background on the expressivity of a given phenotype is essential because this effect complicates our ability to predict phenotype from genotype. Various population biologists and evolutionary geneticists (example, JBS Haldane) have used terms like expressivity of inheritance, penetrance or an equally impressive alternate multiple gene actions or polygenic inheritance, meaning thereby that under some situations (inherent/unknown) more than “one gene” (monogenic control) activity is required for the exact replication of gene activity. In other words, theoretically, expression of a gene may even require assistance from “like minded” gene(s). This is a universal dogma applicable within all living organisms.

The Approach: Methodology Based Comments

Studies that have been referred to in this paper have been published extensively by respective authors on the basis of established techniques over two decades. Briefly, most of these are based on genomic

extractions and processing through molecular genetic techniques of Southern hybridizations [1,11,13,14], molecular cytogenetic techniques and in situ hybridizations [15-19] and also carried out by blasting DNA analysis after gene cloning [2,3,7].

Southern blot/Hybridization studies

Our then newly discovered plant taxon *Isoetes pantii* Goswami et al. [20] (a lycophyte: Isoetaceae- Pteridophyte) had offered numerous rare observations and provided deeper glimpses on evolutionary strategies operating within the genome. Apart from morphological discoveries this taxon exhibited two B chromosomes and a clear sub-metacentric large chromosome, all of these lagged behind the movements during meiosis. Repetitions over several years confirmed that these chromosomes by way of classical cytology -chromosomal behaviour, appeared like being a B chromosome, another triangular small Y chromosome and the large one as an X chromosome. Our Southern-blot experiments offered [1] a clue that the sex chromosomal mechanism has evolved by those basic sequences based on which human Y chromosome has had evolved during human evolution. This experiment had confirmed observations published by Nagl [13] which was the first ever report that human genome has DNA stretches akin to plants was published by Walter Nagl [13]. The genomic DNA of several cultivars of the beans, *Phaseolus coccineus* L and *P. vulgaris* L. was Southern hybridized with a cDNA probe of human cytochrome P450, the enzyme converting androgens into estrogens. Evidence for the existence of an aromatase homologous DNA sequence in these plants was obtained. *In situ* hybridization of a human telomere specific probe to the polytene chromosomes of the embryo suspensor of *P. coccineus* revealed the presence of DNA sequences in the heterochromatic telomeres of the bean chromosomes, which are homologous to the human DNA sequence.

Gene blasting study

Gene blasting was analysed by Blast Gene Bank public data base <http://www.ncbi.nlm.nih.gov>. Our results on genomic DNA sequences from a lower vascular plant taxon, *Isoetes pantii*, compared with human genomic DNA by NCBI Blast Gene Bank public data base have opened up a new line of thinking [2,3,6]. Besides repeating blasting studies on *Isoetes pantii* DNA sequences we could also venture in to another study with *Ginkgo biloba* tree genome which has witnessed evolutionary turmoil's for the last two hundred thousand years. There are a large number of genes of *Ginkgo biloba* which have been sequenced and are available for comparative studies. Table 2 presents homology in detail of *Ginkgo* gene (Chlorophyll a/b binding protein mRNA complete cds) possessing 89% homology with human cDNA clone IMAGE: 5194336, partial cds length 1044 [3]. Search for homologies with some geologically very old genomes whose copies are still represented among surviving genera (plant species in particular) is in progress.

Observation and Discussion

The entire DNA sequences or the genetic makeup of individuals (of one group) is termed as “gene pool” and for taxonomic convenience we designate the parental or basic gene pool as fundamentally responsible which goes on evolving and diversifying during evolutionary stages. Briefly, the hominid gene pool has been evolving and at present we have *Homo sapiens* and we very authentically know that our species has evolved by many chromosomal aberrations, (fissions and fusions etc) including hybridizations among highly evolved apes [21-24].

This is even more remarkable that gene pools often conserve DNA stretches for millions and millions of years but their “expression” in the organism has to be a specific selective process. Many genes continue

