Secret of Lifespan

(Bioinformatics Work Experience Report – 2021)

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CERTIFICATE

This is to certify that the thesis entitled "**Secret of Life span**" is submitted by **Ms.R.Anitha, Mr.C.Jyothi Swaroop, Mr.K.Karthick Raja Ms.T.Sugumariammal, Ms.M.Vinothini, Ms.S.Vinubhashree**, for the award of **B.Tech Bioinformatics** under my guidance and supervision for a period of three months from **09.02.2021** to **28.04.2021.** This work is original and entirely carried out by the candidate for the fulfilment of project work. This work has not been submitted in part or in full for the awarded for any other degree, Diploma, Fellowship or other titles of any university and institutions. No part of the thesis is a reproduction from any other sources, either published or unpublished without acknowledgement

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DECLARATION

I hereby declare that the thesis entitled on “**Secret of Life span**” submitted by me for the degree of Undergraduate in B. Tech-Bioinformatics is the result of my original and independent research work carried out under the guidance of **Dr. S. SUDHAKAR**, Professor, Department of Biotechnology, Manonmaniam Sundaranar University, Tirunelvei-627012 and it has not been submitted for the award of any degree, diploma, associateship, fellowship of any University or Institution.

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Abstract:

It has been proved that telomere repeat has played a vital role in ageing. The tandem repeats of TTAGGG in telomere is an exclusive responsibility for ageing but the same repeat is also present in interior sequence of the chromosomes. Their presence and role of intrinsic TTAGGG in the chromosome are not yet studied completely. In the present study we took four insect's genome, 18 vertebrate's genome and 6 microorganisms. The intrinsic TTAGGG repeats were studied using a newly developed program using R language. The data show all the insect's genome has one repeat per 1200-2200 bases. The vertebrate genome has one repeat per every 3000-7000 bases. Finally, the repeats also have been studied in fungus and protozoans which has one repeat per every 5000-11000 bases. Based on the data we can conclude that the intrinsic TTAGGG has major role in genome organization and that's why their presence is conserved among six phyla such as Arthropod, Chordata, Ascomycota, Nematoda, Epicomplexa, Euglenozoa. The generated data will be useful for synthetic biology laboratory and for genome organization. There is a direct correlation of the presence of Forward repeat TTAGGG and Reverse complementary repeat CCCTAA of the telomeric sequence, this finding suggests that the 5' and 3' ends are protected by the telomere TTAGGG and CCCTAA.

INTRODUCTION

Introduction:

Chromosomes are a complex network of proteins and DNA that help DNA to organize during cell division and protects it. In 1842, Karl Wilhelm von Nageli, a swiss botanist discovered a structure which later known as chromosomes. In 1882, Wilhelm Hofmeister denoted the term as “chromosomes”. In 1883, Wilhem *roux* speculated chromosomes as a carrier of genetic data. Unlike the prokaryotic DNA, the DNA of eukaryotes is organized on chromosomes having centromere, telomere, p arm and q arm.

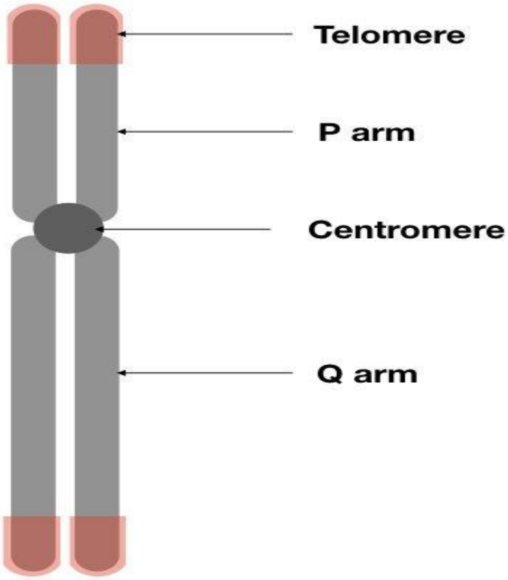

Fig1: Graphical representation of chromosome and their parts

Different organisms have a different chromosomes number based on their genome size. For example, the number of chromosomes in different organisms are Given below,

Table:1 shows the list of organisms, number of chromosomes and their genome size

Organism	**Number Of Chromosomes(n)**	**Genome Size(in Mb)**
Human	23	2827.97
Drosophila melanogaster	6	137.6
Tortoise	24	2300
Caenorhabditis elegans	6	100.2

Chromosomes not only carry transcribed genes and their regulatory DNA sequences, but also contain regions that are required for the stability and maintenance of the chromosome as a unit. These include centromeres, telomeres and origins of replication.

Centromere and arms are the main components of a chromosome:

Centromere:

The Centromere was first discovered by Walter flemming in 1880's a German biologist. The centromere is not only located at the center of the chromosome based on the centromere location, it is categorized into metacentric, sub metacentric, acrocentric, and telocentric. A constricted, narrow, and rounded region of a chromosome which holds chromatids called centromere.

During the process of cell division, and once the replication is in process, the centromere plays a crucial role to copy the exact one from the parent chromosome properly. Due to the proper attachment of centromere to the spindle fiber, the single cell cycle gets completed.

Arms:

The centromeres are attached with **q arm** and **p arm**. Although, based on the location of the centromere, the length of the arm varies. Arms has complex network of protein and

DNA where genes are located. The densely packed region near centromere and the end region in arms is called heterochromatin region (a gene less region, rich in non-coding DNA). On the other hand, except heterochromatin the loosely packed region is known as the euchromatin region (a gene-rich region). The tip of each arm is protected by the structure called telomeres (1).

Telomeres:

In 1975-1977, Elizabeth Blackburn, working as a postdoctoral fellow at Yale University with Joseph G. Gall, discovered the weird nature of telomeres, with their straightforward recurrent polymer sequence repeated DNA sequences composing chromosome ends. Blackburn, Carol Greider, and Jack Szostak were awarded the 2009 noble Prize in Physiology or drug for discovery of however chromosomes are protected by telomeres and the enzyme telomerase (2).

Telomere is located at the end on the chromosome accompanied by the Shelterin protein. Telomere is made up of short repetitive sequence (3). For example, telomere sequence in insect has TTAGG (4), *C.elegan* has TTAGGC (5), Humans and animals has TTAGGG. Telomeres are also structurally complex, with repetitive sequence, including simple telomeric repeats and more complex telomere-associated sequences (6). And the telomere protects the chromosome from every damage like, nucleolytic degradation, repair, UV radiation effects, redundant recombination, inter chromosomal fusion and from more damages. Telomeres plays an extraordinary role in protecting genetic information. During every cell division the telomere also divide but, small amount of telomere will degrade during every cell cycle. The chromosomes are shortened by about 25-200bp for every replication, that shortening of telomeres are varies among different organisms.

Once the end of the telomere length reaches a crucial limit, the cell undergoes caspase mediated cell death. Therefore, telomere length might be functioning as a mechanism to work out the lifetime of a cell and organisms. And one of the interesting features about telomere is, that the telomere is present in cancer cells. In cancer cell, telomere have a lot of infinite capability for cell division, one in which of vital changes they create in cancer cell is the presence of telomeres is high, in order that molecular clock goes away, and those cells can keep dividing, despite they should get to the end of the lifespan. By using this way cancer cell primarily trick the human body into thinking that they should keep replicating (7).

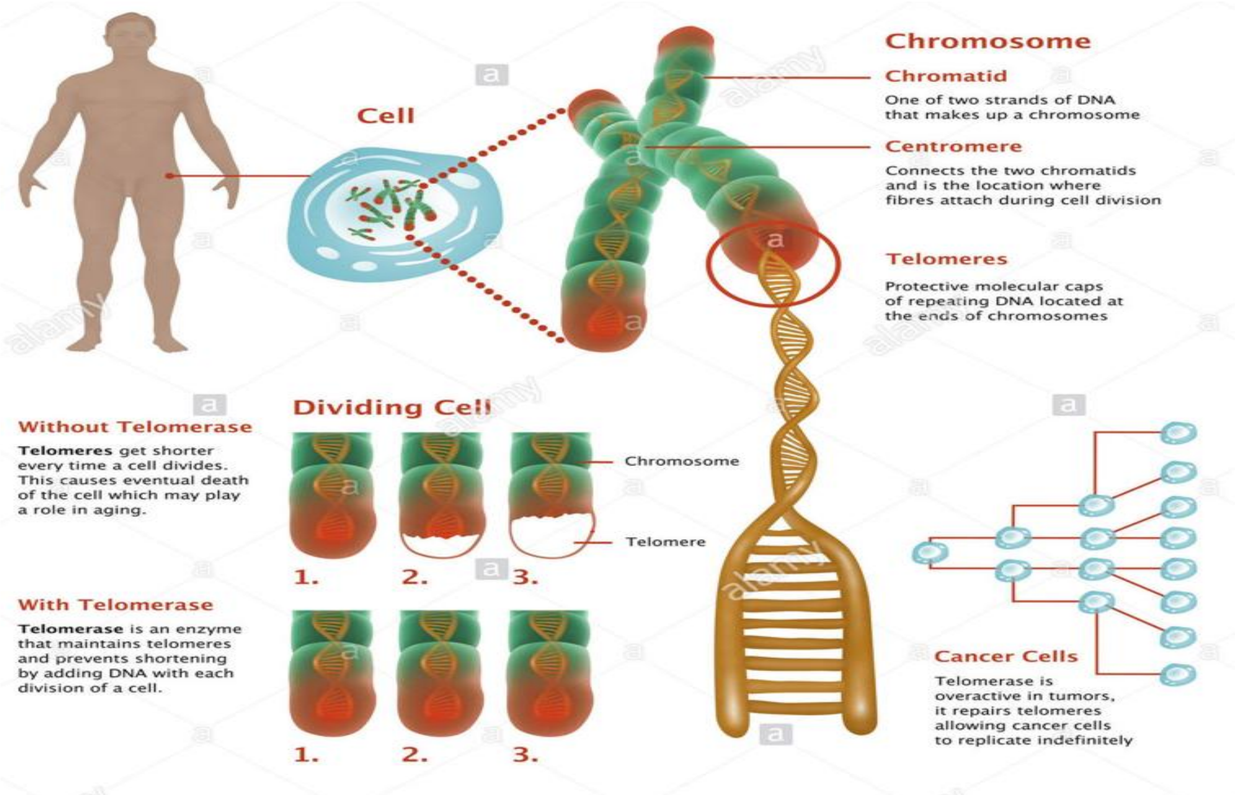

Fig 2: During every cell division the telomere also divide but, small amount of telomere will get degrade during every cell cycle.

Telomere not only present at the end of the chromosomes, but also present in the internal site of the chromosomes (8).

In addition to their location at terminal positions, telomeric-like repeats are also present at internal sites of the chromosomes (intrachromosomal or interstitial telomeric sequences, ITSs). According to their sequence organization and genomic location, two completely different sorts of ITSs is identified: (i) heterochromatic ITSs (het-ITSs), large (up to hundreds of kb) stretches of telomeric-like DNA localized in centromeres, and (ii) short ITSs (s-ITSs), short stretches of telomeric hexamers distributed at internal sites of the chromosomes. Het-ITSs are solely delineate in some vertebrate species and that they most likely represent the remnants of evolutionary chromosomal rearrangements. Instead, s-ITSs are most likely present in all the mammalian genomes although they have been described in detail only in some completely sequenced genome.

Telomerase:

The enzyme telomerase is responsible for the length of the telomeres by addition of guanine-rich repetitive sequences. Telomerase is a reverse transcriptase enzyme that carries its own RNA sequence which used as a template to elongate telomere by adding guanine rich repetitive sequences. Due to the presence of the telomerase the chromosome would not become more and more shorted in every replication of the cell cycle. But the fruit fly *Drosophila melanogaster* does not have telomerase, instead it uses retrotransposons to maintain telomerase. As reported by Miriam Aparecida Giardini et al., under certain circumstances, yeast and human cells that lacks telomerase activity, as well as some telomerase-negative tumor lineages, can maintain their telomeres using a recombination-based DNA replication mechanism known as alternative lengthening of telomeres (9). The enzyme telomerase is active in germ cell and during early embryogenesis, stem cell, cancer cells, but absent or low level in most of the somatic cell.

The enzyme telomerase binds to a special RNA molecule that contains a sequence complementary to the telomeric repeat. It extends (adds nucleotides to) the overhanging strand of the end polymer telomere DNA using the complementary RNA as a template. Once the overhang is long enough, an identical strand is often created by the conventional polymer replication mechanism (that is, using an RNA primer and DNA polymerase), producing double-stranded DNA. In human physical cells proliferation potential is strictly restricted and senescence follows roughly 50-70 cell divisions (10).

Telomere Shortening:

Dyskeratosis is a rare genetic form of bone marrow failure, the inability of the marrow to produce sufficient blood cells which is characterized by the shortening of telomeres. The bone marrow failure syndrome Dyskeratosis was diagnosed with other symptoms like the triad of abnormal skin, malformation of the nails, and white, thickened patches on the mucous membranes of the mouth. This suggest that telomeres play a role in these conditions, which all involve tissues that rapidly divide. Telomeres shorten with age and progressive telomere shortening leads to apoptosis. Shorter telomeres have been implicated in genomic instability and oncogenesis (11)(12).

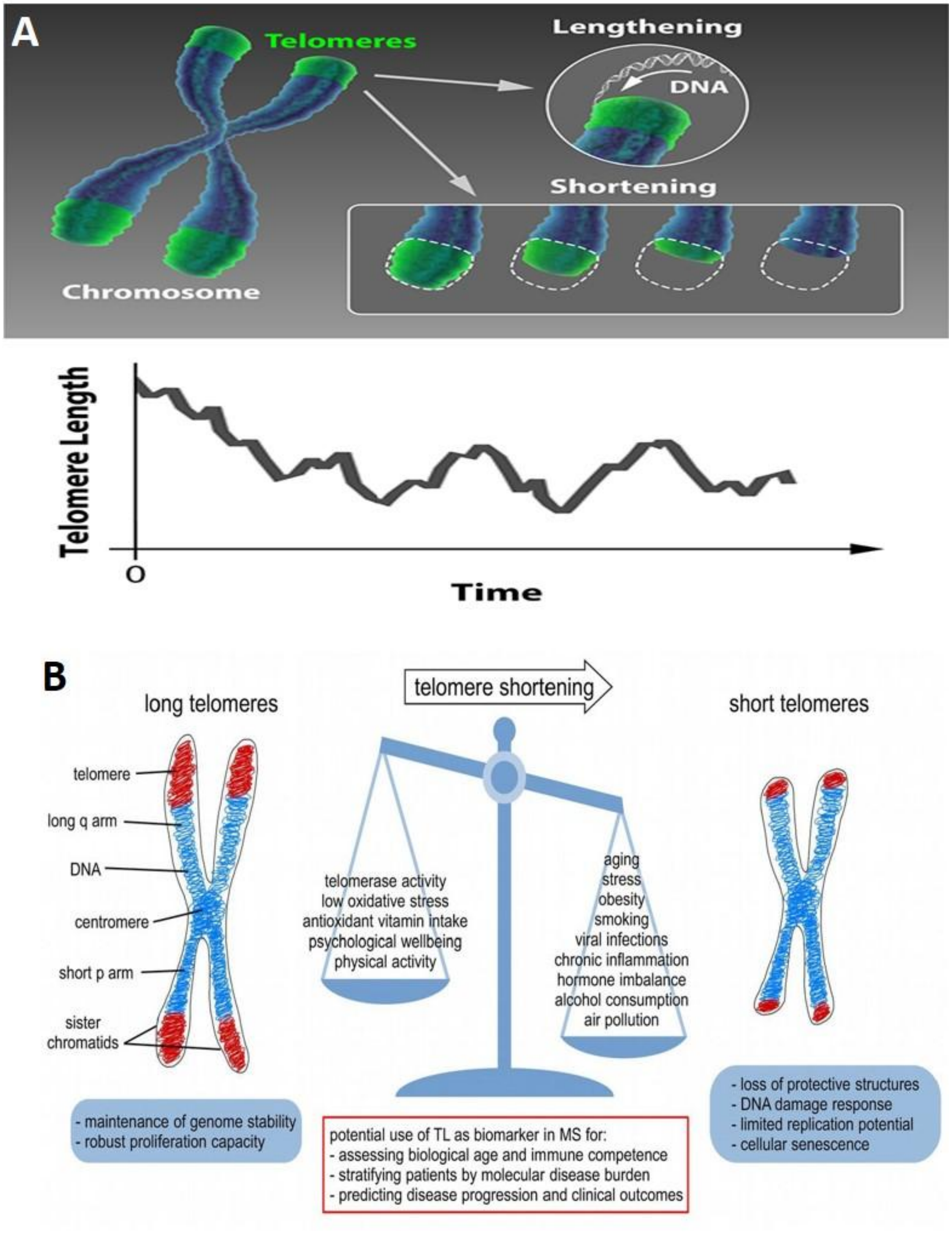

Fig 3: **(A)** Telomere shortening increase when the lifespan decreases. **(B)** The telomere length is also decrease due to stress, obesity, smoking and als due to hormonal imblance.

The decrease of telomere is varying between both men and women. One study showed that in a group of 48 years old men and women, there was a significance difference in telomere length of about 320 bp. Men’s telomere shorten rate is more when compared to women. Telomere length being associated with age and with the aging process.

Some external factors can accentuate telomere shortening, too. For example, smoking, Alcohol consumption, stress (G repeats are particularly sensitive to oxidative stress) or work condition can play a role, as well as poor health (obesity, inflammation, cardiovascular disease). Many of these factors are present in our genome itself, in such a way that it seems programed to make our bodies age. The sequence of telomeric DNA contains guanine in significant proportions. However, guanine shows a high risk of oxidation into “8 – oxo guanine,” which is a composite causing many malfunctions in the genome that are not easily fixed. Its composition itself could affect telomere aging (13).

REVIEW OF LITERATURE

Review of Literature:

Simple to Complex Organisms:

As we are looking for pattern of ageing in organisms, we took organisms from simple to complex forms. We took organisms from various phylum such as *Trypanosoma brucei*(Euglenozoa), *Plasmodium falciparum*(Apicomplexa), *Neurospora crassa*(Ascomycota), *Thermophilic fungi*(Ascomycota), *Saccharomyces cerevisiae*(Ascomycota), *Caenorhabditis elegans*(Nematoda), *Drosophila melanogaster*(Arthropod), *Bombyx mori*(Arthropod), *Apis mellifera*(Arthropod), *Aglais io*(Arthropod) *Danio rerio*(Chordate), *Xenopus laevis*(Chordate), *Homo sapiens*(Chordate), *Equus caballus*(Chordate), *Gopherus evgoodei*(Chordate), *Bos taurus*(Chordate), *Oryctolagus cuniculus*(Chordate), *Anas platyrhynchos*(Chordate), *Canis lupus*(Chordate), *Gallus gallus*(Chordate), *Strigops habroptilus*(Chordate), *Felis catus*(Chordate), *Balaenoptera musculus*(Chordate), *Camelus dromedarius*(Chordate), *Tursiops truncates*(Chordate), *Scyliorhinus canicular* (Chordate), *Taeniopygia guttata*(Chordate), and *Ailuropoda melanoleuca*(Chordate). The richness of the diversity is high among organisms.