Vital and Basic Functions	Few Typical Characteristics	Reviews/Suggested references/see Modern text books also
1. Cell structure/ cell division /functions Respiration-Growth -Enzymes-genes Cell kinetics Mitochondrial DNA	Plant cells, besides having plasma membrane have additional covering: Cell wall made up of mainly cellulose (additional compounds like chitin may be added to some class; viz Fungi) Mitochondrial DNA functions are as per requirement of the cell. The greatest evolutionary molecular discipline of a eukaryotic chromosome is that chromatin must be touched to the plasma membrane as is found in prokaryotic DNA (Chromosome). This rare feat in <i>Allium cepa</i> chromosomes was observed under influence of the magnetic field exposure (Figure 1).	Goswami [46]
2. Mitosis	Chromosomal divisions are exactly same in plants and; mitotic pathways (Interphase-to-telophase), related coiling and condensation of chromosomes, presence of chromomeres: packing of telomeres at both the ends; strict play of spindle fibers' apparatus; required ATP role and interplay of many enzymes and proteins; perfect role of centromeres on chromosomes. In humans monozygotic co twins offer perfect validity to the exactness of mitotic divisions; as well as identical "Time and Place"of genes as evidenced by the cotwins (Figure 2).	Goswami [49]
3. Meiosis	The chromosomal complement of each individual undergoes very strict and stringent events during meiosis; the identification of homologous chromosomes by homologues themselves, then pairing, then undergoing coiling and condensation related molecular events, movements of bivalents and finally separating chromosomes to be transported by Spindle fibers to opposite poles. All these molecular Mechanisms are controlled by genes and there are Are enzymes specifically recruited for perfect Separations thereby handing over half the number of chromosomes to gametes (Figures 3 and 4) An Any error, may cause problem to the individual	Modern Text books of (molecular) genetics (Barchi et al.)
4. Chromosome structural and Functional Organization	In eukaryotes, the majority of the DNA resides in the nucleus where it is packaged into a highly condensed structure called chromatin. The primary and repeating units of chromatin are the nucleosomes, which consist of 147 bp of DNA wrapped around an octamer of histone proteins formed by two copies of each of the core histones H2A, H2B, H3 and H4, with the linker histone H1 bound to the DNA between nucleosomes (reviewed in Luger et al.). The processes of fission and fusion of deleted chromatids to give rise to new chromosomes; accepting foreign DNA and various mechanisms of aberrations which help in new chromosomal complements and help in speciation are exactly same in plants and animals and all these mechanisms involve active role of DNA sequences.	Mirabella et al. [64]
5. Molecular genetics/Repetitive DNA/ and Replication and transcription mechanisms	The centromeric DNA of most eukaryotes consists of tandem repeats (TRs) that bind centromeric specific proteins and help in repairing double stranded breaks. Telomerase role in chromosomes of eukaryotes Telomerase catalytic subunit homologs from fission yeast and human Repetitive DNA sequence motifs repeated hundreds or thousands of times in the genome makes up the major proportion of all the nuclear DNA in most eukaryotic genomes.	Presting [9]; Greider et al. [17]; Nakamura et al. [28]; Tardat and Dejardin [10]
6. Mechanism of Inheritance/Gene Functions	All eukaryotes follow the various modes of inheritance; including those like genomic imprinting etc. Genes behave as units of expression and classical recessive modes of inheritance like albinism (absence of melanin pigment) are the same among animals as in humans (Figure 5).	Text books of Genetics
7. DNA methylation/	In eukaryotes, DNA methylation only occurs at cytosine residues. Epigenetics is inherent molecular phenomenon resulting in heritable changes to gene expression that occurs without alterations to the DNA sequence. The regulation of chromatin by epigenetic mechanisms plays a central role in gene expression and is essential for development and maintenance of cell identity and function. Besides DNA in mitochondria, freely found chromatin is universal which activates the innate immunity (cytosolic DNA-sensing cGAS-STING (cyclic GMP-AMP) synthase linked to stimulator of interferon genes)	Biscotti et al. [59], Mirabella et al. [64]
8. Genome stability/	The DNA replication and transcription machineries share a common DNA template. Intricacies of molecular mechanisms (enzymes etc.) are same and under control of specific DNA sequences Methylation of nucleotides provides a molecular means to reversibly mark genomic DNA. Bacteria can methylate adenosine or cytosine to identify and degrade invading DNA and to track mismatch repair and the progress of genome duplication before cell division.	Zhixun et al. [12]; Schübeler [29]; Sankaer et al. [55]; Mirabella et al. [64]
9. Adaptations (various mechanisms are operative in all genomes)	All eukaryotes (plants and animals) strictly follow Mendelian inheritance patterns, sex linked inheritance, cytoplasmic inheritance epigenetic inheritance; silencing and expressive genes; pseudogenes; genomic imprinting; non linked genetic inheritance and many other modes of transmission as and when are discovered. Chromosomal DNA has many mechanisms (breaks, translocations, duplications) to cause shrinkage, expansion, and equilibrium have developed to find the optimal balance between genomic stability and plasticity Evolutionary adaptations and innovations indicate towards the genetic basis for the development of plants and animals, their respective shapes and size (evodevo) common gene expressions in diversified organisms depend upon how the regulatory regions of the genome have evolved	Modern text books of genetics; Schbert et al. [55]; Editorial: Nature Genetics May; Modern text books of genetics.

10. Revival of "Relic genes and Random; Or/ "early expression" of advanced traits	Our studies in the past have shown that sometimes genes are expressed in some primitive plants and show those features which actually are regular features of advanced genera (see e.g., Figure 6). Also contrary to this, certain genes express in some Living taxa (e.g., See Figure 7) and express those traits which were present in their geologically far distantly placed ancestors (Figure 8) proving that genomes possess those conserved DNA sequences for millions of years. Furthermore, a plant gametophyte is not expected to possess tracheids but under environmental stress, (?) a fern gametophyte has been described to bear tracheids in nature.	Khandelwal et al. [39]; Goswami [47,48]; Goswami et al. [21]; Bajpai et al. [6]; Goswami [34,37]; Goswami et al. [32]
---	--	---

Table 1: Some common evolutionary strategies among eukaryotes (Authors overlap in references).

Gene Locus	Total No. nucleotides	a+t	g+c	Multiple Sequence
L23107 <i>Ginkgo</i> nuclear Encoded chloroplast Chlorophyll a/b binding protein mRNA, Complete cd	(997)	210+200	293+294	aaa=11; ttt=09 (0.0200)
AY971577 <i>Ginkgo biloba</i> Male- specific marke Sequence	(1080)	285+366	209+220	aaa=14 (0.0129) No other
AF331704 Levopimaradiene Synthase mRNA	(2705)	786+716	623+580	aaa=62 (0.0388); ttt=43
CBO 75045 hx14d05.b1 <i>Ginkgo</i> megasporophyll (NYBG) <i>Ginkgo biloba</i> cDNA clone hx 14d05	(528)	191+156	97+84	aaa=26 (0.0342); ttt=13
CBO 75036 <i>Ginkgo</i> Megasporophyll cDNA Clone hx 14c06 mRNA Sequence	(315)	107+99	73+36	aaa=21 (0.01206); ttt=17
CBO75054 <i>Ginkgo</i> Megasporophyll (NYBG) <i>Ginkgo biloba</i> cDNA clonex14e05 mRNA sequence 5086 hz78g11.b1	(276)	96+90	51+39	aaa=10 (0.0 543); ttt=05
<i>Ginkgo</i> microsporophyll (NYBG) <i>Ginkgo biloba</i> mRNA sequence cDNA clone hz78g11	(433)	150+140	75+68	aaa=28 (0.0113); ttt=21
CBO95158 <i>Ginkgo</i> microsporophyll (NYBG) <i>Ginkgo biloba</i> cDNA clone qr91g12 mRNA sequence	(371)	110+119	94+48	aaa=12 (0.0862); ttt=20
CBO94367 hz 69 b05.b1 <i>Ginkgo</i> microsporophyll(NYBG) <i>Ginkgo biloba</i> cDNA clone hz69b05 sequence	(417)	149+129	70+69	aaa=21 (0.1007); ttt=21
hz69a11 <i>Ginkgo</i> microsporophyll(NYBG) <i>Ginkgo biloba</i> cDNA clone hz69a11 mRNA sequence	(543)	153+142	127+121	aaa=20 (0.05340); ttt=09
AY884151 Trehalose-6-Phosphate synthase gene	(4047)	1109+1189	1015+734	aaa=77 (0.04373); ttt=100
AY695796 <i>Ginkgo biloba</i> Defensin precursor mRNA complete sequence	(534)	158+154	139+83	aaa=21 (0.05394); ttt=12
AY 750963 <i>Ginkgo biloba</i> Dihydroflavonol-4-reductase mRNA	(1451)	407+388	339+317	aaa=36 (0.0437); ttt=29
AY574248(LPSgene) (Levopimaradiene synthase)	(6497)	2024+2032	1223+1208	aaa=167 (0.0534); ttt=146
AY959313 <i>Ginkgo biloba</i> Clone 3 athilalike retrotransposon reverse transcriptase like (RT) gene, partial sequence	-241	71+89	44+31	aaa=04 (0.05394); ttt=09

Table 2: Distribution of base pairs among 15 genes of *Ginkgo biloba* which Show homology with some human DNA sequences (genes).

to express “as such” [25] and lot many features are exactly same for millions of years with a loss or gain of some additional traits among a particular group of organisms. For example, a handy small aquatic weed *Isoetes* ranging in height from less than 10 cms to maximum of 100 cms is the descendant of giant lycopods of Carboniferous which were tall trees (nearly, 6 meters). Except loss in the height, these plants are exhibiting almost the same anatomical and reproductive features [26,27]. In order to make the related aspects of gene expressions, conservation and reappearance of relic traits (genes) more vividly explained, hereunder are presented a few relevant examples in Tables 1 and 2. And a few are illustrated in Figures 1-8. Some important considerations are presented below.

Table 1 informs on some of the most widely accepted homologies in gene functions among all organisms thus suggesting an actual proof that lot many DNA sequences are present among unicellular organisms, multicellular and highly evolved plants, animals as well as in human cells. All eukaryotes have exactly same array of structures and functions of genetic systems; to mention a few: (Table 1) chromosome structure, its internal highly complicated chromatin, arrangement of deeper structure of centromere, telomere; as well as mitotic, meiotic alignments, orderly events of coiling and condensation; pairing of homologous chromosomes and too many molecular events which are strictly under the control of enzymes and accurate gene functions controlling these vital events [10,25,28,29].

DNA sequences from living plants representing geologically far distant populations (Gene pools representing relic genes)

Isoetes L. (Lycophytes-Isoetaceae-Pteridophyta): The discovery of development of micro spores (male) and mega spores (female) within one and the same sporangium [30,31] in an aquatic weed (Figure 7), a lycophyte, *Isoetes pantii* Goswami et al. [32], then referred as a startling discovery in the plant kingdom, continued to be an enigmatic problem since then. Both male as well as female spores were discovered to be fertile [32] produced respective gametophytes and developed sex organs, but mixed with these spores, there were abnormal-appearing larger megaspores which resembled no living but some fossil spores [31] described to have occurred among fossil lycopods (Figure 8A-8E). No species of *Isoetes* or any related genus is known to possess such spores. Furthermore, a sex chromosomal mechanism (X-Y) been consistently observed, which has never been known in any other lycophyte [31,33,34] and the evolution of sex chromosomes within the genome has been selectively assisted by evolving a new line of chromosomal evolution within this species *Isoetes pantii*. Details of these discoveries are dealt separately [34,35] but the inherent theme of this background is regarding understanding the importance of transmission of DNA sequences conserved since millions of years within the “lycophyte-Isoetes-gene pool which ultimately compelled to match with human Y chromosome DNA stretches with Southern blots. This is because human Y chromosome evolution is an evolutionary demonstration of fissions, fusions and hetero chromatinization of chromosome segments and subsequent translocations from a few autosomes of early hominids [21,23].

At this time, this was possible to assume that DNA sequences can be continued to ceaselessly multiply, be copied, be fused and also spliced so as to generate new gene-chromosome pathways and amplify within the genome of evolving organisms. The most remarkable point of argument is that a DNA sequence stretch or a gene may be, rarely though, found in a totally unrelated species without any evolutionary significance.



Figure 1: *Allium cepa* (onion) cell showing completely uncoiled chromosomes under magnetic field exposure. Note that nuclear membrane has disappeared and totally uncoiled chromatin (chromosomes) ends are pierced in plasma membrane, this is an essential phase in prokaryotic chromosomes (DNA) before replication.



Figure 2: Monozygotic twins confirm that thousands and thousands of mitotic divisions are strictly same and all phases of divisions (coiling and uncoiling of chromosomes; installation of spindle fibres, longitudinal divisions of centromeres, and movements of chromatids to opposite poles with finally their becoming full chromosomes by exact faultless DNA synthesis in sub phase of Interphase) are perfect. Furthermore, the “Time and Place” of gene actions is monitored and is under genetic control.

Ginkgo biloba (Ginkgoales: Gymnosperms): Ginkgoales comprising many species and at least sixteen genera had flourished worldwide during the distant past, in the Triassic (200 million yrs ago) but now is represented by a single living species *Ginkgo biloba*, commonly known as “maiden hair tree”. *Ginkgo* is found in nature in the remote mountains in China but has been extensively planted in Japan, Korea and in fact in many parts of the world at various places also for yielding edible ovules. From evolutionary points of view *Ginkgo* is one of the most significant plants in the plant kingdom. Due

to remarkable antiquity, Seward in 1938 [27] considered *Ginkgo biloba* as an emblem of changelessness keeping the secrets of immeasurable past. All related fossil species, example, *Baiera*, *Ginkgoidium* and *Ginkgoites* etc had dichotomous open venation in the leaves and with the exception of Trichophyton were like *Ginkgo biloba* in possessing long and short shoots, a feature unique to this group of plants [27]. *Ginkgo* is morphologically distinct and has earlier been referred as a “living fossil”, a valid reason for molecular biologists and evolutionary geneticists to decipher DNA sequences, and search for conserved sequences for comparative studies. The genus has more than 200 genes already sequenced. The intention of homology search for 25 genes was to find out whether known genes with their functions can be traced in human genome. There are 15 genes out of the 28 blasted ones to have good homology (Table 2) but no *Ginkgo* gene, has been found to possess at least 50 nucleotides in a sequence in concordance to any human gene except gene L23107. This is of paramount importance; a homology of 89% of a *Ginkgo* gene L23107 controlling chlorophyll a/b binding protein, a kind of function which cannot be found in humans!! Nevertheless, this is an encouraging observation to be investigated on many more genes. Indisputably this is a matter of chance with no evolutionary obligation on lineage/ evolutionary relationship. But here we want to hypothesize that higher percentage of concordance in the DNA sequence of a gene (say 80% of the sequence) may account for geological persistence of the version of that gene (conserved through billions of years in the present context). These DNA sequences must have been lodged as integral part of sub gene pools much before the divergence of plants and animals [36]. So, the genomes are elastic phylogenetically and can traverse through geological distances. Obviously, revised and or, modified versions of genes may be found in totally unrelated species [2,3,34].