Speed of the Animals:

Movement is key to animal behavior, governing the way animals use habitats, move with conspecifics, avoid predators, get food, and even talk over human-modified landscapes. The need of feat speed has been the greatest single factor in the progressive evolution of animal kind. Speed is additionally seemingly to associate effect on an animal's ability to watch its surrounding and notice the presence of predators, mates, and food. As an example, if extraordinarily little increase in speed (even at low speeds) decrease the flexibility to appear at, then animals in risky environments might favor short, quick movements interspersed with quick scans. The animals which generally move slower showed higher lifespan than animals moving faster and some of the values correlated supporting this hypothesis. Ranging from slow moving animal tortoise to fast moving rabbit (14)(15).

Telomere Length:

The exact causes of aging are still not understood, and it is unclear why some species live less than 1 day, while other species live more than 400 years, that is still a question mark. Some research suggests that telomeres are related to the aging process, but a clear relationship between the life span of a species and initial telomere length has not been observed still now. Here, we measure the telomere lengths position of different species. However, whether telomere length is a universal determinant of species longevity is not known (16). To determine whether telomere shortening can be a single parameter to predict species longevities, here we measured in parallel the telomere length of a wide variety of species (birds and mammals) based on their telomere repeats with very different life spans and body sizes, including *Trypanosoma brucei*(Protozoan), *Plasmodium falciparum*(Protozoan), *Neurospora crassa*(Fungi), *Thermophilic fungi*(Fungi), *Saccharomyces cerevisiae*(Yeast), *Caenorhabditis elegans*(Nematode), *Drosophila melanogaster*(Fruit fly), *Bombyx mori*(Silk worm), *Apis mellifera*(Honey bee), *Aglais io*(European peacock butterfly) *Danio rerio*(Zebre fish), *Xenopus laevis*(Frog), *Homo sapiens*(Human), *Equus caballus*(Horse), *Gopherus evgoodei*(Tortoise), *Bos taurus*(Cow), *Oryctolagus cuniculus*(Rabbit), *Anas platyrhynchos*(Mallard duck), *Canis lupus*(Dog), *Gallus gallus*(Chicken), *Strigops habroptilus*(Owl parrot), *Felis catus*(Cat), *Balaenoptera musculus*(Blue whale), *Camelus dromedarius*(Camel), *Tursiops truncates*(Dolphin), *Scyliorhinus canicula*(Cat shark), *Taeniopygia guttata*(Zebra finch), *Ailuropoda melanoleuca*(Gaint panda). Humans have relatively short telomere lengths from 5 to 15 kbx, and yet humans have much longer life spans than mice, which can start with telomere lengths around 50 kb.

Human telomeres shorten at a rate of ∼70 bp per year, while mice telomeres shorten at a rate of 7,000 bp per year. These different rates of telomere shortening between human, and mice could explain the different longevities of mice and humans. Here, to address whether telomere length and telomere shortening rates could explain species longevity. Laboratory mice were included as a control, a rate of telomere shortening of around 7,000 bp per year, which is 100-fold faster than that reported in humans (16).

The Mechanism of Telomere Protection:

Nearly a century ago, Muller and McClintock independently discovered that natural chromosome ends in fruit flies and maize are resistant to fusion, in contrast with ends generated by DNA breakage. The word telomere was used to describe chromosome ends sealed against rearrangement or, in modern parlance, with “end protection”.

In general, telomeric repeats have one guanosine-rich strand (G-strand) and one cytosine-rich strand (C-strand) synthesized as the leading and lagging strands, respectively. Across organisms, tracts of telomeric repeats vary in length from a few to a few thousand repeats and have a G-strand 3 overhang that varies from a few to more than a hundred nucleotides. Although telomeric sequences vary between species, fundamentally, telomeres and telomerase function very similarly throughout the eukaryotes.

At least in vertebrate cells, the relatively long G-strand overhang can invade the adjacent duplex to produce a lasso-like structure known as a telomeric loop (t-loop). Telomere-bound proteins organized by DNA interaction suppress DNA degradation and repair reactions that would be aberrant for authentic chromosome termini (17)(18).

In eukaryotes, end maintenance could have relied on telomere extension by an ancestral reverse transcriptase (RT) encoded within self-splicing introns. Across extant eukaryotes, the nearly ubiquitous solution to the end-replication problem is a specialized RT, telomerase (19).

Telomere-associated proteins can regulate lengths of telomere tracts by modulating access of telomerase or affecting conventional DNA replication machinery. In mammals, telomeric DNA associates with a six-protein complex called shelterin (20). The telomere of the mammals consists of TTAGGG repeats packed with the DNA binding proteins known as TRF1 and TRF2. Bothe the protein which contains similar C terminal MYb domain that instructs the sequence specific binding to telomeric DNA (21).

A schematic model of mammalian telomere-associated proteins and a proposed model of the telomeric complex in *A. thaliana* summarizes recent knowledge in mammalian and plant telomere biology and provides a clear comparison of conserved structures at chromosome termini (22).

In contrast with these Dipteran insects, some fruit flies have different mechanisms of telomerase-independent telomere maintenance. In Drosophila melanogaster, two non-LTR retrotransposons, HeT-A and TART, retro transpose specifically onto the telomeric ends of the chromosomes. HeT-A does not encode reverse transcriptase but can retro transpose on the chromosomal ends with a reverse transcriptase, possibly derived from the TART element. On the other hand, TART also requires HeT-A, which encodes the gag protein, to access the telomere region. The interdependent retro transposition of HeT-A and TART is a major system for telomere maintenance in D. melanogaster (24)(23).

Telomere Repeats:

In most organisms, telomeric DNA consists of tandem arrays of simple sequence, the end of the telomere repeat is G rich. Although there is diversity in the composition of telomeric repetitive sequences among different organisms, some sequences are characteristic for whole taxonomic groups. The human telomeric sequence consist of **TTAGGG hexa-repeats**, for example, has been found in all vertebrates (6). As well as the plant kingdom telomeric sequence consists of **TTTAGGG hepta-repeats** (25).

Insects represent the most numerous groups of organisms in the animal kingdom, with a variety of cytogenetic systems. Three different types of DNA telomere organization have been described in this group: a **pentanucleotide sequence repeat TTAGG**, from the silkworm Bombyx mori, HeT-A and TART transposable elements in Drosophila melanogaster, and complex tandem repeats in the midge genus Chironomus. Thus, telomere repeats of TTAGG is present in insects and other arthropods (4).

Caenorhabditis elegans telomeric sequences consists hexamer repeats of **TTAGGC** (5). The 14 linear chromosomes of ***Plasmodium falciparum*** are bounded by closely related G-rich repeats, and the most frequent type, of telomere repeat motifs consists of **GGGTTTA** and **GGGTTCA** (26).

Telomere Associated Aging Disorders:

Short telomeres and telomere dysfunction have been linked to numerous disorders. Genes which are involved in the expression and regulation of shelterin proteins or telomerase, have been associated with some genetic disorders with mutation. For the better survival of an organism, their genomic stability is more important. Diseases like aplastic anemia, dyskeratosis congenital, idiopathic pulmonary fibrosis are characterized within the individuals with shorter telomeres. Critically short telomeres trigger what has been termed replicative senescence, which serves as a stress or DNA damage signaling mechanism to protect genome integrity and prevent further proliferation of cells that may harbor genetic alterations. In addition, shortened telomeres have been also associated with an increased risk of cardio-vascular disease, liver cirrhosis, hypertension, atherosclerosis, and cancer. Telomere shortening has been shown to accompany physical disease states that are associated with aging and stress exposure (27).

Organism of Different Habitats:

An environment is a specific kind of surrounding that is good for the existence and growth of certain plants and animals. Habitats or biomes are determined by the climate and geography of the region as well as the animals and plants inhabiting the area. Most animal and bird species are adapted to survive in specific habitats and cannot live in other types of habitat.

For example, whale is adapted to live in marine habitats and cannot survive in deserts or other terrestrial habitats. Similarly, Camel cannot live in marine water or arctic regions as they are adapted for warm terrestrial habitats like grasslands and desserts. But some organisms like Tortoise and Frog (Reptiles) lives both in terrestrial and water. Animals living in extreme cold habitats may migrate to warmer regions during the winter, coming back to their original habitats again during the warm seasons (28).

Lifespan of Organisms:

The life span is the period between the birth and death of an organism. It is the duration of existence of existence of an individual. The link between size and lifespan was first remarked on by Aristotle (350 BC). He made a connection between fire and life which was interestingly prescient: A lesser flame is consumed by a greater one, for the nutriment, to wit the smoke, which the former takes a long period to expend is used up by the big flame quickly. Life span of an organism is inversely proportional to its metabolic rate, that means higher the metabolism, the slower its metabolism. Life span cannot necessarily correlate with their sizes. Reproduction ensures the continuity of the different species.

Evolution of Insects:

Insects are more diversified group when compared with animals and humans. In evolution insects are second evolved after microorganisms to the earth. The phylogenetic analysis among the arthropods has been already identified by the researchers as shown in the image below (29).

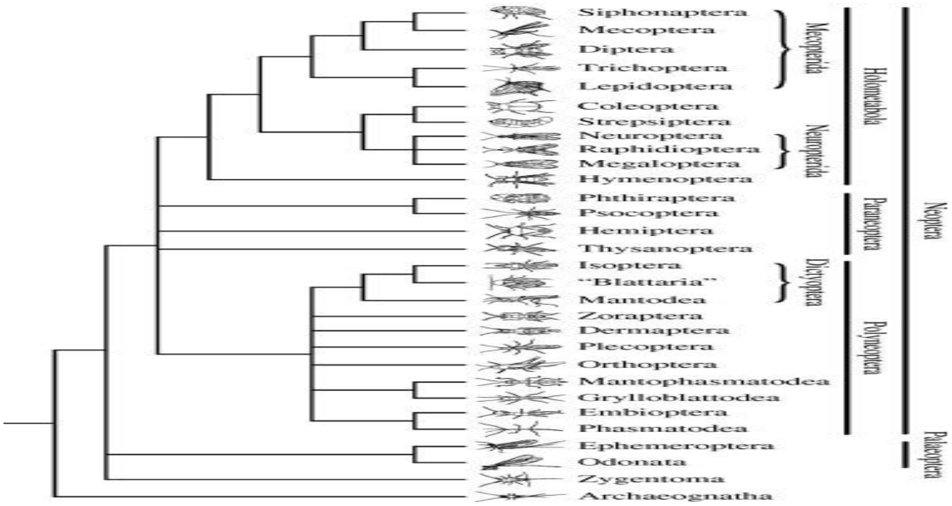

Fig 4: The picture shown that the construction phylogenetic tree among insects under the phylum arthropods.

MATERIALS
AND
METHODS

Materials and Methods:

We downloaded 28 organisms whole genome sequence with all chromosomes in fasta format from NCBI based on different habitat such as *Trypanosoma brucei*(Protozoan), *Plasmodium falciparum*(Protozoan), *Neurospora crassa*(Fungi), *Thermophilic fungi*(Fungi), *Saccharomyces cerevisiae*(Yeast), *Caenorhabditis elegans*(Nematode), *Drosophila melanogaster*(Fruit fly), *Bombyx mori*(Silk worm), *Apis mellifera*(Honey bee), *Aglais io*(European peacock butterfly), *Danio rerio*(Zebre fish), *Xenopus laevis*(Frog*)*, *Homo sapiens*(Human), *Equus caballus*(Horse), *Gopherus evgoodei*(Tortoise), *Bos taurus*(Cow), *Oryctolagus cuniculus*(Rabbit), *Anas platyrhynchos*(Mallard duck), *Canis lupus*(Dog), *Gallus gallus*(Chicken), *Strigops habroptilus*(Owl parrot), *Felis catus*(Cat), *Balaenoptera musculus*(Blue whale), *Camelus dromedarius*(Camel), *Tursiops truncates*(Dolphin), *Scyliorhinus canicula*(Cat shark), *Taeniopygia guttata*(Zebra finch), *Ailuropoda melanoleuca*(Gaint panda). Different species have a different number of chromosomes based on their genome size.

As we, identify the telomeric position, the downloaded sequences are run in R studio using R programming language, and we generated the telomere position in excel file as csv format and also we generated a histogram graph for pictorial representation. We generated the telomeric positions of Forward Repeat (TTAGGG), Reverse Repeat (GGGATT), Forward Complementary Repeat (AATCCC), Reverse Complementary Repeat (CCCTAA) of four combinations.

Program:

```
library("seqinr")

# read the file
a <- read.fasta("chr22.fa", as.string=TRUE)

#take only the sequence
b <- getSequence(a, as.string=TRUE)


#Find the position of ttaggg(ForwardRepeat)
c <- words.pos("ttaggg", b)
ForwardRepeat <- c-6

#Generate file with position
write.csv(ForwardRepeat, "position of ttaggg chr22.csv", row.names=FALSE, )

#plot the frequency
hist(ForwardRepeat, 500,density=2, xlab = "Repeats per 500bps",border="red",col="red", ylab ="Number of repeats", xlim=c(0,250000000), ylim=c(0,400))


#Find the position of gggatt(ReverseRepea)
d <- words.pos("gggatt", b)
ReverseRepeat <- d-6

#Generate file with position
write.csv(ReverseRepeat, "position of gggatt chr22.csv", row.names=FALSE)

#plot the frequency
hist(ReverseRepeat, 500,density=2, xlab = "Repeats per 500bps",border="red",col="red", ylab ="Number of repeats", xlim=c(0,250000000), ylim=c(0,400))


#Find the position of aatccc(ForwardComplementaryRepeat)
e <- words.pos("aatccc", b)
ForwardComplementaryRepeat <- e-6

#Generate file with position
write.csv(ForwardComplementaryRepeat, "position of aatccc chr22.csv", row.names=FALSE)

#plot the frequency
hist(ForwardComplementaryRepeat, 500,density=2, xlab = "Repeats per 500bps",border="red",col="red", ylab ="Number of repeats", xlim=c(0,250000000), ylim=c(0,400))


#Find the position of ccctaa(ReverseComplementaryRepeat)
f <- words.pos("ccctaa", b)
ReverseComplementaryRepeat<- f-6

#Generate file with position
write.csv(ReverseComplementaryRepeat, "position of ccctaa chr22.csv", row.names=FALSE)

#plot the frequency
hist(ReverseComplementaryRepeat, 500,density=2, xlab = "Repeats per 500bps",border="red",col="red", ylab ="Number of repeats", xlim=c(0,250000000), ylim=c(0,400))
```

Fig 5: R programing language used to generate position of telomeric repeats in excel and also generate a histogram graph**.**

R Programming:

R is a language and environment for applied mathematics computing and graphics. The official R software environment is a GNU package. R language is like S language and that is developed by Bell laboratories (formerly AT&T, now Lucent Technologies) by John Chambers and colleagues. R may be considered as a distinct implementation of S. There are some necessary variations, however abundant code written for S runs unaltered under R. Although R has a command line interface, there are several third-party graphical user interfaces, such as RStudio, an integrated development environment, and Jupiter, a notebook interface.

R provides a wide variety of statistical (linear and nonlinear modelling, classical statistical tests, time-series analysis, classification, clustering, …) and graphical techniques, and is highly extensible. R programming is also useful for data science, perception.

R programming created a big revolution in Big Data analytics and in data science. R is a Free Software under the terms of the Free Software Foundation’s GNU General Public License in source code form. It compiles and runs on a wide variety of UNIX platforms and similar systems (including FreeBSD and Linux), Windows and MacOS.

The capabilities of R extended through user-created packages, which allow specialized statistical techniques, graphical devices, import/export capabilities, reporting tools etc. These packages are developed primarily in R, and sometimes in Java, C, C++ and Fortran. The R packaging system is also used by researchers to create compendia to organize research data, code and report files in a systematic way for sharing and public archiving. A core set of packages is included with the installation of R, with more than 15,000 additional packages are available.

R Studio:

RStudio is the premier integrated development environment for R. It is available in open source and commercial editions on the desktop (Windows, Mac, and Linux) and from a web browser to a Linux server running RStudio Server or RStudio Server Pro.

Comparative analysis:

The histogram graphs and dot plots were generated using various combinations of the TTAGGG repeat then the average repeat value and average ratio repeat value of each organism were analyzed with both pictorial and numerical data. Then graphs and charts were generated based on the data obtained. Then these data were assessed for finding a pattern in the values corresponding to the different lifespan of different organisms.

Number of Telomere Repeats:

From the available data from excel file, we calculated.

$$\textbf{Total Repeat Ratio} = \frac{\textbf{Size (In bp)}}{\textbf{Total Repeats}}$$

We found, internal repeat ratio. From chromosome, we exclude 40,000 bp from 5' end and 40,000 bp from 3' end. Then from the remaining internal repeat of the chromosomes are taken to calculate internal repeat ratio.

$$\textbf{Internal Repeat Ratio} = \frac{\textbf{Size (-80,000)}}{\textbf{Internal Repeats}}$$

RESULT

Result:

Genome:

We chose 28 organisms from different habitat of different phylum. In general animals living in aquatic conditions had bigger genome size in comparison with animals living in terrestrial habitat. However, the genome size did not have any correlation with the lifespan or the survival rate of the animal. For example, frog which is small with the genome size is 2718.4mb and the animal in aquatic such as shark and whale which is large that also has genome size of 4043.7mb and 2105.3mb. And the chromosome number varies between organisms based on the size of the chromosomes. In general, complex organisms had more chromosomes in comparison with simple life forms. All the 28 species are shown in the below table.