Genomic reshuffles and evolutionary reversals: Appearance of traits that was once present in fossil forms

Ophioglossum L: Almost all species of *Ophioglossum* investigated for chromosome numbers have been found to have intraspecific cytotypes with highly variable numbers. These are some of the rarest examples that a great majority of species have inconstant chromosome numbers; species varying to possess from haploid, $n=90, 100, 110, 120$ to 240 number of bivalents in meiosis; $2n=240, 360, 500, 1400$ chromosomes in root tip mitoses. In other words, there is not a single species which can be known to have a stable chromosome count. Despite very high grade of polyploidy, each and every species behaves as a “diploid” because, this is believed that “Paleopolyploidy influences” prevent multivalent formations during meiosis. Goswami [37,38] opines that these unstable chromosome counts are also genetic mechanisms as strategies for adaptations because, this is well known that high grades of ploidy offers adaptive values for tolerance of extreme climatic variations. Quite likely inconstant acquisition of number of chromosomes among the species is actually inherently imposed by evolutionary-genomic load. There are many features which appear in some plants of this genus (*Ophioglossum*) which are present in other higher groups of plants; particularly periderm production [39] in stems of a few plants (Figure 6). This indicates the early onset of genes and also, means that the genome of these plants already has genes for many features which, in later part of evolution, have become characteristics of higher group of plants.

Isoetes pantii: As mentioned above *Isoetes pantii* plants have had exhibited the regular development of highly unusual mega spores (Figures 7 and 8) inside the microsporangia which are not comparable to mega spore ever produced by any living lycophyte including any

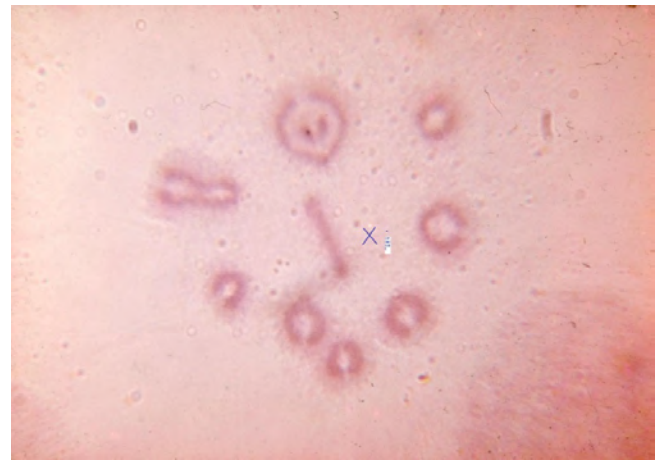


Figure 3: Diakinesis in the grasshopper, *Poecilocerus pictus*; pairing in bivalents and non-pairing long rod shaped X-chromosome; note the terminal chiasma still holding homologous chromosomes (nine bivalents+X chromosome) just before the onset of anaphasic-separation.. By and large, pairing and separation etc are under perfect molecular genetic control.

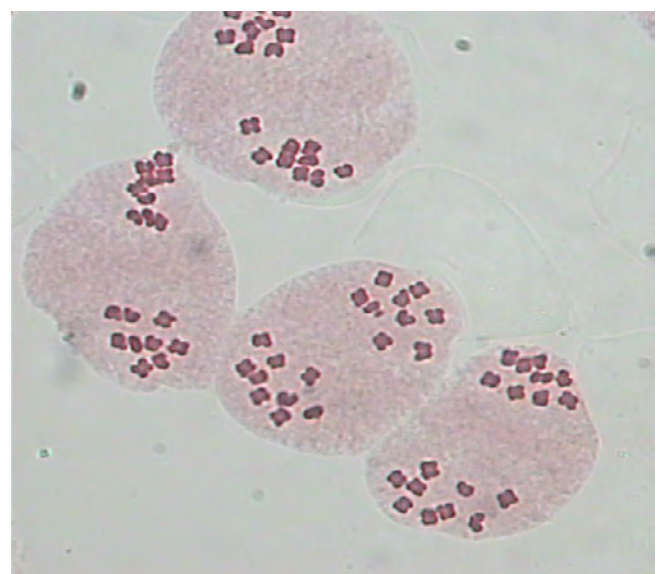


Figure 4: End of first phase of meiosis in a plant *Achillea millefolium* ($2n=18$ chromosomes) This slide shows the halving of parental chromosomal complement which results after Anaphase I when equal number of separated chromosomes (nine) reach the opposite poles.

species of the genus *Isoetes*. On the contrary, these spores are almost similar or are comparable to spores produced by fossil relative-lycophods which were present during Upper Triassic period (nearly, 160-180 million years ago). These spores are direct testimony to the revival of those genes which were then active; became “lost” thereafter and then have reappeared or have been activated in the present time. However these have been restricted within plants belonging to *Isoetes pantii* since this species is a natural hybrid with the evolved sex chromosome mechanism, quite likely natural hybridization assisted with genomic reshuffle might have triggered those genes.

Loss and gains in evolution

There are examples from plants. In bryophytes (non-vascular



Figure 5: Albinism is a two gene recessive disorder (*aabb*) inherited in human families and so also among animals. This recessive trait is caused by lack of melanin compound in the skin; all expressions of the trait (eye brows etc.) are same brown. Individuals with albinism cannot tolerate bright sunlight; may develop skin cancers.

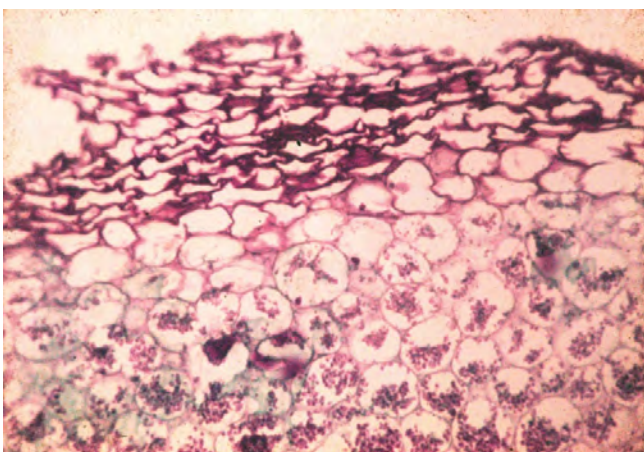


Figure 6: The rhizome (stem) in transverse section of *Helminthostachys zeylanica* (related to genus to *Ophioglossum*) shows periderm; this small plant belongs to lower vascular plants and the production of periderm is a feature of higher group of plants. This is indicative of early onset of gene expression which also means that the genome of this lower group of plant possesses all those genes which regularly express in higher plants. Additionally, some *Ophioglossum* (not all species) plants also show the secondary growth producing periderm meaning thereby that species differ in expression of these genes among different species.

mainly terrestrial plants) the plant body is essentially a haploid plant bearing a sporangium wherein sporocytes are haploid and mitotically divide to produce more or less identical spores. Japanese workers have discovered X-Y mechanism in *Marchantia polymorpha*. This has been shown by more sophisticated experiments by Okada et al. [40,41] that the liverwort *Marchantia polymorpha* not only has X and Y chromosome mechanism but has human Y chromosome specific DNA MSY-sequences [42,43]. These results confirm our observations [1,34,35] that the genes or specific stretches of DNA may be fundamentally same and may be molecularly similarly operative for the appearance of sex chromosomes, be the plant or animal or even man. Except in *Marchantia polymorpha* and *Isoetes pantii* the msy genes

have not been investigated so far, though among non-flowering plants there are a few plants like an alga, Chara, a bryophyte, *Sphaerocarpus donelli* and the gymnosperm *Ginkgo biloba* also have sex chromosomes [26,44,45].

Since new chromosomes arise from within the genome, from the same chromosomal complement by fission and fusions (breaks and reunions on different segments; translocations [46-48]). Furthermore, the instance of hybridization also helps in enriching the genome by adding foreign DNA. This is best illustrated by the chromosomal complement of *Isoetes pantii* whose parents are supposed to be hexaploid (*I. sampathkumarini* $2n=66+1$) and a diploid *Isoetes coromandelina* ($2n=22+1$ B chromosome). The hybrid, *I. pantii* has $2n=48$ in which, there are two extra ($33+1+11+1=46$ chromosomes). This has been explained by observing too many breaks, many fluctuating counts and presence of two B chromosomes having received, one each by both the parents [34,35,49]. Quite likely fissions and fusions have resulted in reallocating genes to new chromosomes [47,48] and we have 48 chromosomes in roots of these plants. Additionally, follow-up studies on population cytogenetics over 45 years we have encountered many segregates having evolved $2n=60$ and $2n=72$ chromosomes. These plants appear to be better adapted and original populations are on decline [37]. There are hundreds of examples where the loss and gain of genes, chromosomes and traits, their reappearance as well as disappearance in the related taxa of plants and animals have been studied [14,40].

Random Distribution of Genes

Several conserved genes present on X chromosomes of Eutherians are located on autosomes of Marsupials. DXYS1 sequences are present on both the X and Y chromosomes in man but in apes these have been identified only on X chromosome not on Y. Highly conserved sequence

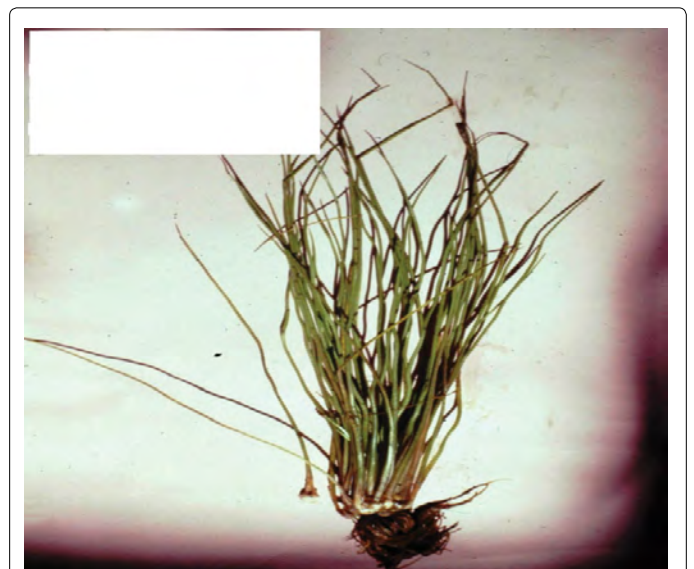
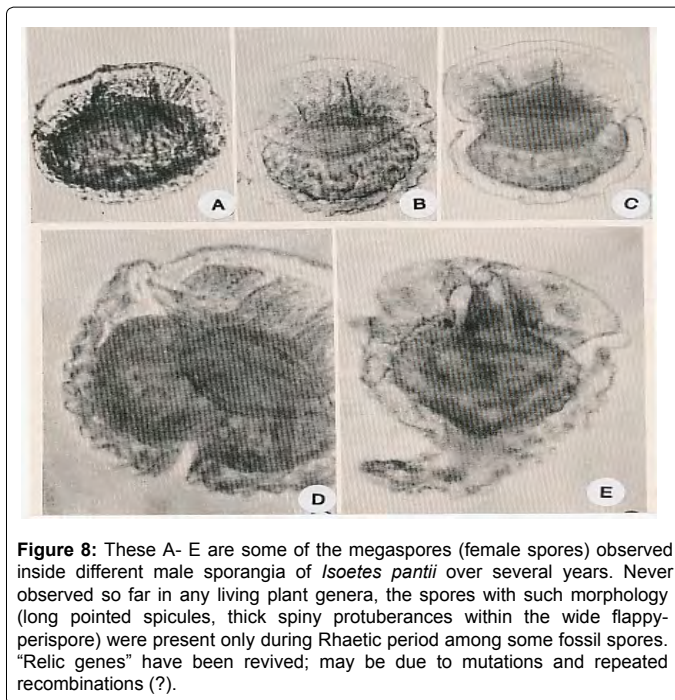


Figure 7: *Isoetes pantii* Goswami & Arya is an aquatic weed exhibiting fundamental discoveries in the plant kingdom. The genus *Isoetes* itself is a testimony to the enormous amount of evolution in reduction of the plant size; the ancestors of these quillworts were giant trees in Carboniferous. The strangest part is that except the loss of genes which control enormous height of plants, all morphological and anatomical features are exactly same. Such genera in the biological world have demonstrated that there are losses, gains and inherent conservation of genes in evolution.



family (GATA) n is present in Yeast, mouse and man. We have lately found them in plants too.