Organisms	Phylum	Chromosome No	Genome Size (in Mb)
Saccharomyces cerevisiae	Ascomycota	16	11.6
Plasmodium falciparum	Apicomplexa	14	23.509
Thermophilic fungi	Ascomycota	6	35.7
Neurospora	Ascomycota	7	43
Trypanosoma brucei	Euglenozoa	11	52.57
C. elegan	Nematoda	6	100.2
Drosophila	Arthropod	6	137.6
Honeybee	Arthropod	16	236
Butterfly (European peacock)	Arthropod	31	382
Silkworm	Arthropod	28	530
Chicken	Chordate	35	1000
Zebra finch	Chordate	31	1068.99
Duck	Chordate	33	1136.42
Owl parrot	Chordate	25	1190
Zebra fish	Chordate	25	1679
Camel	Chordate	37	2084.54
Whale	Chordate	23	2105.3
Horse	Chordate	32	2270
Tortoise	Chordate	24	2300
Cat	Chordate	19	2320
Giant panda	Chordate	21	2371.8
Dolphin	Chordate	22	2385.75
Dog	Chordate	40	2400
Cow	Chordate	30	2715.85
Frog	Chordate	18	2718.4
Rabbit	Chordate	22	2780.37
Human	Chordate	23	2859.97
Catshark	Chordate	31	4043.7

Table 2: Shows the 28 species which belongs to different phylum with chromosome number and genome size. In this table the species *Thermophilic fungi, C. elegan, Drosophila melanogaster* which has the lowest chromosome number 6 when compared to other species. Dog has higher chromosome number 40 among all the species. The organisms which have similar number of chromosomes such as, Dolphin and Rabbit has 22 chromosomes, Whale and Human has 23 chromosomes, Owl parrot and Zebra fish has 25 chromosomes, European peacock butterfly, Zebra finch and Cat shark has 33 chromosomes. As shown in the above table.

Lifespan:

It is not essential that life span of organisms should be correlated with their sizes. For example, the sizes of duck and parrots are not quite different, but their life spans show great difference. And there is no correlation between life span with the genome size of the organisms. For example, the genome size of Xenopus(frog) and human are almost having same genome size of about 2.5 Gb approximately. But their life is different Xenopus lives up to 15 years and human lives up to 80 years. Whatever is the life span, death of every organism is must. It means no individual is immortal except some single-celled (e.g., Amoeba) organisms, *C.elegan* is an eternal species.

S.No	Organisms	Lifespan (In Months)	Lifespan (In Days)
1	Thermophilic fungi	0.3	7
2	Saccharomyces cerevisiae	0.5	14-15
3	C. elegan	0.5	12-18
4	Neurospora	0.7	24
5	Trypanosoma bruceie	0.7	20-24
6	Honeybee	0.5-1	14-28
7	Plasmodium falsiparum	0.5-1	16-32
8	Silkworm	2	61
9	Drosophila	2-3	91
10	Butterfly (European peacock)	11	330
11	Zebra finch	24-60	720-1800
12	Zebrafish	42-65	1277-1977
13	Rabbit	24-84	730-2555
14	Duck	60-120	1825-3650
15	Chicken	60-120	1825-3650
16	Cat shark	144	4380
17	Dog	120-156	3650-4745
18	Xenopus	180	5475
19	Cat	120-180	3650-5475
20	Panda	180-240	5475-7300
21	Cow	216-264	6480-7920
22	Horse	300-360	9125-10950
23	Camel	480	14400
24	Dolphin	480-720	14600-21900
25	Human	840-1080	25550-32850
26	Whale	960-1080	29200-32850
27	Owl parrot	1140	34675
28	Tortoise	960-1800	29200-54750

Table 3: Shows the lifespan of all 28 species in months and in days. Tortoise has long lifespan in this table which lives up to 150 years (1800 months). The species with lower lifespan is *Thermophilic fungi,* which has the maximum lifespan of 7 days.

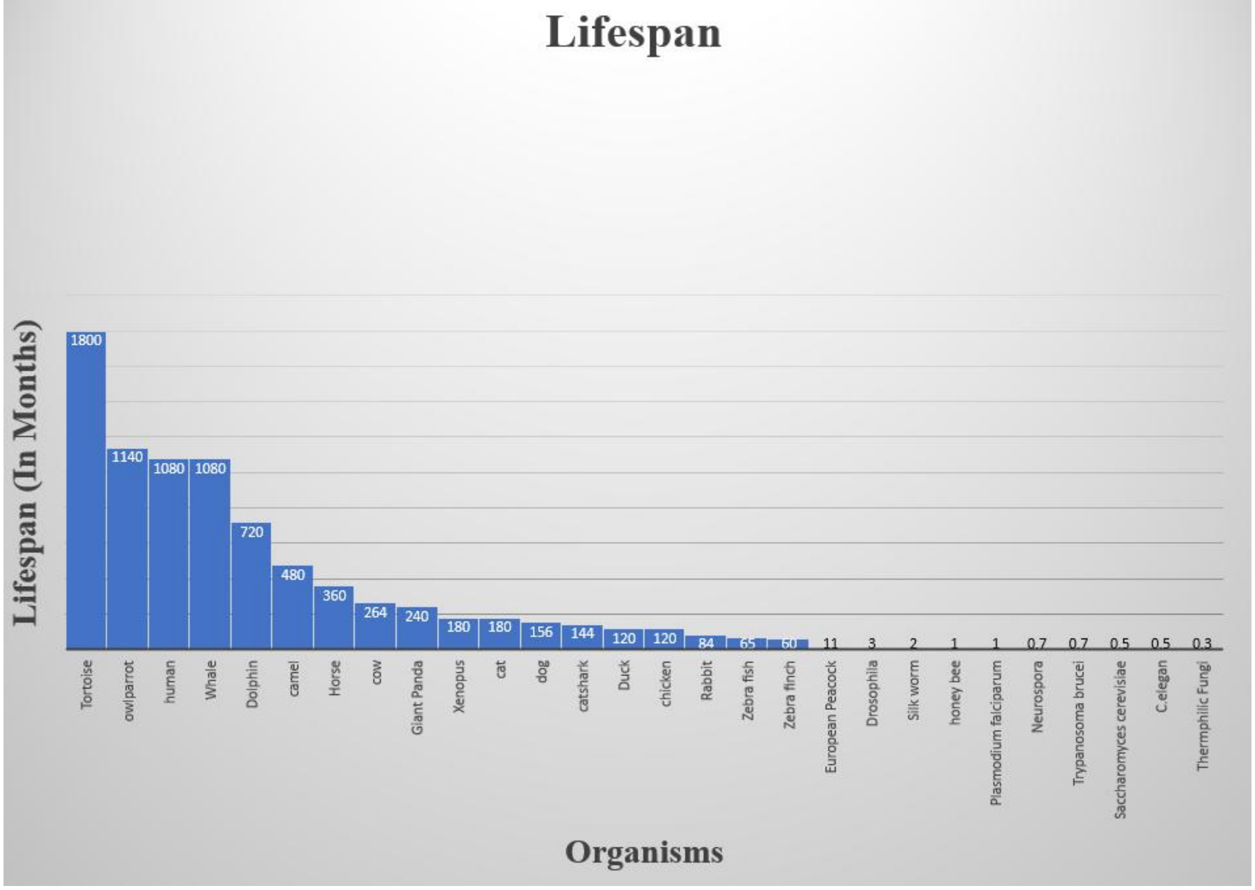

Fig 6: Shows the graphical representation of lifespan of all 28 species.

Table 4: Shows the organisms Ration average is divided based on their habitat.

Organisms	**Phylum**	**Ratio Average**			
		FR	**RR**	**FCR**	**RCR**
		Insects			
Drosophila (Penta)	Arthropod	1691.7	1045	1061	1707
Silkworm (Penta)		1238.36	1321	1317	1233
Honeybee (Penta)		2207.21	1090	1061	2626
European Peacock (Penta)		1446.92	1401	1385	575
		Aquatic Animals			
Zebra fish		5419	6778	6745	5371

Tortoise	Chordata	4333	3659	3627	4226
Dolphin		4799	4093	3951	4548
Catshark		5794	2657	2337	5640
Whale		5215	4063	4086	5194
Xenopus		3608	4765	4719	3684
Terrestrial Animals					
Human	Chordata	6088	2928	3364	6160
Horse		4979	4702	4689	4995
Cow		5797	3279	2533	5868
Rabbit		5864	4995	5033	5848
Dog		4513	3723	3743	4616
Giant Panda		4872	4249	4244	4898
Camel		4835	4249	4257	4953
Cat		5260	3955	3951	5145

In above table, organisms are grouped based on habitat and repeat ratio values, from that insects have a 1000-2000 direct repeat ratio values, Aquatic animals have a 3000-6000 direct repeat ratio values and Terrestrial animals have a 4000-6000 direct repeat ratio values.

The ratio average of forward repeat and reverse complementary repeat were similar in all categories of animals. Similarly, reverse repeat and forward complementary repeat had similar values of average ratio in all categories of animals.

The aquatic animals had higher average ratio in reverse repeat and forward complementary repeat in comparison with terrestrial animals.

Table:

The below tables show size of the organisms is differing from the genome size of the organisms. The table shows that, all the 6 chromosomes in drosophila varies in size and the penta telomeric repeats TTAGG repeats are differ in all the chromosomes, as shown in the table. The highest repeat is 18309 in chromosome 3R and the lowest repeat is 989 in chromosome 4. But the highest ratio is in chromosome X and the lowest ratio is in chromosome 4. Finally, the average ratio is 1690.7, average total repeat is 12773.32 and average internal repeat is 12734.6 in drosophila.

Thermothielavioides terrestris **(Thermophilic fungi):**

Table 5.1: Shows Total repeat, Total repeat ratio, Internal repeats, Internal repeat ratio of Forward repeat (TTAGGG). The total repeats and internal repeats are high in chromosome 1 and low in chromosome 6. Average for total repeats, internal repeat, total repeat ratio and internal repeat ratio are 1046.5, 1005.166, 6028.19 and 6347.665.

Chromosomes	Size (In bp)	Total Repeat	Total Repeat Ratio	Internal Size (Total size-80,000)	Internal Repeats	Internal Repeat Ratio
1	10101509	1788	5649.61	10021509	1755	5,755.84
2	9477512	1577	6009.83	9397512	1520	6,235.20
3	4786945	986	4854.91	4706945	947	5,054.85
4	4578922	729	6281.10	4498922	699	6,550.67
5	4396881	687	6400.11	4316881	644	6,827.45
6	3570487	512	6973.60	3490487	466	7,661.98
Average		**1046.5**	**6028.19**		**1005.166**	**6347.665**

C. elegan:

Table 5.2: Shows Total repeat, Total repeat ratio, Internal repeats, Internal repeat ratio of Forward repeat (TTAGGC). The total repeats and internal repeats are high in chromosome 5 and low in chromosome 6. Average for total repeats, internal repeat, total repeat ratio and internal repeat ratio are 3246.2, 3236.8, 6118.6 and 6462.

Chromosomes	Size (In bp)	Total Repeat	Total Repeat Ratio	Internal Size (Total size-80,000)	Internal Repeats	Internal Repeat Ratio
1	20594552	3742	5506.36	20514552	3734	5493.98
2	20116996	3466	3804.09	2039996	3462	5883.88
3	19436473	3197	6079.59	19356473	3182	6083.11
4	21017644	2890	7272.54	20937644	2886	7254.90
5	23638155	3914	6039.38	23558155	3896	6046.75
6	18190508	2271	8009.91	18110508	2261	8009.95
Average		**3246.2**	**6118.6**		**3236.8**	**6462**

***Drosophila melanogaster*:**

Table 5.3: Shows Total repeat, Total repeat ratio, Internal repeats, Internal repeat ratio of Forward repeat (TTAGG). The total repeats and internal repeats are high in chromosome 3R and low in chromosome 4. Average for total repeats, internal repeat, total repeat ratio and internal repeat ratio are 12773.32, 12734.6, 1691.7 and 1690.7.

Chromosomes	Size (In bp)	Total Repeat	Total Repeat Ratio	Internal Size (Total size-80,000)	Internal Repeats	Internal Repeat Ratio
2L	23513712	13315	1765.9	23433712	13257	1767.6
2R	25286936	14785	1710.3	25206936	14724	1711.9
3L	28110227	16677	1685.5	28030227	16629	1685.6
3R	32079331	18309	1752.1	31999331	18281	1750.4
4	1348131	989	1363.1	1268131	936	1354.8
X	23542271	12565	1873.6	23462271	12520	1873.9
Average		**12773.32**	**1691.7**		**12734.6**	**1690.7**

Neurospora:

Table 5.4: Shows Total repeat, Total repeat ratio, Internal repeats, Internal repeat ratio of Forward repeat (TTAGGG). The total repeats and internal repeats are high in chromosome 1 and low in chromosome 6. Average for total repeats, internal repeat, total repeat ratio and internal repeat ratio are 3246.2, 3236.8, 6118.6 and 6462.

Chromosomes	**Size (In bp)**	**Total Repeats**	**Total Repeat Ratio**	**Internal size (Total size-80,000)**	**Internal Repeats**	**Internal Repeat Ratio**
1	9798893	1692	5791.3079	9,718,893	1633	5,951.55
2	4478683	906	4943.3587	4,398,683	861	5,108.80
3	5274802	942	5599.5774	5,194,802	903	5,752.82
4	6000761	1045	5742.3550	5,920,761	1004	5,897.17
5	6436246	1080	5959.4870	6,356,246	1035	6,141.30
6	4218384	778	5422.0874	4,138,384	718	5763.76
7	4255303	920	4625.3293	4,175,303	866	4,821.36
Average		**1051.8**	**5440.500**		**1002.85**	**5633.82**

Trypanasoma brucei:

Table 5.5: Shows Total repeat, Total repeat ratio, Internal repeats, Internal repeat ratio of Forward repeat (TTAGGG). The total repeats and internal repeats are high in chromosome 11. The total repeats low in chromosome 1 and internal repeats are low in chromosome 2 and 3. Average for total repeats, internal repeat, total repeat ratio and internal repeat ratio are 3246.2, 3236.8, 6118.6 and 6462.

Chromosome	Size (in bp)	Total Repeat	Total Repeat Ratio	Internal Size (Total Size-80000)	Internal Repeats	Internal Repeat Ratio
1	739879	60	11210.3	859879	64	11560.60
2	895117	70	12787.4	815117	61	14674.04
3	1469848	70	20997.8	1389848	61	24095.86
4	1432056	135	10607.8	1352056	126	11365.52
5	1385737	168	8248.4	1305737	161	8607.06
6	1184041	150	7893.6	1104041	136	8706.18
7	2224448	272	8178.1	2144448	249	8933.52
8	2225824	266	8367.8	2145824	253	8797.72
9	2160261	256	8438.5	2080261	245	8817.39
10	3899268	469	8314.004	3819268	452	88626.69
11	4531609	525	86316	4451609	513	8833.54
Average		**222.4545**	**10334.11**		**211**	**11183.46**

Plasmodium falciparum:

Table 5.6: Shows Total repeat, Total repeat ratio, Internal repeats, Internal repeat ratio of Forward repeat (TTAGGG). The total repeats and internal repeats are high in chromosome 11. The total repeats low in chromosome 1 and internal repeats are low in chromosome 2 and 3. Average for total repeats, internal repeat, total repeat ratio and internal repeat ratio are 222.4545, 211, 10334.11 and 11183.46.

Chromosomes	Size (In bp)	Total Repeats	Total Repeat Ratio	Internal size (Total size-80,000)	Internal Repeats	Internal Repeat Ratio
1	739879	60	11210.3	859879	64	11560.60
2	895117	70	12787.4	815117	61	14674.04
3	1469848	70	20997.8	1389848	61	24095.86
4	1432056	135	10607.8	1352056	126	11365.52
5	1385737	168	8248.4	1305737	161	8607.06
6	1184041	150	7893.6	1104041	136	8706.18
7	2224448	272	8178.1	2144448	249	8933.52
8	2225824	266	8367.8	2145824	253	8797.72
9	2160261	256	8438.5	2080261	245	8817.39
10	3899268	469	8314.004	3819268	452	88626.69
11	4531609	525	86316	4451609	513	8833.54
Average		**222.4545**	**10334.11**		**211**	**11183.46**

Saccharomyces cerevisiae:

Table 5.7: Shows Total repeat, Total repeat ratio, Internal repeats, Internal repeat ratio of Forward repeat (TTAGGG). The total repeats and internal repeats are high in chromosome 4. The total repeats low in chromosome 3 and internal repeats are low in chromosome 1. Average for total repeats, internal repeat, total repeat ratio and internal repeat ratio are 92.3125, 80.9375, 8125.73 and 96135.

Chromosome	Size (in bp)	Total Repeats	Total Repeats ratio	Internal Size (Total Size-80000)	Internal Repeats	Internal Repeat ratio
1	230218	33	6976.30	150218	26	8,854.53
2	813184	90	9035.37	733184	80	10,164.8
3	316620	31	10213.54	236620	22	14,391.81
4	1531933	196	7815.98	1451933	190	8,062.80
5	576874	68	8483.44	496874	62	9,304.41
6	270161	40	6754.025	190161	27	10,005.96
7	1090940	125	8727.52	1010940	114	9,569.64
8	562643	78	7213.37	482643	66	8,524.89
9	439888	60	7331.46	359888	51	8,625.25
10	745751	95	7850.01	665751	76	9,812.519
11	666816	87	7664.55	586816	74	9,011.02
12	1078177	127	8489.58	998177	112	9,626.58
13	924431	114	8109.04	844431	101	9,152.78
14	784333	104	7541.66	704333	93	8,433.68
15	1091291	115	9489.48	1011291	102	10,698.93
16	948066	114	8316.36	868066	99	9,576.42
Average		**92.3125**	**8125.73**		**80.9375**	**9613.5**

Honeybee:

Chromosomes	Size (In bp)	Total Repeat	Total Repeat Ratio	Internal Size (Total size-80,000)	Internal Repeats	Internal Repeat Ratio
1	27754200	1544	17,975.51	2,76,74,200	1536	18,017.05
2	16089512	980	16,417.86	1,60,09,512	976	16,403.18
3	13619445	839	16,232.94	1,35,39,445	828	16,351.98
4	13404451	731	18,337.14	1,33,24,451	718	18,557.73
5	13896941	805	17,263.28	1,38,16,941	802	17,228.10
6	17789102	1027	17,321.42	1,77,09,102	1019	17,378.90
7	14198698	678	20,942.03	1,41,18,698	677	20,854.79
8	12717210	859	14,804.66	1,26,37,210	854	14,797.66
9	12354651	717	17,231.03	1,22,74,651	713	17,215.49
10	12360052	704	17,556.89	1,22,80,052	673	18,246.73
11	16352600	821	19,917.90	1,62,72,600	817	19,917.50
12	11514234	704	16,355.44	1,14,34,234	684	16,716.71
13	11279722	729	15,472.86	1,11,99,722	724	15,469.22
14	10670842	655	16,291.36	1,05,90,842	653	16,218.74
15	9534514	529	18,023.65	94,54,514	515	18,358.27
16	7238532	384	18,850.34	71,58,532	365	19,612.41
Average		**794.125**	**17,437.14**		**784.625**	**17584.03**

Table 5.8: Shows Total repeat, Total repeat ratio, Internal repeats, Internal repeat ratio of Forward repeat (TTAGG). The total repeats and internal repeats are high in chromosome 1 and low in chromosome 16. Average for total repeats, internal repeat, total repeat ratio and internal repeat ratio are 794.125, 784.625, 17437.14, 17584.03.

Xenopus (Frog):

Table 5.9: Shows Total repeat, Total repeat ratio, Internal repeats, Internal repeat ratio of Forward repeat (TTAGGG). The total repeats and internal repeats are high in chromosome 1. The total repeats low in chromosome 13 and internal repeats low in chromosome 14. Average for total repeats, internal repeat, total repeat ratio and internal repeat ratio are 38608, 36560.5, 3727.59, 3777.41.

Chromosomes	Size (In bp)	Total Repeats	Total Repeat Ratio	Internal Size (Total size-80,000)	Internal Repeats	Internal Repeat Ratio
1	219802468	57589	3816.74	219,722,468	57567	3,816.81
2	179946965	47524	3786.44	179,866,965	47502	3,786.51
3	181146889	48580	3728.83	181,066,889	48568	3,728.11
4	159726490	42846	3727.92	159,646,490	42549	3,752.06
5	144167370	37336	3861.35	144,087,370	37314	3,861.48
6	120483113	31942	3771.93	120,403,113	31927	3771.20
7	144084680	40544	3553.78	144,004,680	40520	3,553.91
8	121245977	33625	3605.82	121,165,977	33598	3,606.34
9	159361991	43852	3634.08	159,281,991	43827	3,634.33
10	136570856	42506	3212.97	136,490,856	36755	3,713.53
11	155008753	36506	4246.11	154,928,753	42497	3,645.63
12	128359586	35754	3590.07	128,279,586	35737	3,589.54
13	126821045	25609	4952.20	126,741,045	25593	4,952.17
14	89646544	35409	2531.74	89,566,544	24196	3,701.70
15	120101378	31964	3757.39	120,021,378	31953	3,756.18

16	98932710	27672	3582.96	98,852,710	27643	3576.04
17	117834370	29614	3979.00	117834370	29597	3,981.29
18	104563341	33561	3757.39	104,483,341	29294	3,566.71
Average		**38,608**	**3727.59**		**36560.5**	**3777.41**

Cat:

Table 5.10: Shows Total repeat, Total repeat ratio, Internal repeats, Internal repeat ratio of Forward repeat (TTAGGG). The total repeats and internal repeats are high in chromosome 8. The total repeats and internal repeats are low in chromosome 16. Average for total repeats, internal repeat, total repeat ratio and internal repeat ratio are 24400.26, 24041.526, 5260.75, 5339.774.

Chromosomes	Size (In bp)	Total Repeat	Total Repeat Ratio	Internal Size (Total size-80,000)	Internal Repeats	Internal Repeat Ratio
1	242100913	32701	7,403.47	242,020,913	32628	7,420.03
2	171471747	32701	5,243.62	171,391,747	28271	6,065.28
3	143202405	28344	5,052.30	143,122,405	28205	5,077.19
4	208212889	40130	5,188.45	208,052,889	40103	5,191.95
5	155302638	29944	5,186.43	155,222,638	29873	5,198.76
6	149751809	29708	5,040.79	149,671,809	29694	5,043.16
7	144528695	28019	5,158.23	144,448,695	27960	5,169.12
8	222790142	43296	5,145.74	222,710,142	43212	5,155.74
9	161193150	31133	5,177.56	161,113,150	30848	5,225.40
10	117648028	23017	5,111.35	117,568,028	22934	5,129.85
11	90186660	17803	5,065.81	90,106,660	17444	5,170.067
12	96884206	18566	5,218.36	96,804,206	18510	5,234.15
13	96521652	19511	4,947.03	96,441,652	19291	5,003.45

14	63494689	12354	5,139.60	63,414,689	12317	5,155.04
15	64340295	13485	4,771.24	64,260,295	13135	4,898.38
16	44648284	8420	5,302.64	44,568,284	8270	5,398.82
17	71664243	13782	5,199.84	71,584,243	13663	5,245.132
18	85752456	16416	5,223.71	85,672,456	16270	5,270.58
X	130557009	24275	5,378.24	130,477,009	24161	5,403.62
Average		**24400.26**	**5260.75**		**24041.526**	**5339.774**

Panda:

Table 5.11: Shows Total repeat, Total repeat ratio, Internal repeats, Internal repeat ratio of Forward repeat (TTAGGG). The total repeats and internal repeats are high in chromosome 1. The total repeats and internal repeats are low in chromosome 20. Average for total repeats, internal repeat, total repeat ratio and internal repeat ratio are 22376, 22355.76, 4872.19, 4873.26.

Chromosomes	**Size (In bp)**	**Total Repeat**	**Total Repeat Ratio**	**Internal Size (Total size-80,000)**	**Internal Repeats**	**Internal Repeat Ratio**
1	212770937	43151	4930.85	212690937	43139	4930.36
2	199809881	41309	4836.96	199729881	41297	4836.43
3	147627920	30198	4888.67	147547920	30180	4888.93
4	144794249	29969	4831.47	144714249	29948	4832.184
5	130990914	27427	4775.98	130910914	27418	4774.63
6	131587389	27053	4864.06	131507389	27026	4865.96
7	141533052	28509	4964.504	141453052	28483	4966.23
8	129245720	27043	4779.27	129165720	27025	4779.49
9	103688518	21099	4914.38	103608518	21069	4917.58

10	110580333	22622	4888.18	110500333	22605	4888.313
11	110513224	22133	4993.14	110433224	22114	4993.81
12	81781225	16883	4843.99	81701225	16863	4844.99
13	92459488	19079	4846.14	92379488	19055	4848.044
14	106650358	21919	4865.66	106570358	21880	4870.67
15	91612352	18656	4910.61	91532352	18641	4910.27
16	91341929	18867	4841.36	91261929	18843	4843.28
17	42246006	8533	4950.897	42166006	8519	4949.642
18	38124791	7789	4894.696	38044791	7776	4892.59
19	35683536	7239	4929.35	35603536	7216	4933.97
20	30944335	6343	4878.501	30864335	6321	4882.824
X	112850221	24075	4687.44	112770221	24053	4688.406
Average		**22376**	**4872.1956**		**22355.76**	**4873.268**

Dolphin:

Table 5.12: Shows Total repeat, Total repeat ratio, Internal repeats, Internal repeat ratio of Forward repeat (TTAGGG). The total repeats and internal repeats are high in chromosome 1. The total repeats and internal repeats are low in chromosome 21. Average for total repeats, internal repeat, total repeat ratio and internal repeat ratio are 26014.909, 26002.5, 4093.252, 4091.835.

Chromosomes	**Size (In bp)**	**Total Repeat**	**Total Repeat Ratio**	**Internal Size (Total size-80,000)**	**Internal Repeats**	**Internal Repeat Ratio**
1	183742880	38296	4797.97	183662880	38122	4817.77
2	176472748	37851	4662.30	176392748	37712	4677.36
3	171421769	34189	5013.95	171341769	34175	5013.66
4	144183200	28593	5042.6	144103200	28477	5060.34
5	137487549	28066	4898.722	137407549	28053	4898.14

6	115599616	23990	4818.66	115519616	23405	4935.68
7	114015307	24927	4573.97	113935307	22586	5044.51
8	108430135	23014	4711.49	108350135	23009	4709.032
9	105335178	22711	4638.07	105255178	21718	4846.45
10	102812509	20327	5057.93	102732509	20277	5066.46
11	102167733	19957	5119.39	102087733	19912	5126.95
12	89330967	18360	4865.52	89250967	17701	5042.14
13	88485069	17565	5037.58	88405069	17550	5037.33
14	88483154	19612	4511.68	88403154	19020	4647.91
15	86293990	17220	5011.27	86213990	17212	5008.95
16	83508544	18042	4628.56	83428544	18028	4627.72
17	78442772	19442	4034.707	78362772	17914	4374.39
18	78151963	14277	5473.98	78071963	14274	5469.52
19	58636127	14277	4107.03	58556127	12606	4645.099
20	58467291	12678	4611.71	58387291	11772	4959.84
21	35682248	7634	4674.122	35602248	7624	4669.76
X	128693445	24340	5287.32	128613445	24336	5284.9
Average		**22062.1818**	**4799.024**		**21612.86**	**4907.45**

Rabbit:

Table 5.13: Shows Total repeat, Total repeat ratio, Internal repeats, Internal repeat ratio of Forward repeat (TTAGGG). The total repeats and internal repeats are high in chromosome 1. The total repeats and internal repeats are low in chromosome 21. Average for total repeats, internal repeat, total repeat ratio and internal repeat ratio are 17750.4, 17740.64, 5864.5, 5862.1.

Chromosomes	**Size (In bp)**	**Total Repeat**	**Total Repeat Ratio**	**Internal Size (Total size-80,000)**	**Internal Repeats**	**Internal Repeat Ratio**
1	194850757	34523	5644.0	194770759	34518	5642.5
2	174332312	31067	5611.4	174252312	31053	5611.4
3	155691105	27476	5666.4	155611105	27466	5665.5
4	91394100	15840	5769.8	91314100	15828	5770.9
5	37992211	6437	5902.1	37912211	6416	5909.0
6	27502587	4417	6226.5	27422587	4403	6228.1
7	173684459	30523	5690.2	173604459	30513	5689.5
8	111795807	19050	5868.5	111715807	19042	5866.8
9	116251907	20265	5736.5	116171907	20256	5735.1
10	47997241	7956	6032.8	47917241	7950	6027.3
11	87554214	15122	5789.8	87474214	15115	5787.2
12	155355395	27210	5709.4	155275395	27204	5707.8
13	143360832	24782	5784.8	143280832	24772	5783.9
14	163896628	28630	5724.6	163816628	28614	5725.0
15	109054052	18790	5803.8	108974052	18786	5800.8
16	84478945	14779	5716.1	84398945	14767	5715.3
17	85008467	15029	5656.2	84928467	15020	5654.3
18	69800736	11857	5886.8	69720736	11852	5882.6
19	57279966	9649	5936.3	57199966	9644	5931.1
20	33191332	5341	6214.4	33111332	5334	607.5
21	15578276	2249	6926.7	15498276	2246	6900.3
X	111700115	19517	5723.2	111620775	19495	5725.6
Average		**17750.4**	**5864.5**		**17740.64**	**5862.1**

Whale:

Table 5.14: Shows Total repeat, Total repeat ratio, Internal repeats, Internal repeat ratio of Forward repeat (TTAGGG). The total repeats and internal repeats are high in chromosome 1. The total repeats and internal repeats are low in chromosome Y. Average for total repeats, internal repeat, total repeat ratio and internal repeat ratio are 24400.26, 24041.526, 5260.75, 5339.774.

Chromosomes	Size (In bp)	Total Repeat	Total Repeat Ratio	Internal Size (Total size-80,000)	Internal Repeats	Internal Repeat Ratio
1	184938300	36699	5039.3	184858300	36687	5038.7
2	175897734	35030	5021.3	175817734	35019	5020.6
3	171266408	33750	5074.5	171186408	33734	5074.5
4	144968589	28307	5121.2	144888589	28286	5122.2
5	140689829	26848	5240.2	140609829	26824	5241.9
6	116510015	22585	5158.7	116430015	22557	5161.5
7	113414938	22231	5101.6	113334938	22217	510.2
8	110314666	21982	5018.4	110234666	21959	5020.0
9	107421550	20772	5171.4	107341550	20760	5170.5
10	104744437	20484	5113.4	104664437	20464	5114.5
11	104068540	20528	5069.5	103988540	20503	5071.8
12	91445419	17494	5227.2	91365419	17482	5226.2
13	90635089	17893	5065.1	90555089	17874	5066.3
14	90457838	17598	5140.2	90377838	17582	5140.3
15	88470553	18103	4887.0	88390553	18090	4886.1
16	86152963	16966	5077.9	86072963	16950	5078.0
17	81207215	15680	5179.0	81127215	15656	5181.8
18	79663398	15105	5273.9	79583398	15095	5272.1
19	60735208	11908	5100.3	60655208	11895	5099.2
20	60304989	11792	5114.0	60224989	11762	5120.3
21	36241783	7000	5177.3	36161783	6985	5177.0

X	128877148	22747	5665.6	128797148	22714	5670.3
Y	2349494	339	6930.6	2269494	319	7114.4
Average		**20080**	**5215.9**		**20061.4**	**5224.7**

Human:

Table 5.5: Shows Total repeat, Total repeat ratio, Internal repeats, Internal repeat ratio of Forward repeat (TTAGGG). The total repeats and internal repeats are high in chromosome 1. The total repeats and internal repeats are low in chromosome Y. Average for total repeats, internal repeat, total repeat ratio and internal repeat ratio are 22596.541, 22564.21, 6088.79, 6134.934.

Chromosomes	Size (In bp)	Total Repeat	Total Repeat Ratio	Internal Size (Total size-80,000)	Internal Repeats	Internal Repeat Ratio
1	249250621	43299	5749.79	249170621	43180	5770.51
2	243199373	45535	5318.77	243119373	45520	5340.94
3	198022430	37576	5277.30	197942430	37576	5267.79
4	191154276	35439	5367.53	191074276	35429	5393.16
5	180915260	34457	5268.59	180835260	34441	5250.58
6	171115067	32045	5330.32	171035067	32045	5337.34
7	159138663	28758	5541.07	159058663	28727	5536.904
8	146364022	27161	5343.69	146284022	27150	5387.99
9	141213431	22749	6083.78	141133431	22742	6205.85
10	135534747	24812	5302.55	135454747	24759	5470.93
11	135006516	25360	5326.89	134926516	25360	5320.44
12	133851895	24726	5390.28	133771895	24642	5428.61
13	115169878	17806	6422.55	115089878	17806	6362.54
14	107349540	16964	6309.83	107269540	16964	6323.36
15	102531392	15622	6528.61	102451392	15563	6583.01
16	90354753	14211	6357.05	90274753	14211	6352.46
17	81195210	13993	5950.12	81115210	13951	5814.29

18	78077248	14301	5619.89	77997248	14296	5455.88
19	59128983	8936	6559.99	59048983	8893	6639.94
20	63025520	11452	5626.96	62945520	11452	5496.47
21	48129895	6496	7190.58	48049895	6468	7428.86
22	51304566	6007	8460.13	51224566	6007	8527.48
X	155270560	29135	5355.75	155190560	29014	5348.82
Y	59373566	5477	10449.15	59293566	5345	11093.28
Average		**22596.541**	**6088.79**		**22564.21**	**6134.934**

Tortoise:

Table 5.16: Shows Total repeat, Total repeat ratio, Internal repeats, Internal repeat ratio of Forward repeat (TTAGGG). The total repeats and internal repeats are high in chromosome 1. The total repeats low in chromosome 21and internal repeats are low in chromosome 24. Average for total repeats, internal repeat, total repeat ratio and internal repeat ratio are 22742.3, 20863, 4337.7, 4370.1.

Chromosomes	**Size (In bp)**	**Total Repeat**	**Total Repeat Ratio**	**Internal Size (Total size-80,000)**	**Internal Repeats**	**Internal Repeat Ratio**
1	370335144	84130	4401.93	370295144	84117	4402.14
2	299447175	61411	4442.11	299367175	67411	4440.92
3	225143049	53459	4211.50	225063049	53450	4210.72
4	155918640	38599	4039.44	155838640	38589	4038.42
5	147425149	33700	4374.63	147345149	5587	4373.94
6	137797752	31922	4316.70	137717758	51624	4356.22
7	131611970	35659	3690.84	131531970	35411	3714.43
8	113972862	28321	4024.32	113892862	28301	4024.34
9	108927930	65447	4380.58	108847930	25428	4280.63
10	86493507	19237	4496.20	86413507	19215	4497.19
11	81157593	18500	4386.89	81077593	18488	4385.41
12	44291995	10150	4363.74	44211995	10121	4368.34
13	34052379	7707	4418.37	33972379	7691	4417.16
14	34023795	7555	4503.48	33943795	7540	4501.82
15	30016314	7050	4257.63	29936314	7035	4255.33
16	26755340	6460	4141.69	26675340	6083	4385.22
17	24966275	5553	4495.99	24886275	5532	4498.60

18	23166772	5871	3955.96	23086772	5662	4077.49
19	22456854	5564	4036.09	22376854	5055	4423.67
20	19814879	5254	3771.37	19734809	5202	3793.69
21	18349496	3162	5803.12	18269496	3140	5818.31
22	17272096	3936	4388.23	17192090	3922	4383.50
23	15774734	3510	4494.22	15694734	3485	4503.51
24	12531862	3660	4711.22	12451862	2631	4732.74
Average		**22742.3**	**4337.7**		**20863**	**4370.1**

Parrot:

Table 5.17: Shows Total repeat, Total repeat ratio, Internal repeats, Internal repeat ratio of Forward repeat (TTAGGG). The total repeats and internal repeats are high in chromosome 1. The total repeats and internal repeats are low in chromosome 23. Average for total repeats, internal repeat, total repeat ratio and internal repeat ratio are 7785, 7651.24, 5849.31, 6091.68.

Chromosomes	**Size (In bp)**	**Total Repeat**	**Total Repeat Ratio**	**Internal Size (Total size-80,000)**	**Internal Repeats**	**Internal Repeat Ratio**
1	155644563	28283	5,503.11	155,564,563	28271	5,503.11
2	123023803	21663	5,678.98	122,943,803	21651	5,678.98
3	89082643	15429	5,773.71	89,002,643	15416	5,773.71
4	86460390	15065	5,739.15	86,380,390	14855	5,739.15
5	83240647	14501	5,740.33	83,160,647	12880	5,740.33
6	76431904	12902	5,924.03	76,351,904	12886	5,924.03
7	70131234	12070	5,810.37	70,051,234	12020	5,810.37
8	63488934	10907	5,820.93	63,408,934	10878	5,820.93
9	44431488	7279	6,104.06	44,351,488	7212	6,104.06
10	43764472	7433	5,887.86	43,684,472	7406	5,887.86
11	39187110	6419	6,104.86	39,107,110	6286	6,104.86
12	27433492	5035	5,448.55	27,353,484	4824	5,448.55
13	16476160	2595	6,349.19	16,396,160	2581	6,349.19
14	12884122	2091	6,161.70	12,804,122	2071	6,161.70
15	12307978	2024	6,081.01	12,227,978	2012	6,081.01
16	8419051	1457	5,778.34	8,339,051	1442	5,778.34

17	7441144	1491	4,990.70	7,361,144	1485	4,990.70
18	6734548	1033	6,519.40	6,654,548	1022	6,519.40
19	5789228	902	6,418.21	5,709,228	887	6,418.21
20	5645757	807	6,995.98	5,565,757	785	6,995.98
21	5492648	1280	4,291.13	5,412,648	994	4,291.13
22	2907026	1030	2,822.35	2,827,026	520	2,822.35
23	2785283	370	7,527.79	2,705,283	363	7,527.79
W	37425726	5517	6,783.70	37,345,726	5505	6,783.70
Z	101869369	17042	5,977.54	101,789,369	17042	101,789,369
Average		**7785**	**5849.31**		**7651.24**	**6091.68**

Zebra fish:

Table 5.18: Shows Total repeat, Total repeat ratio, Internal repeats, Internal repeat ratio of Forward repeat (TTAGGG). The total repeats and internal repeats are high in chromosome 1. The total repeats and internal repeats are low in chromosome 25. Average for total repeats, internal repeat, total repeat ratio and internal repeat ratio are 9915.6, 9885.5, 5419.2, 5428.7.