We have also well proven record of distribution of identical gene sequences on different human chromosomes and on dog, pig, rat and crane (snake) etc. This can be emphasized here that higher percentage of concordance in the DNA sequences of a few genes among some plants and animals including man, may account for geological persistence of certain DNA stretches/versions of genes conserved through billions of years probably due to random distribution [50,51]. These DNA sequences must have been lodged as integral part of sub-gene pools much before the divergence of plants and animals (in the Pre-Cambrian to Cambrian: approximately four to five thousand million years ago). The genomes are elastic from evolutionary point of view and have phylogenetically travelled through millions of years and spread over among diversified organisms world over at all times since the advent of life on the earth. Certainly therefore, a gene, present in one organism at one chromosome domain may be present for the different or related similar function at a different domain in another organism, and thus in no way is an exclusive, "bonafide resident" within/of that organism.

The genomes of eukaryotic species contain numerous types of highly to moderately repetitive DNA elements, such as the Alu sequence in humans, B1 in mouse, L1 in mammals, del2 in *Lilium spp.*, Tourist in cereals and Kpnl in *Pennisetum spp.* Repeated sequences comprise a large proportion of plants' genome. In Rice 50% genome includes repeated sequences [52]. Similarly, maize (78%), wheat (83%) rye, (92%) and onion (95%) have quite high proportion of repeated sequences. This is further intriguing that closely related species can have similar distributions or can show marked dissimilar pattern and also distantly related species do have identical or similar distribution patterns of specific repetitive elements. Not only that, even the same organism, for example, in the chicken, repetitive sequences even differ in between its micro chromosomes and macro chromosomes [53].

However, as the biological complexities evolved and reproductive excesses provoked limitations on adaptations on account of

automatically generated selection pressures (natural selection), multiple options should have been available for evolutionary strategies. These options might not have influenced the structural and functional integrity of the genome probably due to an immediate or even, urgent but uniform "wrapping-packaging" of the genetic machinery in to linear chromosomes among cells evolving as eukaryotes. Evolution of chromosome systems [49] undertook all physical, regulatory and selective responsibilities of changes either forcibly or naturally operative on the genomes. Certain dogmatic rules were framed for each domain. For example, pairing of homologous segments in homologous chromosomes in meiosis; those chromosomes, which remain unpaired, lag behind; nondisjunction can lead to unequal segregation, which in turn, can question fertility of the product and finally, meiosis can screen away any "foreign intrusion" and safe guard vitality of the genome, are some of the biological attributes of chromosome systems. Obviously, natural hybridization and also mutations, will abruptly disrupt meiotic selections of the species because of altered and addition of DNA stretches within the sub-gene pool. These genetic phenomena might have been able to generate different selection pressures for the survival of species and genera. Needless to mention, such incidences over millions of years must have paved way for compartmentalization and differences in strategies for future evolutions. Certainly then, it can be assumed that random distribution of DNA sequences would have lasted only until majority of cells, over millions of years, evolved and added maximum quota of accommodative genetic material capable of molecular functions and retaining physical and biological attributes of a living cell. In other words, genetically overloaded cells incapable of performing essential vital functions must have lagged behind in evolution and millions of such cells might have been eliminated (died out).

Summary

The evolution of DNA molecule and its inherent tendency to go on replicating within primitive cells during the earliest phases of biological evolution must have installed within cells which can be designated as "in built-genetic clock". This inherent tendency and architectural ease of the DNA molecule (double helix loaded with bases of template origins) should be considered as one of the fundamental characteristics of ceaseless multiplication and random distribution of DNA sequences among evolving and multiplying cells thereby increasing not only the millions and millions copies of cells but also, enriching inherent genome of those cells by adding DNA stretches to the parent genome.

The nuclear genetic information of organisms is locked in the DNA molecule in prokaryotes and the eukaryotes have linear chromosomes [54] and the total genetic makeup of chromatin (both nuclear as well as cytoplasmic) constitutes the genome. Genomes are stable but in the evolutionary processes lot many phenomena go on enriching and offering changes [55]. The number of genes in eukaryotes varies from-5000 (Bakers' yeast) to-100,000 (hexaploid wheat) which are linearly arranged in specific number of chromosomes (The number of chromosomes varies from one (01) in the ant *Myrmecia pilosula* to as many as 1400 chromosomes in a somatic cell of *Ophioglossum reticulatum* a pteridophytic plant (related to ferns). Modern studies employing restriction enzyme analysis, gene cloning and DNA sequencing has brought an explosion of knowledge of molecular biology establishing that genome of higher organisms contains many pseudogenes, multigene families, repetitive DNA sequences and transposons [19,22,56,57]. Many more categories of DNA inclusions are being discovered which are proving to be of great evolutionary relevance. One of the biggest surprises that the whole-genome

sequencing era has brought to us is the amount of non-genic, especially transposable element derived sequences that comprise the bulk of chromosomal DNA in many eukaryotes. New chromosomal-DNA sequencing data have lately revealed new classes of such elements. Most eukaryotes carry repetitive sequence which occur in tandem arrays in the vicinity of centromeres, telomeres and have also been found in interstitial regions of chromosomes [57-67].

Practically the entire distribution of DNA sequences in the human genome and in genomes of all major classes of living organisms fall in to following six categories:

1. DNA sequences for basic functions are uniformly similar in all organisms. Theoretically, it appears that about 50 to 75% DNA sequences have been randomly distributed among all evolving and multiplying cells during Pre Cambrian before bisecting the genomes into prokaryotes and eukaryotes.
2. DNA sequences for fundamental structural organizations of chromosomes in eukaryotes are the same (nucleosomes etc). The genes controlling mitotic and meiotic cell divisions are essentially same in eukaryotes. This is also important to recall in prokaryotes that DNA ends are attached to plasma membrane and most remarkably this is repeated by eukaryotic chromosome as an "evolutionary tribute" that in interphase of mitosis in eukaryotes, the long chromatin threads attach to the nuclear membrane. That the eukaryotic chromosome has this inherent potentiality for such an attachment was once proved when the magnetic field exposure resulted in totally uncoiled chromosomes, removal of nuclear membrane, and chromosome ends were seen pierced in the plasma membrane.
3. Sequences that are dispersed among prokaryotes and a large number of lower groups of plants and animals viz. retrospoons like PLTEs but not in higher animals like mammals; which means that every major group achieved new or additional copies of genes during the evolutionary processes. Decidedly, as we already know, chromosomal mechanisms (aberrations, polyploidy as well as natural hybridizations) have played a great role.
4. Sequences recently being detected among plants and animals including man viz. telomeric, centromeric as well as some specific genes and parts thereof, support random distribution of DNA stretches during earliest phases of cellular evolution (4000-4500 million years ago).
5. Certain deeply conserved DNA sequences which rarely express among genomes with very special or relic characters might have been triggered by certain mutations and recombination of silent genes (by being activated). Most often, these traits may not last for hundreds of generations.
6. A large number of specialized sequences evolved and unaltered after selection for specific functions among all organisms as per their evolutionary status, might still be deep seated within the genomes; mainly among those organisms whose genomes have undergone biological screenings of evolutionary strategies since Permian -Palaeozoic and yet survived in modern times.

Acknowledgements

I humbly dedicate this paper to my dear student Late Dr. Arun Kumar Bajpai who had translated my vision and experience in his experiments and helped me in formulating the concept as outlined in this brief review.

References

1. Goswami HK, Chandorkar MS (1994) Highly conserved DNA sequence in *Isoetes pantii*. *Indian Fern Journal* 11: 53-55.
2. Bajpai AK, Goswami HK (2002) Human Genome may share some genes with plant gene pool. *Bionature* 22: 63-65.
3. Goswami HK, Kang SC, Goswami R, Bajpai AK (2006) DNA sequences do not abide with Phylogenetic Distance. *Bionature* 26: 1-12.
4. McLayght A, Hokamp K, Wolfe KH (2002) Extensive genomic duplication during early Chordate evolution. *Nature Genetics* 31: 200-204.
5. Goswami HK (2009) Dispersal of Genes in evolution II. Conserved DNA sequences are evolutionary signals in the Human Genome. *Bionature* 29: 38-46.
6. Bajpai AK, Goswami R, Goswami HK (2004) *Isoetes* V Genomic reshuffle AY695796 *Ginkgo biloba* defensin precursor mRNA complete sequence (A): DNA sequences. *Bionature* 24: 25-46.
7. Altschul SF, Madden TL, Schaffer AA, Jhang J, Jhang Z, et al. (1997) Gapped Blast and PSI-Blast: a new generation of protein database search programs. *Nucleic Acid Res* 25: 3389-3402.
8. Gianfrancesco F, Musumeci S (2004) The Evolutionary conservation of the human chitotrisidase gene in rodents and primates. *Cytogenet Genome Res* 105: 54-56.
9. Presting GG (2018) Centromeric retrotransposons and Centromere function. *Science* 49: 79-84.
10. Tardat M, Dejaridin J (2018) Telomere establishment and its maintenance during mammalian development. *Chromosoma* 127: 3-18.
11. Pennisi E (1996) Gene linked to commonest cancer. *Science* 272: 1583-1584.
12. Fournier T, Schacherer (2017) Genetic backgrounds and hidden trait complexity in natural populations. *Curr Opin Genet Dev* 47: 48-53.
13. Nagl W (1991) Two human DNA sequence (Aromatase: centromere) detected in *Phaseolus* (Fabaceae) by respective blot and in situ hybridization. *Polish Bot Stud* 2: 159-164.
14. Mikolos GLG (1985) Localized highly repetitive DNA sequences in vertebrate and invertebrate genomes. In: *Molecular Evolutionary Genetics*. Plenum Press, New York, USA, pp: 1-94.
15. Ferguson-Smith MA, Yang F, O'Brien PCM (1998) Comparative mapping using chromosome sorting and painting. *ILAR J* 39: 200-208.
16. Goodwin EH, Meyne J (1990) Strand specific FISH reveals orientation of chromosome 18 alphoid DNA. *Cytogenet Cell Genet* 63: 126-127.
17. Greider CW, Blackburn EH (1989) A telomeric sequence in the RNA of *Tetrahymena* telomerase required for telomere repeat synthesis. *Nature* 337: 331-337.
18. Yang F, Graphodatsky AS, O'Brien CMP, Colabella A, Solanki N, et al. (2000) Reciprocal chromosome painting illuminates the history of genome evolution of the domestic cat, dog and human. *Chromosome Research* 8: 393-404.
19. Skaletsky H, Kuroda-Kawaguchi T, Minx PJ, Cordum HS, Hillier L, et al. (2003) The male-specific region of the human Y chromosome is a mosaic of discrete sequence classes. *Nature* 423: 825-837.
20. Goswami HK, Arya BS (1970) A New species of *Isoetes* from Narsinghgarh, Madhya Pradesh. *J Ind Bot Soc* 49: 130-137.
21. Vogel F, Motulsky AG (1986) *Human Genetics: Problems and Approaches*. Springer Verlag, Berlin, p: 807.
22. Zhang Z, Gerstein M (2004) Large Scale analysis of Pseudogenes in the Human Genome. *Curr Opin Genet Dev* 14: 328-335.
23. Willard HF (2003) *Genome Biology: Tales of the Y chromosome*. *Nature* 423: 810-813.
24. Kuhlwillm M, Gronau I, Hubisz MJ, Filippo C, Prado-Martinez J, et al. (2016) Ancient gene flow from early modern humans into Eastern Neanderthals. *Nature* 530: 429-433.
25. Schachl T, Steiner FA (2017) Structure of centromere chromatin: from nucleosome to chromosomal architecture. *Chromosome* 126: 443-455.
26. Smith GM (1956) *Cryptogamic Botany Vol I and Vol II*. McGraw Hill Publications,