Chromosomes	Size (In bp)	Total Repeat	Total Repeat Ratio	Internal Size (Total size-80,000)	Internal Repeats	Internal Repeat Ratio
1	59578282	10615	5612.3	59498282	10501	5665.9
2	59640629	11406	5228.8	59560629	11386	5231.0
3	62628489	11713	5346.9	62548489	11671	5359.3
4	78093715	12248	6376.0	78013715	12243	6372.1
5	72500376	13149	5513.7	72420376	13131	5515.2
6	60270059	11129	5415.5	60190059	11091	5426.9
7	74282399	14114	5263.0	74202399	14088	5267.0
8	54304671	10101	5376.1	54224671	10096	5370.3
9	56459846	10622	5315.3	56379846	10612	5312.8
10	45420867	8273	5490.2	45340867	8250	5495.8
11	45484837	8408	5409.7	45404837	8369	5424.3

12	49182954	9123	5391.0	49102954	9114	5387.6
13	52186027	9963	5237.9	52106027	9954	5234.6
14	52660232	9534	5523.4	52580232	9520	5523.1
15	48040578	8972	5354.5	47960578	8861	5412.5
16	55266484	10108	5467.5	55186484	10096	5466.1
17	53461100	10052	5318.4	53381100	10033	5320.5
18	51023478	9582	5324.9	50943478	9573	5321.5
19	48449771	8850	5474.5	48369771	8844	5469.2
20	55201332	10334	5341.7	55121332	10317	5342.7
21	45934066	8653	5308.4	45854066	8639	5307.7
22	39133080	7458	5247.1	39053080	7452	5240.6
23	46223584	9006	5132.5	46143584	8975	5141.3
24	42172926	7703	5474.8	42092926	7653	5500.1
25	37502051	6776	5534.5	37422051	6669	5611.3
Average		**9915.6**	**5419.2**		**9885.5**	**5428.7**

Silkworm:

Table 5.19: Shows Total repeat, Total repeat ratio, Internal repeats, Internal repeat ratio of Forward repeat (TTAGG). The total repeats and internal repeats are high in chromosome 23. The total repeats and internal repeats are low in chromosome 28. Average for total repeats, internal repeat, total repeat ratio and internal repeat ratio are 12886.7, 12378.28, 1238.2, 1275.9.

Chromosomes	**Size (In bp)**	**Total Repeat**	**Total Repeat Ratio**	**Internal Size (Total size-80,000)**	**Internal Repeats**	**Internal Repeat Ratio**
1	20666287	15976	1293.5	20586287	15962	1289.7
2	8396445	7370	1139.27	8396445	6314	1298.1
3	15212953	13101	1161.2	15132953	12040	1256.8
4	18737234	14748	1270.4	18657234	14738	1265.9
5	19061979	15399	1237.8	18981979	14745	1287.3
6	16650604	12937	1287.0	16570604	12850	1289.5
7	13944894	10949	1273.6	13864894	10928	1268.4

8	16262221	12688	1281.7	16182221	12594	1284.9
9	16796068	12856	1306.4	16716068	12796	1306.3
10	17614771	15706	1121.5	17534771	13667	1283.0
11	20440007	15633	1307.4	20360007	15581	1306.7
12	17580608	13789	1274.97	17500608	13746	1273.1
13	17735081	13708	1293.77	17655081	13544	1303.5
14	13345518	10434	1279.0	13265518	10386	1277.2
15	18440292	14493	1272.3	18360292	14418	1273.4
16	14337292	11344	1262.4	14257292	11158	1277.7
17	16840672	13348	1261.6	16760672	13029	1286.4
18	15699053	18498	848.6	15619053	12662	1233.5
19	14801489	11586	1277.3	14721489	11343	1297.8
20	12370531	9814	1260.4	12290531	9737	1262.2
21	15310392	12663	1209.0	15230392	11935	1276.1
22	18482526	14612	1264.8	18402526	14413	1276.8
23	21465692	16819	1276.2	21385692	16770	1275.2
24	17359173	14132	1228.3	17279173	13846	1247.9
25	14548897	11842	1228.5	14468897	11314	1278.8
26	11473476	9227	1243.46	11393476	9021	1262.9
27	10930128	8579	1274.0	10850128	8522	1273.1
28	10609739	8578	1236.85	10529739	8533	1234.0
Average		**12886.7**	**1238.2**		**12378.28**	**1,275.90**

Cow:

Table 5.20: Shows Total repeat, Total repeat ratio, Internal repeats, Internal repeat ratio of Forward repeat (TTAGGG). The total repeats and internal repeats are high in chromosome 1. The total repeats and internal repeats are low in chromosome 25. Average for total repeats, internal repeat, total repeat ratio and internal repeat ratio are15103, 28627.67, 5797.97, 7630.92.

Chromosomes	Size (In bp)	Total Repeat	Total Repeat Ratio	Internal Size (Total size-80,000)	Internal Repeats	Internal Repeat Ratio
1	158534110	25938	6112.04	158454110	25935	6109.66

2	136231102	22543	6043.16	136151102	22539	6040.68
3	121005158	20970	5770.39	120925158	20957	5770.15
4	120000601	20131	5930.98	119920601	20110	5963.23
5	120089316	21237	5654.72	120009316	20134	5960.53
6	117806340	19186	6140.22	117726340	18884	6234.18
7	110682743	19042	5812.55	110602743	19030	5812.02
8	113319770	19962	5676.77	1133239770	19956	5678.91
9	105454467	17424	6052.25	105454467	17397	6061.64
10	103308737	19610	5268.161	103228737	18796	5492.05
11	106982474	18017	5967.86	106902474	17996	5940.34
12	87216183	13951	6251.6	87136183	13940	6250.8
13	83472345	15436	5407.64	83392345	14650	5692.31
14	82403003	14788	5572.28	82323003	14774	5572.15
15	85007780	14710	5778.91	84927780	14701	5777
16	81013979	15358	5275.03	80933979	10424	7764.19
17	73167244	12704	5759.38	73087244	12116	6032.29
18	65820629	12073	5451.88	65740629	11780	5880.69
19	63449741	11286	5621.6	63369741	11277	5619.37
20	71974595	11666	6169.6	71894595	11656	6168.03
21	69862954	11919	5861.47	69862954	11904	5868.86
22	60773935	10586	5740.88	60693035	10569	5742.55
23	52498615	9156	5733.79	52418615	9139	5735.7
24	62317253	10399	5992.67	62237253	10385	5992.99
25	42350435	7294	5806.2	42270435	7281	5805.58
26	51992305	8908	5836.58	51912305	8901	5832.18
27	45612108	7804	5844.79	45532108	7743	5880.42
28	45940150	7896	5818.15	45860150	7883	5817.6
29	51098607	8698	5874.75	51018607	8673	5882.46
30	139009144	24405	5742.99	138929144	24199	5741.11
Average		**15103**	**5797.97**		**28627.67**	**7630.92**

Butterfly:

Table 5.21: Shows Total repeat, Total repeat ratio, Internal repeats, Internal repeat ratio of Forward repeat (TTAGG). The total repeats and internal repeats are high in chromosome 1. The

total repeats are low in chromosome 27 and internal repeats is low in chromosome 30. Average for total repeats, internal repeat, total repeat ratio and internal repeat ratio are 1220.3, 1219, 9785.5, 10041.6.

Chromosomes	Size (In bp)	Total Repeat	Total Repeat Ratio	Internal Size (Total size-80,000)	Internal Repeats	Internal Repeat Ratio
1	15533955	1442	10772.50	15453955	1498	10316.39
2	14849406	1392	10667.67	14769406	1389	10633.12
3	14762480	1402	10529.58	14722480	1398	10531.10
4	14727120	1491	9877.34	14647120	1486	9856.74
5	14640259	1394	10542.33	14560259	1385	10512.82
6	14637429	1432	10221.66	14557429	1426	10208.57
7	14559244	1436	10138.74	14479244	1428	10139.52
8	14198653	1350	10517.52	14118653	1342	10520.60
9	13920324	1376	10116.51	13840324	1370	10102.42
10	13780858	1378	10000.62	13700851	1370	10000.62
11	13511320	1300	10393.32	13431320	1298	10347.70
12	13368958	1283	10420.07	13288958	1277	10406.38
13	13340570	1230	1084.99	13260570	1221	10860.41
14	1331544	1241	10729.60	13235441	1237	10699.62
15	13087440	1239	10560.48	13007440	1230	10575.15
16	12944774	1231	10515.65	12864774	1221	10536.26
17	12249620	1234	9926.75	12169620	1227	9918.19
18	11867531	1137	10437.58	11787531	1123	10496.46
19	11734116	1145	10248.13	11654116	1143	10196.07
20	11121304	1102	10110.27	11041304	1097	10064.99
21	10603326	1007	10527.61	10523326	996	10565.58
22	13050283	1058	9782.87	10270283	1054	9744.10
23	10170685	1032	9855.31	10090685	1026	9834.97
24	10082432	1004	10042.26	10002432	1000	10002.43
25	9897174	964	10266.77	9817174	960	10226.22
26	9706448	949	10228.08	9626448	963	9996.31
27	8713913	911	9565.21	8633913	989	8729.94
28	8622819	979	8807.78	8542819	966	8843.49
29	8552921	1004	8518.84	8472921	989	8567.15
30	7426551	935	7942.83	7346551	932	7882.56
Z	17545335	1754	10003.04	17465335	1751	9974.49
Average		**1220.3**	**9785.5**		**1219**	**10041.6**

Zebra finch:

Table 5.22: Shows Total repeat, Total repeat ratio, Internal repeats, Internal repeat ratio of Forward repeat (TTAGGG). The total repeats and internal repeats are high in chromosome 2. The total repeats and internal repeats are low in chromosome 29. Average for total repeats, internal repeat, total repeat ratio and internal repeat ratio are 5680.31, 5620.46, 5496.35, 5581.4.

Chromosomes	Size (In bp)	Total Repeat	Total Repeat Ratio	Internal Size (Total size-80,000)	Internal Repeats	Internal Repeat Ratio
1	114375790	19858	12358	114,295,790	19847	5,758.84
1A	70879221	12545	5,649.9	70,799,221	12532	5,649.47
2	151896526	25737	5,901.87	151,816,526	25731	5,900.14
3	111449612	18926	5,888.70	111,369,612	18911	5,889.14
4	71343966	12118	5,887.43	71,263,966	12105	5,887.15
4A	19376786	3408	5,685.67	19,296,786	3394	5,685.55
5	61898265	10636	5,819.69	61,818,265	10623	5,819.28
6	34836644	6316	5515.61	34,756,644	6264	5,548.63
7	38159610	6754	5,649.92	38,079,610	6729	5,659.02
8	30964699	5519	5,610.56	30,884,699	5519	5,596.06
9	25566760	4300	5,945.75	25,486,760	4300	5,927.15
10	20434694	3789	5,393.16	20,354,694	3789	5,372.04
11	21061567	3704	5,686.16	20,981,567	3704	5,664.56
12	20382777	3603	5657.16	20,302,777	3603	5,634.96
13	18433556	3186	5,785.79	18,353,556	3186	5,760.68
14	16445707	2756	5967.23	16,365,707	2756	5,938.21
15	13709395	2333	5,876.29	13,629,395	2333	5,842.00
17	11203372	2002	5,596.08	11,123,372	2002	5,556.12
18	11222577	3408	3,293.00	11,142,577	1965	5,670.52
19	10986837	2034	5,401.59	10,906,837	2022	5,394.08
20	15002346	2720	5515.56	14,922,346	2620	5,695.55
21	7641456	1546	4,942.72	7,561,456	1529	4,945.36
22	4625764	919	5,033.47	4,545,764	910	4,995.34
23	6774791	1227	5,521.42	6,694,791	1209	5,537.46
24	7443780	1541	4,830.48	7,363,780	1516	4,857.37
25	2793977	561	4,980.35	2,713,977	546	4,970.65

26	6843016	1256	5,448.26	6,763,016	1237	5,467.27
27	5448099	1035	5,263.86	5,368,099	1014	5,293.98
28	5729701	985	5,816.95	5,649,701	962	5,872.87
29	1126259	204	5520.87	1,046,259	181	5,780.43
W	20846394	4486	4,646.98	20,766,394	4473	4,642.60
Z	78982076	12358	6,391.16	78,902,076	12343	6,392.45
Average		**5680.31**	**5496.35**		**5620.46**	**5581.40**

Shark:

Table 5.23: Shows Total repeat, Total repeat ratio, Internal repeats, Internal repeat ratio of Forward repeat (TTAGGG). The total repeats and internal repeats are high in chromosome 1. The total repeats and internal repeats are low in chromosome 31. Average for total repeats, internal repeat, total repeat ratio and internal repeat ratio are 23563.065, 22587.83, 5794.207, 5819.48.

Chromosomes	Size (In bp)	Total Repeat	Total Repeat Ratio	Internal Size (Total size-80,000)	Internal Repeats	Internal Repeat Ratio
1	313568160	313488160	53731	5835.89	53702	5837.55
2	289498315	289418315	50137	5774.14	49849	5805.90
3	277254249	277174249	49137	5642.47	48898	5668.416
4	244324502	244244502	41237	5924.89	41046	5950.507
5	233859027	233779027	40474	5778.006	40069	5834.41
6	225974235	225894235	38714	5837.016	38709	5835.703
7	211474833	211594833	35641	5939.08	35562	5950.03
8	199962141	199882141	35688	5603.06	34562	5783.29
9	198790641	198710641	34387	5780.98	34271	5798.22
10	191882600	191802600	33518	5724.76	33472	5730.24
11	169802008	169722008	29709	5715.507	29696	5715.32
12	165189515	165109515	28136	5871.11	27930	5911.55
13	163470629	163390629	27885	5862.31	27879	5860.71
14	160845508	160765508	27432	5863.43	27421	5862.86
15	147036345	146956345	25483	5769.98	25432	5778.403

16	144966053	144886053	25099	5775.71	25080	5776.96
17	133841611	133761611	21357	6266.87	21349	6265.47
18	131918509	131838509	17977	7338.18	17969	7336.998
19	106706591	106626591	17977	5935.73	17961	5936.56
20	98274498	98194498	16855	5830.58	16846	5828.95
21	71046048	70966048	12543	5664.199	12508	5673.65
22	30786469	30706469	5366	5737.32	5351	5738.45
23	27685257	27605257	5337	5187.42	5325	5184.09
24	27315460	27235460	5069	5388.73	5056	5386.76
25	26010896	25930896	4361	5964.43	4342	5972.11
26	24906204	24826204	4325	5758.66	4317	5750.8
27	24353605	24273605	4502	5409.508	4476	5423.06
28	20090439	20010439	3412	5888.17	3399	5887.15
29	16133577	16053577	2976	5421.23	2972	5401.61
30	15593260	15513260	2852	5467.48	2651	5851.85
31	12109206	12029206	2138	5663.800	2123	5666.14
Average			**23563.065**	**5794.207**	**22587.83**	**5819.48**

Horse:

Table 5.24: Shows Total repeat, Total repeat ratio, Internal repeats, Internal repeat ratio of Forward repeat (TTAGGG). The total repeats and internal repeats are high in chromosome 1. The total repeats and internal repeats are low in chromosome 31. Average for total repeats, internal repeat, total repeat ratio and internal repeat ratio are 15214.625, 15063.40, 4979.34, 5031.84.

Chromosomes	**Size (In bp)**	**Total Repeat**	**Total Repeat Ratio**	**Internal Size (Total size-80,000)**	**Internal Repeats**	**Internal Repeat Ratio**
1	188260577	38418	4,900.32	188,180,577	38388	4,904.15
2	121350024	24141	5,026.71	121,270,024	24116	5,031.93
3	121351753	24070	5,041.61	121,271,673	24036	5,048.74
4	109462549	21914	4,995.09	109,382,549	21850	5,009.72
5	96759418	20081	4,818.45	96,679,418	20003	4,837.24
6	87230776	17936	4,863.44	87230776	17477	4,991.17
7	100787686	21301	4,731.59	100787686	20288	4,967.84
8	97563019	19561	4,987.62	96,679,418	19491	5,005.54

9	85793548	17006	5,044.89	87,150,776	16974	5,054.40
10	85155674	17005	5,007.68	85,075,674	16918	5,033.43
11	61676917	12808	4,815.49	61,596,917	12727	4,846.14
12	36992759	7180	5,152.19	36,912,759	6880	5,376.85
13	43784481	8574	5,106.65	43,704,481	8517	5,140.83
14	94600235	19095	4,954.18	94,520,235	19043	4,967.71
15	92851403	19133	4,852.94	92,771,403	19117	4,857.00
16	88962352	18120	4,909.62	88,882,352	18027	4,934.95
17	80722430	15879	5,083.59	80,642,430	15849	5,093.21
18	82641348	17370	4,757.70	82,561,348	16442	5,026.23
19	62681739	12672	4,946.47	62,601,739	12628	4,963.71
20	65343332	14085	4,639.21	65,263,332	13450	4,858.24
21	58984458	11663	5,057.40	58,904,458	11602	5,083.99
22	50928189	10264	4,961.82	50,848,189	10192	4,996.87
23	55556184	11353	4,893.52	97,483,019	11270	4,929.56
24	48288683	10006	4,825.97	48,208,683	9989	4,834.18
25	40282968	7788	5,172.44	40,122,968	7776	5,180.42
26	43147642	8330	5,179.78	43,067,642	8311	5,191.63
27	40254690	7921	5,082.02	40,174,690	7904	5,092.95
28	47348498	9095	5,205.99	47,268,498	9075	5,217.46
29	34776120	6898	5,041.47	34,696,120	6868	5,063.50
30	31395959	6042	5,196.28	31,315,959	5985	5,245.77
31	26001039	5017	5,182.58	25,921,039	4918	5,286.91
X	128206784	26142	4,904.24	128,126,784	25918	4,946.63
Average		**15214.625**	**4979.34**		**15063.40**	**5031.84**

Duck:

Table 5.25: Shows Total repeat, Total repeat ratio, Internal repeats, Internal repeat ratio of Forward repeat (TTAGGG). The total repeats and internal repeats are high in chromosome 1. The total repeats and internal repeats are low in chromosome 30. Average for total repeats, internal repeat, total repeat ratio and internal repeat ratio are 6448.3, 6370, 4826.3, 5046.

Chromosomes	Size (In bp)	Total Repeat	Total Repeat Ratio	Internal Size (Total size-80,000)	Internal Repeats	Internal Repeat Ratio
1	207238429	35486	5840	207158429	35166	5890.8
2	164862000	28775	5729.3	164782000	28655	5750.4
3	120086012	20688	5804.6	120006012	20673	5804.6
4	76269206	13026	5855	76189206	12966	5875.6
5	33853611	19732	3388.6	66776311	19691	3391.0
6	37939480	6467	5865.7	37859480	6346	5964.9
7	39896445	6940	5748.7	39816445	6937	5738.8
8	32618258	5510	5919.8	32538258	5456	5962.6
9	26788864	4803	5577.5	26708864	4800	5563.1
10	22484652	4515	4979.9	22404652	4410	5079.2
11	22598276	4196	5385.6	22518276	4073	5527.3
12	21610006	3755	5754.9	21530006	3719	5803.2
13	23150841	4199	5513	23070841	4140	5571.3
14	20984523	6442	3257.4	20904523	6434	3248.5
15	17872457	3696	4835.6	17792457	3383	5257.8
16	16222536	5937	2732.4	16142536	5896	2737.4
17	1402342	436	3216.3	1322342	395	3339.2
18	12065260	2309	2672.2	11985260	2302	5206.4
19	13129675	2450	5359	13049675	2442	5341.6
20	11966879	2291	5223.4	11886879	2289	5190.7
21	16960004	2981	5687.4	16920004	2898	5838.5
22	8397549	1587	5291.4	8317549	1581	5257.6
23	5328910	1094	4871	5248910	1060	4947.1
24	7636233	1376	5549.5	7556233	1349	5597.2
25	7658487	1809	4233.5	7578487	1428	5303.3
26	3037671	841	3611.9	2957671	823	3589.4
27	6799408	1402	4849.7	6719408	1160	5787.6
28	7028699	1260	5578.3	6948699	1213	5723.8
29	6031659	1442	4182.8	5951659	1401	4245.1
30	214689	45	4770.8	134689	23	5612.0
W	16693329	3001	5562.5	16613329	2998	5539
33	112901	245	406.8	32901	36	843.6
Z	84547829	14059	6013.7	84467829	14069	6011.9
Average		**6448.3**	**4826.3**		**6370**	**5046**

Hen:

Table 5.26: Shows Total repeat, Total repeat ratio, Internal repeats, Internal repeat ratio of Forward repeat (TTAGGG). The total repeats and internal repeats are high in chromosome 1. The total repeats and internal repeats are low in chromosome 32. Average for total repeats, internal repeat, total repeat ratio and internal repeat ratio are 5989.79, 5806.70, 4970.33, 5348.46.

Chromosomes	Size (In bp)	Total Repeat	Total Repeat Ratio	Internal Size (Total size-80,000)	Internal Repeats	Internal Repeat Ratio
1	197608386	34142	5787.83	197528386	34125	5788.37
2	149682049	34142	4384.10	149602049	34125	4383.94
3	110838418	17876	6200.40	110758418	17435	6352.64
4	91315245	11293	8086.00	91235245	11293	8078.92
5	59809098	9729	6147.50	59729098	9723	6143.07
6	36374701	7146	5090.21	36294701	7057	5143.07
7	36742308	5481	6703.57	36662308	5470	6702.43
8	30219446	4496	6721.40	30139446	4479	6729.05
9	24153086	3481	6938.54	24073086	3470	6937.48
10	21119840	4661	4511.18	21039840	4660	4514.98
11	20200042	6585	3067.58	20120042	5241	3838.97
12	20387278	3425	5952.48	20307278	3419	5939.53
13	19166714	4124	4647.60	19086714	4123	4629.32
14	16219308	3963	4092.68	16139308	3912	4125.58
15	13062184	2432	5370.96	12982184	2404	5400.24
16	2844601	399	7129.32	2764601	396	6981.31
17	10762512	2613	4118.83	10682512	1631	6549.67
18	11373140	7187	1582.45	11293140	7160	1577.25
19	10323212	2140	4823.93	10243212	2137	4793.26
20	13897287	2038	6819.08	13817287	2032	6799.84
21	6844979	1163	5885.62	6764979	1131	5981.41
22	5459462	990	5514.60	5379462	987	5450.31
23	6149580	1037	5930.16	6069580	1023	5933.11
24	6491222	1045	6211.69	6411222	1014	6322.70
25	3980610	2963	1343.43	3900610	2946	1324.03
26	6055710	882	6865.88	5975710	878	6806.04
27	8080432	6904	1170.39	8000432	5182	1543.88
28	5116882	1927	2655.36	5036882	818	6157.55

30	1818525	528	3444.17	1738525	466	3730.74
31	6153034	2908	2115.89	6073034	2862	2121.95
32	725831	180	4032.39	645831	68	9497.51
33	7821666	3340	2341.81	774166	3339	2318.55
W	6813114	1140	5976.41	6733114	1132	5947.98
Z	82529921	11293	7308.05	82449921	11290	7302.91
Average		**5989.79**	**4970.33**		**5806.70**	**5348.46**

Camel:

Table 5.27: Shows Total repeat, Total repeat ratio, Internal repeats, Internal repeat ratio of Forward repeat (TTAGGG). The total repeats and internal repeats are high in chromosome 1. The total repeats and internal repeats are low in chromosome 36. Average for total repeats, internal repeat, total repeat ratio and internal repeat ratio are 11525.86, 7368.56, 4835.63, 9817.23.

Chromosomes	Size (In bp)	Total Repeat	Total Repeat Ratio	Internal Size (Total size-80,000)	Internal Repeats	Internal Repeat Ratio
1	124715342	25113	4,966.16	124,635,342	25101	4,965.35
2	123797624	24358	5,082.42	123,717,624	24347	5,081.43
3	120724560	24396	4,948.53	120,644,560	24378	4,948.91
4	68336600	14019	4,874.57	68,256,600	14008	4,872.68
5	97468828	19832	4,914.72	97,388,828	19552	4,981.01
6	97504898	20479	4,761.21	86,582,405	20452	4,233.44
7	86662405	17504	4,951.00	86,582,405	17490	4,950.39
8	81230863	16342	4,970.68	81,150,863	16327	4,970.34
9	77266745	15907	4,857.40	77,186,745	15896	4,855.73
10	69117207	14084	4,907.49	69,037,207	14076	4,904.60
11	85443229	19018	4,492.75	85,363,229	18258	4,675.38
12	68281056	13742	4,968.78	68,201,056	13727	4,968.38
13	69976089	14538	4813.32	69,896,089	14522	4,813.11
14	70369702	13489	5,216.82	70,289,702	13471	5217.85
15	57412934	11598	4,950.24	57,332,934	11572	4954.45
16	55652839	11618	4,790.22	55,572,839	11610	4,786.63
17	52130679	10514	4,958.21	52,050,679	10506	4,954.37
18	32939817	6840	4,815.76	32,859,817	6828	4,812.50
19	45218158	9421	4,799.71	45,138,158	9363	4,820.90
20	42996454	8894	4,834.32	42,916,454	8831	4,859.75

21	31123794	6986	4,455.16	31,043,794	6338	4,898.04
22	28606581	5806	4,927.07	28,526,581	5798	4,920.07
23	34524780	6964	4,957.60	34,444,780	4781	7,204.51
24	24767672	4791	5,169.62	24,687,672	4783	5,161.54
25	41725625	8162	5,112.18	41,645,625	8144	5,113.65
26	27902444	5589	4,992.38	27,822,444	5579	4,986.99
27	28600766	5695	5,022.08	28,520,766	5684	5,017.72
28	16041598	3129	5,126.74	15,961,598	3121	5,114.25
29	25940089	5040	5146.84	25,860,089	5027	5,144.23
30	25866843	5254	4,923.26	25,786,843	5237	4,923.97
31	17406307	3463	5,026.36	17,326,307	3441	5,035.25
32	24923383	4991	4,993.6	24,843,383	4968	5,000.68
33	23363481	4700	4,970.95	23,283,481	4692	4,962.37
34	22483259	4465	5,035.44	22,403,259	4445	5,040.10
35	26327613	5349	4,921.96	26,247,613	5328	4926.35
36	7066694	1229	5,749.95	6,986,694	1220	5,726.79
37	121484823	24138	5,032.92	121,404,823	24122	5,032.95
Average		**11,525.86**	**4835.63**		**7368.56**	**9817.23**

Dog:

Table 5.28: Shows Total repeat, Total repeat ratio, Internal repeats, Internal repeat ratio of Forward repeat (TTAGGG). The total repeats and internal repeats are high in chromosome 1. The total repeats and internal repeats are low in chromosome Y. Average for total repeats, internal repeat, total repeat ratio and internal repeat ratio are 13226.075, 12858.37, 4513.22, 4649.40.

Chromosomes	Size (In bp)	Total Repeat	Total Repeat Ratio	Internal Size (Total size-80,000)	Internal Repeats	Internal Repeat Ratio
1	123313939	25944	4753.08	123233939	25921	4754.21
2	86187811	21341	4038.60	86107811	18865	4564.42
3	92870237	19652	4725.73	92790237	18673	4969.21
4	89007665	34142	2606.98	88927665	34134	2605.25
5	89573405	19095	4690.93	89493405	197080	4690.43
6	78268176	16748	4673.28	78188176	16735	4672.13
7	81039452	17009	4764.50	80959452	16984	4766.80
8	75260524	15999	4704.50	75180524	15976	4705.84
9	62002293	13744	4511.22	61922293	13326	4646.72
10	70361000	16092	4372.42	70281000	15613	4501.44

11	75541347	16902	4469.37	75461347	15625	4829.52
12	73497294	16593	4429.41	73417294	15311	4795.06
13	64037277	13259	4829.72	63957277	13236	4832.06
14	61043064	12823	4760.43	60963064	12799	4763.11
15	65200600	14147	4608.79	65120600	14128	4609.32
16	62021213	12556	4939.56	61941213	12555	4933.58
17	65471548	14152	4626.31	65391548	13970	4680.85
18	56883407	11500	4946.38	56803407	11460	4956.66
19	55265241	11943	4627.41	55185241	11532	4785.40
20	58896461	12692	4640.43	58816461	12223	4811.94
21	52140716	11180	4663.74	52060716	11159	4665.35
22	62106979	13286	4674.61	62026979	12556	4940.20
23	53282923	11913	4472.67	53202923	11480	4634.40
24	48838117	10259	4760.60	48758997	10192	4784.04
25	51941001	11882	4371.40	51861001	11863	4371.65
26	40674351	8985	4526.91	40594351	8966	4527.58
27	46248802	9852	4694.35	46168802	9845	4689.56
28	41862212	9829	4259.05	41782212	8720	4791.53
29	42049852	9829	4278.14	41969852	8803	4767.67
30	40414903	8733	4627.83	40334903	8701	4635.66
31	39518933	8013	4931.85	39438933	7980	4942.22
32	39023732	7809	4997.27	38943732	7803	4990.86
33	31649084	7164	4417.79	31569084	6850	4608.62
34	42263871	9113	4637.75	42183871	9086	4642.73
35	26942268	5785	4657.26	26862268	5764	4660.35
36	31065185	7380	4209.37	30985185	6353	4877.25
37	30932408	6966	4440.48	30852408	6528	4726.16
38	24102048	6168	3907.59	24022048	5017	4788.12
X	127069619	27413	4635.37	126989619	27396	4635.33
Y	3937623	1151	3420.04	3857623	1127	3422.91
Average		**13226.075**	**4513.22**		**12858.37**	**4649.40**

From the results generated from csv file of various combinations of TTAGGG (FR), GGGATT(RR), AATCCC (FCR), CCCTAA (RCR) are analyzed based on the obtained as shown below in table form.

Forward Repeat:

Table 6.1: Shows the forward repeat Ratio average, Internal ratio average, Maximum repeat of chromosome, Minimum repeat of chromosome, Average repeat, Internal average repeat. The chromosome 1 has the maximum number of repeats present in all the species. The chromosomes Minimum number of repeats vary between all the species.

Organisms	Ratio Average	Internal Ratio Average	Max Repeat Chr	Min Repeat Chr	Average Repeats	Internal Average Repeats
Drosophila (Penta)	1691.7	1690.7	18309(chr3R)	208(Chr4)	2695.667	2686.5
Silkworm (Penta)	1238.3	1275.9	18498(chr18)	8578(chr28)	12886.75	12378.28
Honeybee (Penta)	2207.2	2714.53	11957(chr1)	4120(chr15)	6283.8125	5123.68
Butterfly (Penta)	1446.92	2036.99	15877(chr1)	5028(chr30)	8724.77	7783.25
Zebrafish	5419	5428.7	14114(Chr7)	6776(Chr25)	9915.68	9885.5
Rabbit	5864.5	5862	34523(Chr1)	2249(Chr21)	17750.45	17740.64
Duck	4826	5062	35486(Chr1)	45(Chr31)	6448	6336
Whale	5215.9	5224.7	36699(1)	339 (ChrY)	20080	20061.4
Xenopus	3608.74	3777.41	57589(chr1)	25609(chr13)	38,246	36560.5
Cow	5797.97	7630.92	25938(chr1)	7294(chr25)	15103	28627.67
Camel	4835.63	9817.23	25113(chr1)	1229(chr36)	11525.86	7368.56
Zebra finch	5496.35	5581.4	25737 (chr2)	204(chr29)	5680.31	5620.46
Dog	4513.22	4649.4	5581.4	5581.4	5581.4	5581.4
Chicken	4970.33	5348.46	34142(chr1)	399(chr17)	5989.79	5806.7
Parrot	7785	6091.68	7527.27(chr23)	2822.35(chr22)	5849.31	7651.24
Tortoise	4333.05	4370.28	84130(ch1)	2660(chr24)	21284.04	21200.41
Dolphin	4799.024	4907.445	38296(chr1)	7634(chr21)	22062.181	21612.86
Catshark	5794.207	5819.48	53731(chr1)	2138(chr31)	23563.064	22587.84
Panda	4872.195	4873.268	43151(chr1)	6343(chr20)	22376	22355.76
Human	6088.79	6134.934	45535(Chr2)	5477(ChrY)	22596.54	22564.21
Horse	4979.34	5031.84	38418(chr1)	5017(Chr31)	15214.625	15063.4
Cat	5260.7	5339.7	32701(chr1)	12354(chr14)	24400.26	24041

C.elegan	13454.83	13500.18	1756(chr5)	1349(chr3)	1527.166667	1520.5
Neuraspora crassa	5440.5	5633.82	1692 (chr1)	778(chr6)	1,051.86	1002.85
Thermophlic Fungi	6028.19	6347.665	1788(chr1))	512(chr6)	1046.5	1005.166
S. cerevisiae	9613.5	9613.5	196(chr4)	31(chr3)	92.31	80.93
P. falciparum	11585.6	25606.19	446(chr3)	83(chr1)	167.7857	76.35
Trypanosoma brucei	10334	11183.4	525(chr11)	66(chr1)	222.4545	211

Reverse Repeat:

Table 6.2: Shows the Reverse repeat Ratio average, Internal ratio average, Maximum repeat of chromosome, Minimum repeat of chromosome, Average repeat, Internal average repeat. The chromosome 1 has the maximum number of repeats present in all the species. The chromosomes Minimum number of repeats vary between all the species.

Organisms	Ratio Average	Internal Ratio Average	Max Repeat Chr	Min Repeat Chr	Average Repeats	Internal Average Repeats
Drosophila (Penta)	1045.8	1052.3	30985(Chr3R)	1123(Chr4)	21929	21870
Silkworm (Penta)	1321.72	1324.45	16354(chr23)	7949(chr28)	12016.32	11966.39
Honeybee (Penta)	1090.56	2048.86	25651(chr1)	6314(chr6)	12669.18	12618.12
Butterfly (Penta)	1401.27	1400.07	12331(ChrZ)	5611(Chr30)	8801.06	8753.96
Zebrafish	6778.1	6771.3	12524(Chr4)	5589(Chr25)	7951.6	7936.08
Rabbit	4995.3	4999.3	42158(Chr1)	2470(Chr21)	21108.8	21095.5
Duck	4074	4083.9	43653(Chr1)	68(Chr31)	7418	7397.2
Whale	4063	4203.7	46530(Chr1)	545(ChrY)	25485	25117.7
Xenopus	4765.31	4873.72	30979(chr37)	1462(chr36)	55662.1	28733.22
Cow	3279.13	2532.33	63041(chr1)	16717(chr25)	34656.53	34643.93
Camel	4249.73	4236.58	45424(chr1)	19213(chr13)	13136.7	13119.78
Zebra finch	2919.2	2894.02	34953 (chr2)	740(chr29)	8756.41	9371.4
Dog	3723.69	3717.67	36156(chrX)	1395(chrY)	15854.75	15854.3
Chicken	3310.92	3374.23	42994(chr1)	576(chr32)	8013.2	7854.7
Parrot	3962.73	4004.48	33418 (Chr1)	804 (chr23)	10343.12	10128.92
Tortoise	3659.46	3660.96	94908(Chr1)	4019(Chr24)	23772.36	23747.7
Dolphin	4093.252	4091.835	45865(Chr1)	8528(Chr21)	26014.909	26002.5

Catshark	2657.575	2579.722	109659(Chr1)	5932(Chr30)	47998.03	47959.9
Panda	4249.607	4249.301	49057(Chr1)	6865(Chr20)	25664.95	25646.9
Human	2928.126	2927.653	93096(Chr1)	8964(ChrY)	46589.58	46581.88
Horse	4702.47	4702.66	40962 (chr1)	5197 (chr31)	16108.03	16091.34
Cat	3955.93	3955.83	60506 (chr1)	10963 (chr16)	32711.57	32691.78
C. elegan	6210.8	6204.02	3851(Chr5)	3073(Chr3)	3304.1	3305.33
Neuraspora	4371.45	4401.1	2134(chr1)	983(chr2)	1313.42	1289.28
Thermophlic Fungi	6443.13	6418.7	1508 (chr1)	605 (chr6)	948.5	939.66
S. cerevisiae	8125.7	9613.5	196 (chr4)	31 (chr3)	92.31	80.93
P. falciparum	17778.18	17904.97	198 (chr4)	58 (chr3)	97.64	92.35
Trypanosoma brucei	5317.24	5369.25	40201 (chr11)	140 (chr1)	3927.81	3912.36

Forward Complementary Repeat:

Table 6.3: Shows the Forward complementary repeat Ratio average, Internal ratio average, Maximum repeat of chromosome, Minimum repeat of chromosome, Average repeat, Internal average repeat. The chromosome 1 has the maximum number of repeats present in all the species. The chromosomes Minimum number of repeats vary between all the species.