- New York, USA.
27. Sporne KR (1974) *The Morphology of Gymnosperms*. 2nd edn. Hutchinson and Co Ltd., London.
 28. Nakamura TM, Morin GB, Chapman KB, Weinrich SL, Andrews WH, et al. (1997) Telomerase catalytic subunit homologs from fission yeast and human. *Science* 277: 955-959.
 29. Schübeler D (2015) Function and information content in DNA methylation. *Nature* 517: 321-326.
 30. Goswami HK, Arya BS (1968) Heterosporous sporangia in *Isoetes*. *Brit Fern Gaz (London)* 10: 39-40.
 31. Goswami HK (1975) The morphogenetics of mixed sporangia in *Isoetes*. *J Ind bot Soc* 54: 210-218.
 32. Goswami HK, Sharma US (1997) Relic Genes in *Isoetes pantii* (Goswami & Arya). *Bionature* 17: 1-6.
 33. Goswami HK (1975) Chromosome studies in natural populations of *Isoetes pantii* with heterosporous sporangia. *Cytologia* 40: 543-551.
 34. Goswami HK (2011) Population cytogenetic studies confirm X-Y mechanism in *Isoetes pantii* (Isoetaceae: Pteridophyta). *Bionature* 31: 13-22.
 35. Bhu I, Goswami HK (1990) New line of chromosomal evolution in *Isoetes*. *Bionature*, p: 10.
 36. Glaessner MF (1979) *Pre Cambrian Animals. Fossil Record and Evolution: Scientific American*, USA.
 37. Goswami HK (2012) Directional selection of Bisexual plants in Natural populations of *Isoetes pantii* (Pteridophyta: Isoetaceae) with Chromosome Evolution. *Acta Botanica Hungarica* 54: 103-115.
 38. Goswami HK (2013) Palaeoploidization and adaptation: An Evolutionary strategy among pteridophytes with a reference to *Ophioglossum L.* *Nucleus (Springer-Verlag)* 56: 69-80.
 39. Khandelwal S, Goswami HK (1977) Periderm in ophioglossaceae. *Acta Soc Bot Polomae* 46: 641-646.
 40. Okada S, Fujisawa M, Sone T, Nakayama S, Nishiyama R, et al. (2000) Construction of male and female PAC genomic libraries suitable for identification of Y chromosome-specific clones from the liverwort *Marchantia polymorpha*. *Plant J* 24: 421-428.
 41. Ishizaki K, Shimizu-ueda Y, Okada S, Yamamoto M, Fujisawa M, et al. (2002) Multicopy genes uniquely amplified in the Y chromosome specific repeats of the liverwort *Marchantia polymorpha*. *Nucleic Acids Res* 30: 4675-4681.
 42. Tanurdzic M, Banks JN (2004) Sex Determining Mechanisms in Land Plants. *The Plant Cell* 16: S61-S71.
 43. Armstrong SJ, Filatov DA (2008) A Cytogenetic view of sex chromosome evolution in plants. *Cytogenet Genome Res* 120: 241-246
 44. Abraham A, Mathew PM (1962) X and Y chromosomes in *Cycas*. *Ann Bot* 26: 261-266.
 45. Stebbins GL (1971) *Chromosomal Evolution in higher plants*. Edward Arnold Ltd., London, UK.
 46. Goswami HK (2001) B chromosomes from both parents in natural hybridization may enforce genomic reshuffle. *Chromosome Research* 9: 110.
 47. Goswami HK (2005) Origin of new chromosomes in the genome of *Isoetes pantii*. *Bionature* 25: 1-10.
 48. Goswami HK (2005) Intragenomic importance of B-chromosomes. *Bionature* 25: 11-20.
 49. Goswami HK (1993) *Origin and Evolution of Chromosome system*. Catholic Press, Ranchi, India.
 50. Singh L, Purdom IF, Jones KW (1980) Sex chromosome associated satellite DNA: evolution and Conservation. *Chromosoma* 79: 137-157.
 51. Rozen S, Skaletsky H, Marszalek JD, Minx PJ, Cordum HS, et al. (2003) Abundant gene conversion between arms of palindromes in human and ape Y chromosomes. *Nature* 423: 873-876.
 52. Zwick MS, Hanson RE, Islam-Faridi MN, Stelly DM, Wing RA, et al. (1997) A Rapid procedure for the isolation of Cot-1 DNA from plants. *Genome* 40: 138-142.
 53. Schmid M, Enderle E, Schindler D, Schempp W (1989) Chromosome banding and DNA replication patterns in bird karyotypes. *Cytogenet Cellgenet* 52: 139-146.
 54. Cohn NS (1964) *Elements of cytology*. Brace & World Inc., Harcourt, New York, USA.
 55. Schubert I, Vu THG (2016) Genome stability and evolution: Attempting a holistic. *Trends in Plant Science* 21: 749-757.
 56. Balakirev ES, Francisco J (2003) Pseudogenes: Are they "Junk" or Functional DNA?. *Ann. Rev. Genetics*. 37: 123-151.
 57. Arkhipova IR (2006) Distribution and Phylogeny of Penelope-Like Elements in Eukaryotes. *Syst Biol* 55: 875-885.
 58. Barchi M, Cohen P, Keeney S (2016) Special issue on Brecent advances in meiotic chromosome structure, recombination and segregation. *Chromosoma* 125: 173-175.
 59. Biscotti MA, Olmo E, Heslop-Harrison JS (2015) Repetitive DNA in eukaryotic genomes. *Chromosome Res* 23: 415-420.
 60. Eames AJ (1936) *Morphology of Vascular plants (Lower Group)*. McGraw Hill Book & Co., New York, NY, USA, p: 433.
 61. Goswami HK, Sharma US (1996) Wild Gametophytes with Tracheids. *Fern Gaz (London)* 15: 87-89.
 62. Goswami HK (2015) Human Genome is Billions of Years older than man: A reemphasis on Random Distribution of DNA sequences during early phases of evolution. *Bionature* 36: 35-43.
 63. Schmutz J, Martin J, Terry A, Couronne O, Grimwood J, et al. (2004) The DNA sequence and comparative analysis of human chromosome 5. *Nature* 431: 268-274.
 64. Mirabella AC, Foster BM, Bartke T (2016) Chromatin deregulation in disease. *Chromosoma* 125: 75-93.
 65. Okada S, Sone T, Fujisawa M, Nakayama S, Takenaka M, et al. (2001) The Y chromosome in the liverwort *Marchantia polymorpha* has accumulated unique repeat sequences harboring a male-specific gene. *Proc Natl Acad Sci* 98: 9454-9459.
 66. Watson JM, Spencer JA, Riggs AD, Graves JA (1991) Sex chromosome evolution: Platypus gene mapping suggests that part of the human X chromosome was originally autosomal. *Proc Natl Acad Sci USA* 88: 11756-11760.
 67. Dou Z, Ghosh K, Vizioli MG, Zhu J, Sen P, et al. (2017) Cytoplasmic chromatin triggers inflammation in senescence and cancer. *Nature* 550: 402-406.