Organisms	Ratio Average	Internal Ratio Average	Max Repeat Chr	Min Repeat Chr	Average Repeats	Internal Average Repeats
Drosophila (Penta)	1061.9	1057.6	31585(chr3R)	1046(chr4)	21902.6	21849.1
Silkworm (Penta)	1317.84	1321.76	15432	6241	12049.25	11987.07
Honeybee (Penta)	1061.3	1061.15	25952(chr1)	6366(chr16)	13078.5	12997.87
Butterfly (Penta)	1385.89	1398.88	12126(chrZ)	5833(chr30)	8897.93	8756.22
Zebrafish	6745	6744.4	12784(chr4)	5502(chr25)	7986.3	7975.9
Rabbit	5033.3	5031.7	41307(chr1)	2414(chr21)	20991.4	20977.7
Duck	4107.7	4133	42717(chr1)	44(chr33)	7270	7344.2
Whale	4086.2	4087.9	46721(chr1)	521(chrY)	25345	25329.2
Xenopus	4719.19	4752.38	45499(chr1)	19474(chr14)	41277.5	29425.83

Cow	2533.21	2532.67	63380(chr1)	16835(chr25)	41079.27	34612.53
Camel	4257.07	4589.84	31051(chr37)	3639(chr28)	13101.32	13085.16
Zebra finch	2953.2	2960.4	35286(chr2)	740(chr29)	9049.87	17477.45
Dog	3743.55	3743.78	35951(chrX)	1293(chrY)	15794.27	15772.47
Chicken	3339.89	3438.94	41891(chr1)	542(chr32)	7509.5	7383.64
Parrot	3965.55	3965.48	33313(chr1)	855(chr23)	10305.2	10281.5
Tortoise	3627.52	3656.94	95466(chr1)	3883(chr24)	23958.08	23880.45
Dolphin	3951.105	4114.39	45285(chr1)	8526(chr21)	25835.73	25823.82
Catshark	2667.77	2669.15	110973(chr1)	5814(chr30)	48113.903	48077.16
Panda	4244.28	4294.75	69134(chr20)	8218(chr19)	28636.52	25363.76
Human	3364.46	2921.58	92887(chr1)	8662(chrY)	46406.08	46395.67
Horse	4689.029	4686.54	40737(chr1)	5430(chr31)	16080.718	16099.4
Cat	3951.24	5145.065	60723(chr1)	11265(chr16)	32714.89	25111
C. elegan	6320.76	6220.9	3998(chr5)	2877(chr6)	3257	3300.66
Neuraspora	4698.64	4722.81	2192(chr1)	1006(chr7)	1237.28	1216.57
Thermophlic Fungi	6685.56	6675.24	1483(chr2)	543(chr6)	922.16	911.66
S. cerevisiae	5685.3	5750.64	259(chr4)	48(chr1,6)	130.18	116
P. falciparum	17978.71	18388.28	168(chr14)	45(chr1)	91.42	84.92
Trypanosoma brucei	5730.85	5729.65	803(chr11)	109(chr1)	359.18	343.36

Reverse Complementary Repeat:

Table 6.4: Shows the Reverse Complementary repeat Ratio average, Internal ratio average, Maximum repeat of chromosome, Minimum repeat of chromosome, Average repeat, Internal average repeat. The chromosome 1 has the maximum number of repeats present in all the species. The chromosomes Minimum number of repeats vary between all the species.

Organisms	Ratio Average	Internal Ratio Average	Max Repeat Chr	Min Repeat Chr	Average Repeats	Internal Average Repeats
Drosophila (Penta)	1707	1706	18400(chr3R)	904(chr4)	12818	12764
Silkworm (Penta)	1233.07	1245.23	17494	6654	12878	12786
Honeybee (Penta)	2626.88	2637.23	10893(1)	3030(16)	5267.25	5200

Butterfly (Penta)	1575.57	1581.77	13177(chr9)	4863(chr30)	8494.93	7767.77
Zebrafish	5371.1	5371.5	13296(chr5)	7045(chr25)	10000.4	9984.7
Rabbit	5848.1	5845.5	34427(chr1)	2151(chr21)	18086	18075.5
Duck	4927	5345.9	35454(chr1)	48(chr31)	1626.5	6055
Whale	5194.6	5152.4	36255(chr1)	379(chrY)	20007.3	20408.2
Xenopus	3684.4	3681.33	57622(chr1)	25697(chr13)	37974.61	37971.44
Cow	5868.18	5872.85	26146(chr1)	7370(chr25)	14905.83	14882.86
Camel	4953.56	4886.31	24763(chr1)	1149(chr36)	11250.83	11716.9
Zebra finch	5553.14	5604.09	25594(chr2)	208(chr29)	5643.56	5614.43
Dog	4616.91	4554.72	26408(chr1)	1899(chrY)	12663.72	14190.55
Chicken	5563.33	5630.16	30866(chr1)	514(chr16)	5138.29	5061.79
Parrot	5871.6	5898.56	27335(chr1)	413(chr22)	7818.92	7745.92
Tortoise	4226.88	4254.09	84284(chr1)	3940(chr24)	21022.12	20954.79
Dolphin	4548.06	4886.68	38120(chr2)	8379(chr21)	22515.73	21908.73
Catshark	5640.17	5734.96	53701(chr1)	2761(chr31)	22909.77	22760.52
Panda	4898.63	4899.21	43759(chr1)	6362(chr20)	22240.33	22221.52
Human	6160.25	6163.39	43072(chr1)	5168(chrY)	22520.92	22487.33
Horse	4995.283	5039.52	38135(chr1)	5103(chr31)	15109.718	14986.46
Cat	5145.065	5153.884	46682(chr1)	8163(chr16)	25111	25061.315
C. elegan	**6497.32**	**6564.1**	4374(chr5)	2233(chr6)	**3241.8**	**3199.1**
Neuraspora	5502.05	5714.55	1762(chr1)	799(chr7)	1043.14	995.71
Thermophlic Fungi	5473.83	5652	1795(chr1)	678(chr5)	1123.66	1077
S. cerevisiae	8157.16	8555.4	165(chr4)	35(chr1,6)	91.81	78.68
P. falciparum	11039.8	21931.42	31196(chr2)	73(chr8)	2379.85	2294.85
Trypanosoma brucei	8874.5	8897.86	534(chr11)	74(chr1)	230.63	220.7

Graphs:

Neurospora crassa:

Chromosome 2:

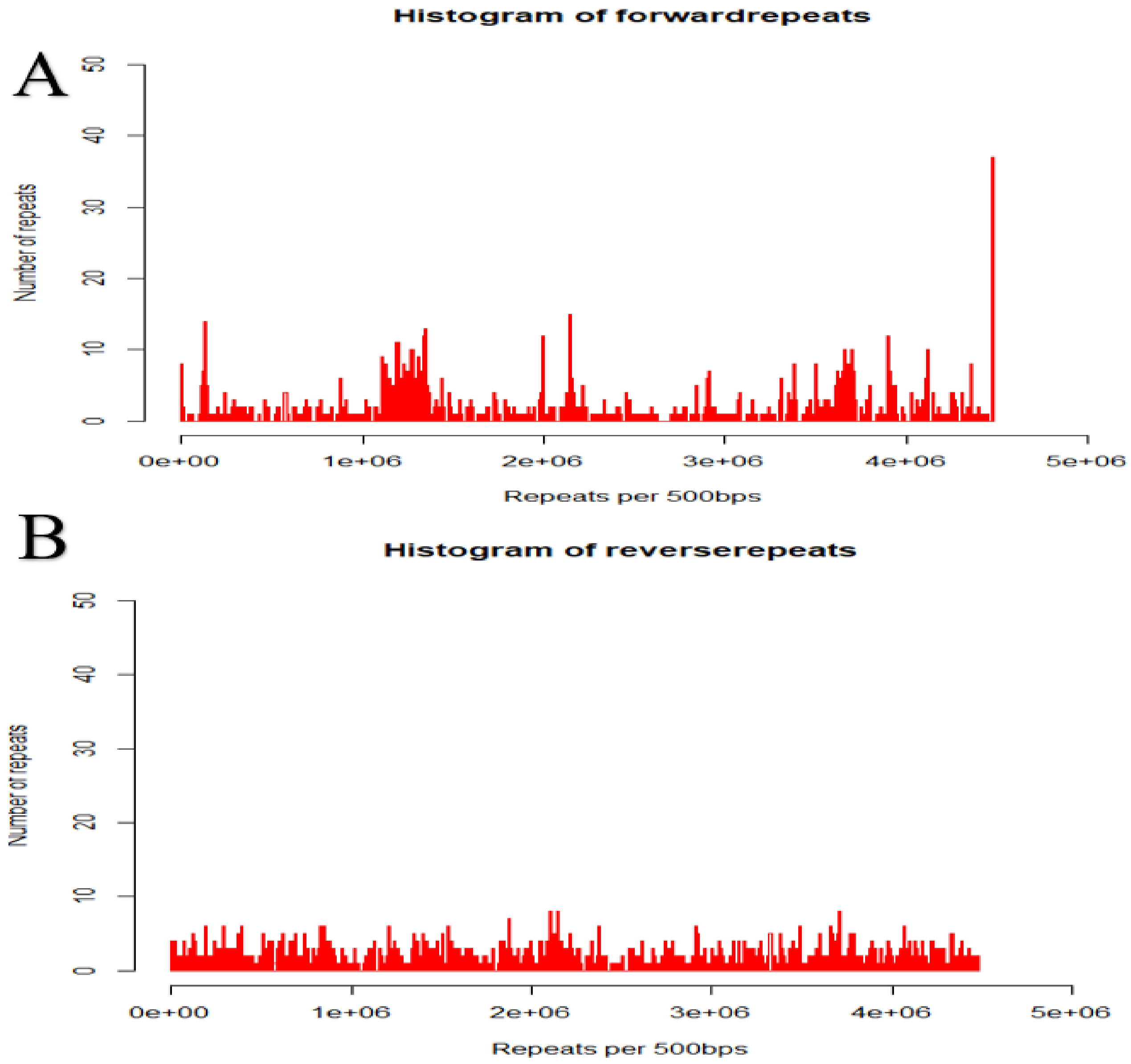

Fig 7.1: (A) Forward repeat graph of *Neurospora crassa* shows high telomeric peek at 3’ of value 40. **(B)** Reverse repeat graph of *Neurospora crassa*, in this graph there is no telomeric peek.

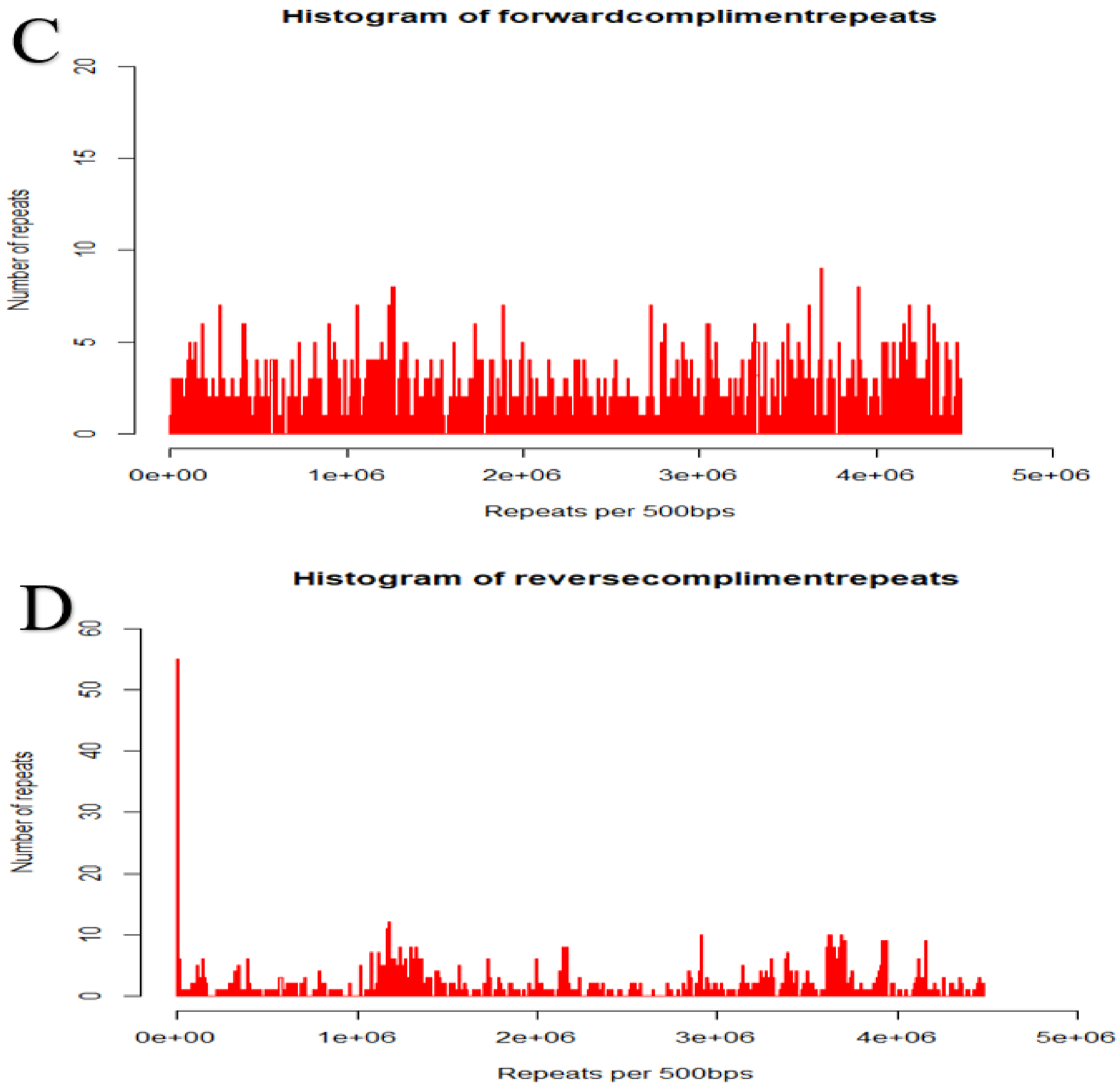

Fig 7.2: (C) Forward complementary repeat graph of *Neurospora crassa* in this graph there is no telomeric peek. **(D)** Reverse complementary repeat graph of *Neurospora crassa*, shows high telomeric peek at 5’ of value 55. Both the graph Forward and Reverse complementary repeat are inversely proportional to each other.

In Neurospora crassa both the Forward and Reverse complementary repeat graphs are inversely proportional to each other in chromosomes 1, 2, 3, 5, 6, and 7.

Dog:

Chromosome 22:

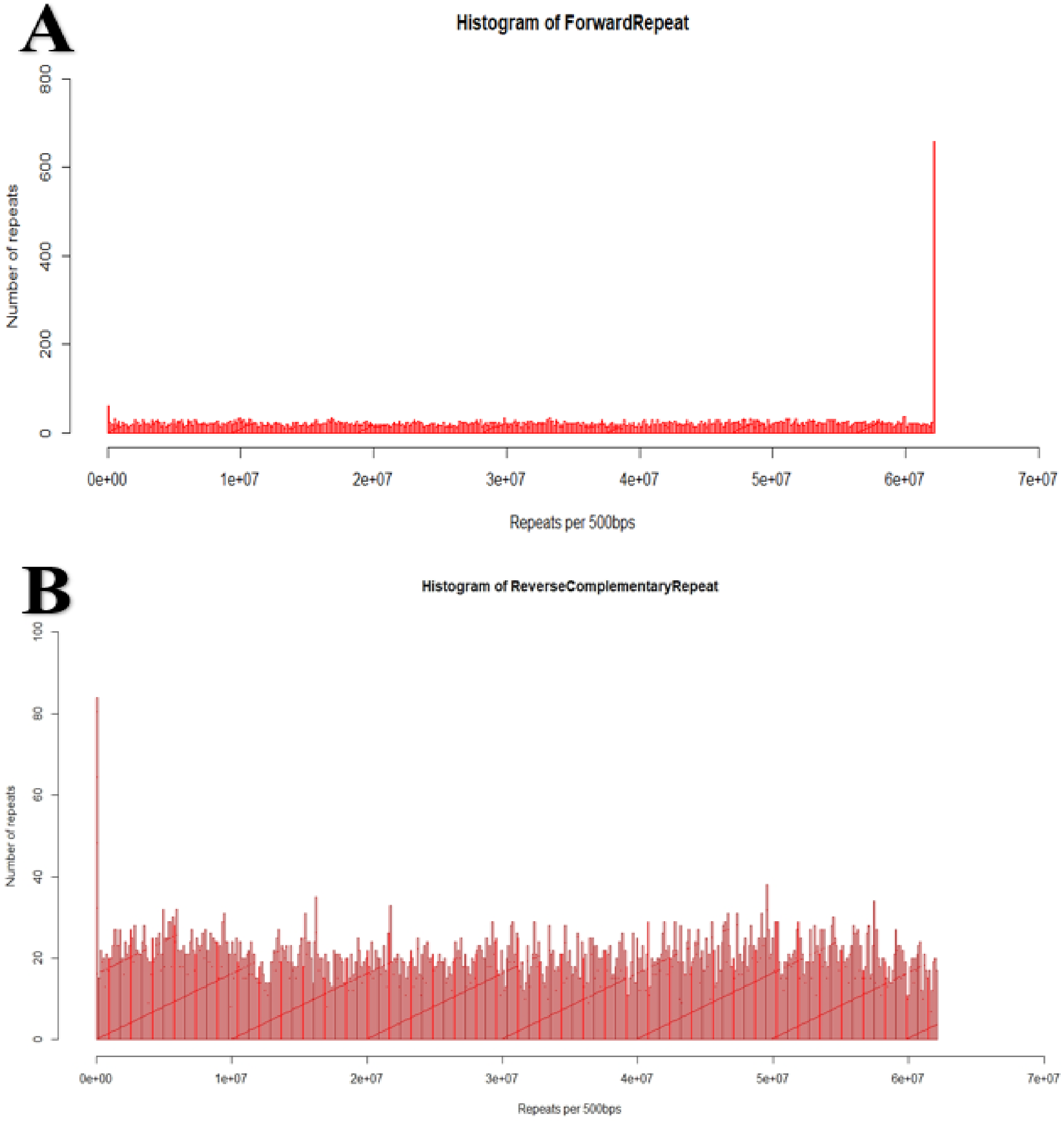

Fig 8: (A) Forward repeat graph of Dog shows high telomeric peek at 3' of value ~700. **(B)** Reverse complementary repeat graph of Dog shows high telomeric peek at 5' of value ~85. Both the graph Forward and Reverse complementary repeat are inversely proportional to each other.

In Dog both the Forward and Reverse complementary repeat graphs are inversely proportional to each other in chromosomes 2, 5, 6, 9, 11, 20, 22, 24, 25, and 28.

Dolphin:

Chromosome 7:

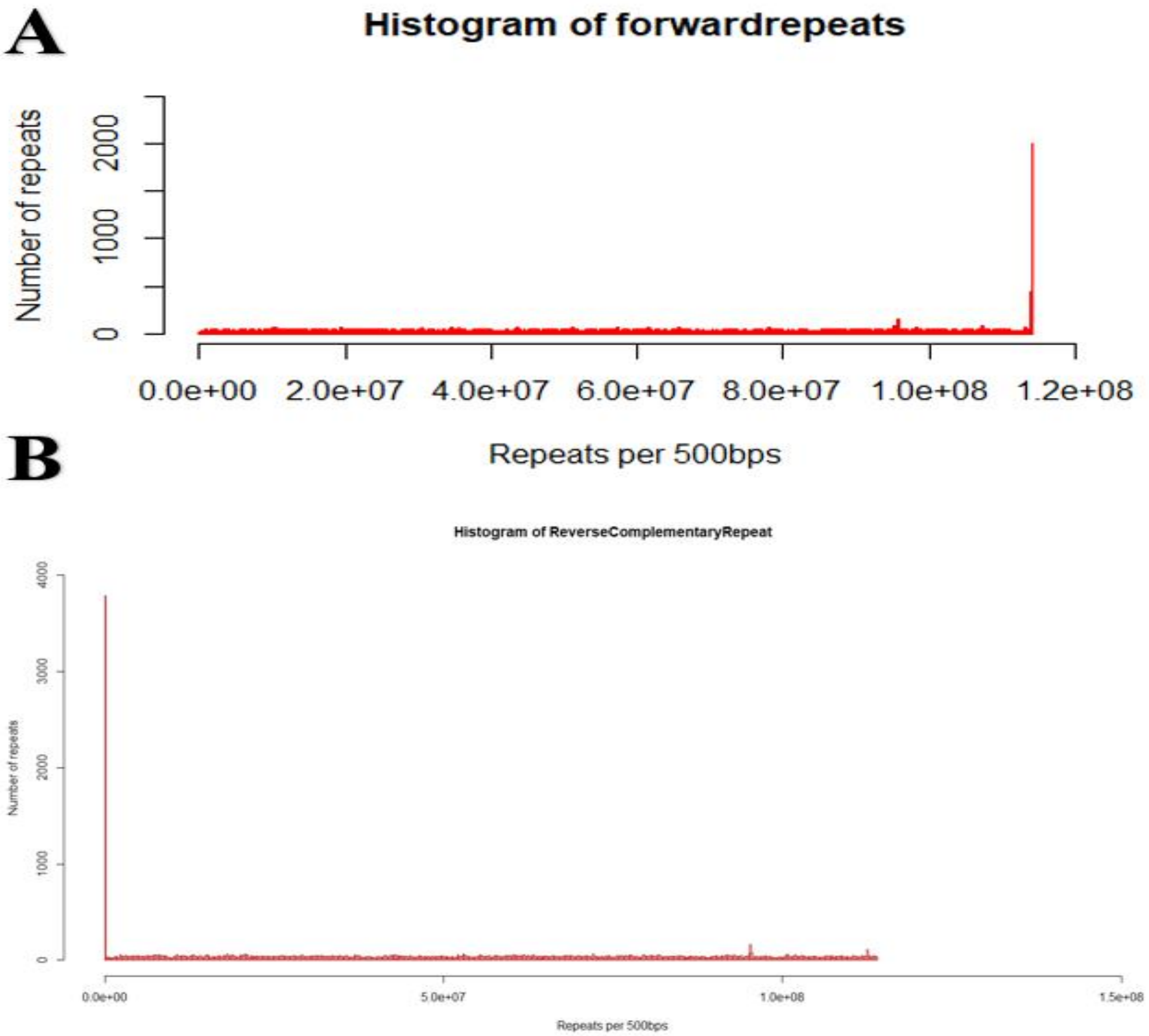

Fig 9: (A) Forward repeat graph of Dolphin shows high telomeric peek at 3’ of value ~2000. **(B)** Reverse complementary repeat graph of Dolphin shows high telomeric peek at 5’ of value ~4000.

Both the graph Forward and Reverse complementary repeat are inversely proportional to each other.

In Dolphin both the Forward and Reverse complementary repeat graphs are inversely proportional to each other in chromosomes 6, 7, 12, 14, 17, 19 and 21.

Duck:

Chromosome 9:

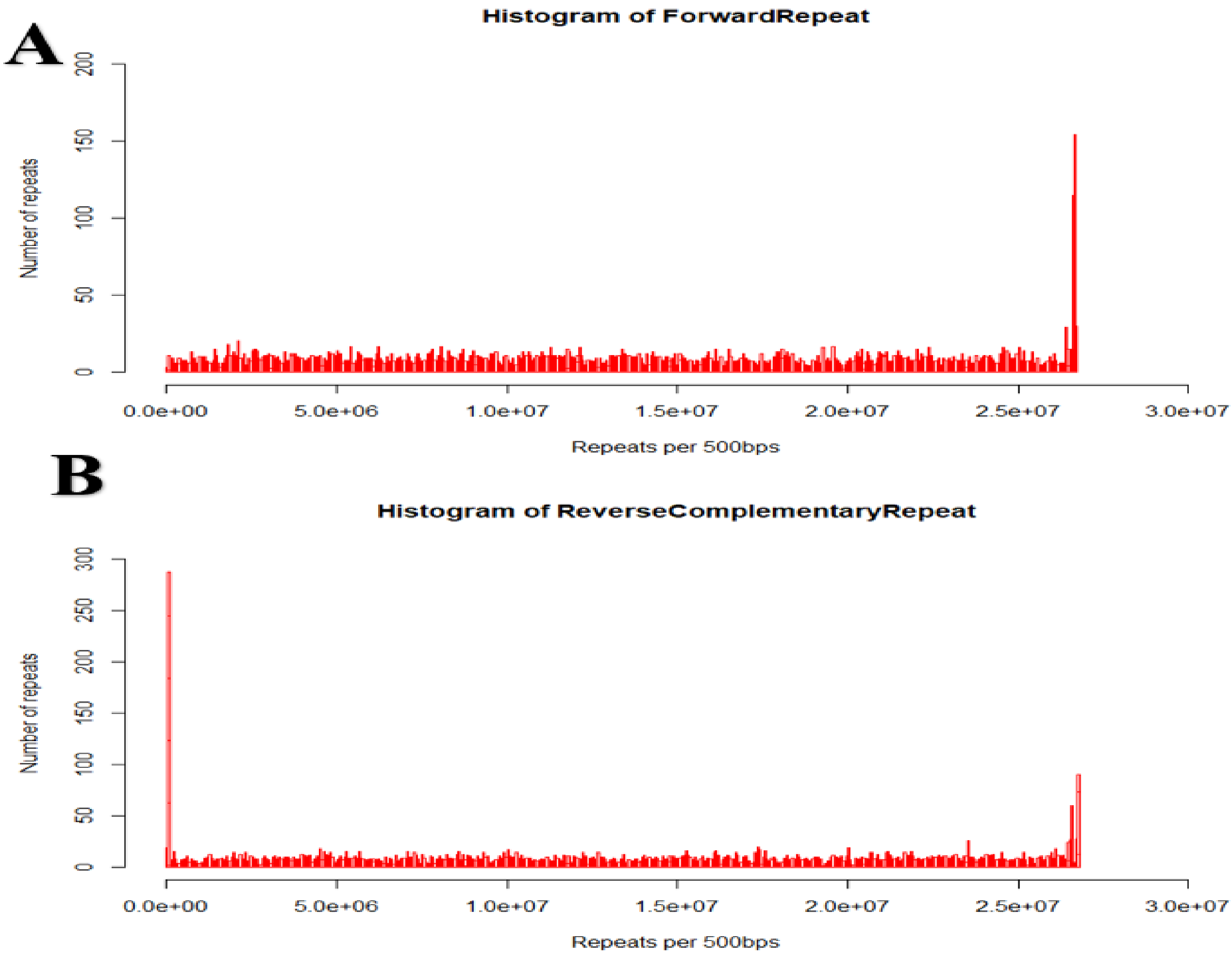

Fig 10: **(A)** Forward repeat graph of Duck shows high telomeric peek at 3' of value ~180. **(B)** Reverse complementary repeat graph of Duck shows high telomeric peek at 5' of value ~300. Both the graph Forward and Reverse complementary repeat are inversely proportional to each other.

In Duck both the Forward and Reverse complementary repeat graphs are inversely proportional to each other in chromosomes 9, 11, 15, 19 and 29.

Hen:

Chromosome 13:

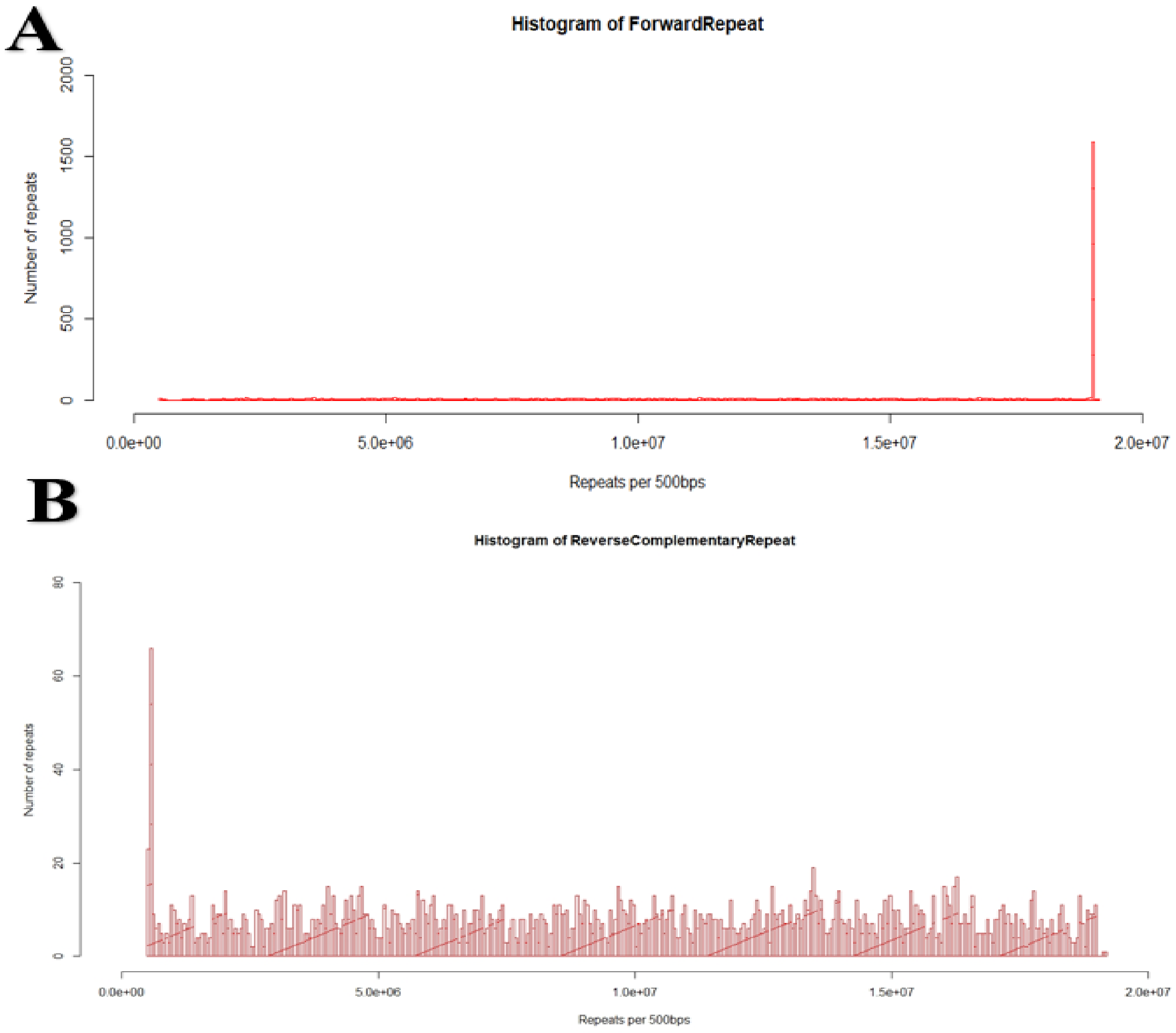

Fig 11: (A) Forward repeat graph of Hen shows high telomeric peek at 3’ of value ~1800. **(B)** Reverse complementary repeat graph of Hen shows high telomeric peek at 5’ of value ~70. Both the graph Forward and Reverse complementary repeat are inversely proportional to each other.

In Hen both the Forward and Reverse complementary repeat graphs are inversely proportional to each other in chromosomes 1, 4, 7, 10, 13, 14, 15, 17, 19, 22, 25, and 27.

From the graph we conclude that the Forward Repeat and Reverse Complementary Repeat are inversely proportional to each other. For example, forward repeat has high peek of telomeric repeat of TTAGGG in 3' and in reverse complementary repeat has high peek of telomeric repeat of CCCTAA in 5' and vice versa. So, from this the chromosome are protected by both forward and reverse complementary repeat (30). Likewise, we analyzed the organisms such as Duck, Hen, Dog are also showing the similar pattern. And the average ratio and average repeats of forward and reverse complementary repeat are also same in all the organisms that we analyzed. So, the hypothesis is both the forward and reverse complementary repeat plays a curical role in lifespan.

DISCUSSION

Discussion:

Genome size has no correlation with lifespan:

Based on the genome size of different species we cannot be able to predict the lifespan of all organisms. Because the whole genome size of the microorganisms is around 50-100 mb and the whole genome size of the insects is around 100-500 mb and the whole genome size of vertebrates has 1Gb (Hen) to 4Gb (Shark). The microorganisms which are the first exist to the world after that insects and finally the vertebrates. The genome size of Xenopus is 2.7Gb and the genome size of the human is 2.8 Gb. Both the organism’s genome size is almost similar, but their life span is different. Xenopus can live up to 15 years, but human can live up to 70-80 years. So, there is no correlation between genome size with lifespan. This is called as G value paradox (31).

Similarity among arthropods:

As we took four insects which belong to arthropods phylum such as *Drosophila melanogaster* (Fruit fly), *Bombyx mori* (Silkworm), *Apis mellifera* (Honeybee), *Aglais io* (European peacock butterfly). Insects as the Penta telomeric repeats TTAGG. From the results, the average ratio of these insects comes under 1200-2200 per repeats. From the final graph we conclude that, the insects are separated based on the evolution as shown in the above figure. Based on evolution Lepidoptera and Diptera are evolved first and then Hymenoptera (fig 4) (29).

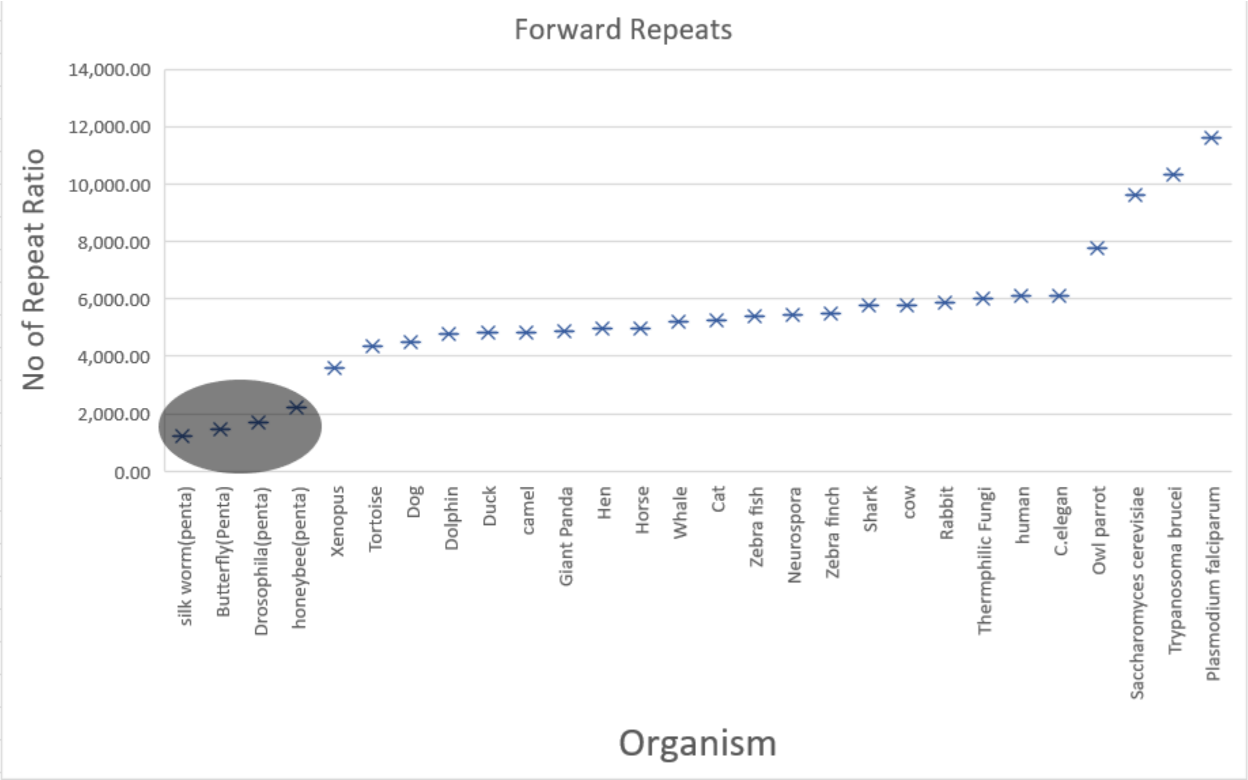

Fig 12: Shows that cluster of insects together and it is separated based on the evolution.

Comparison between organisms:

As we took 28 species for analysis, based on phylum such as Chordata, Arthropoda, Ascomycota, Euglenozoa, Nematoda, Apicomplexa. From the result, the insects (Arthropoda) as the average ratio of 1200-2200, vertebrate (Chordata) as the ratio of 3000-7000, the protozoans and the fungus as 5000-13000 per repeat. Saccharomyces cerevisiae has lowest number of repeat 31 and tortoise has higher repeats of 84130.

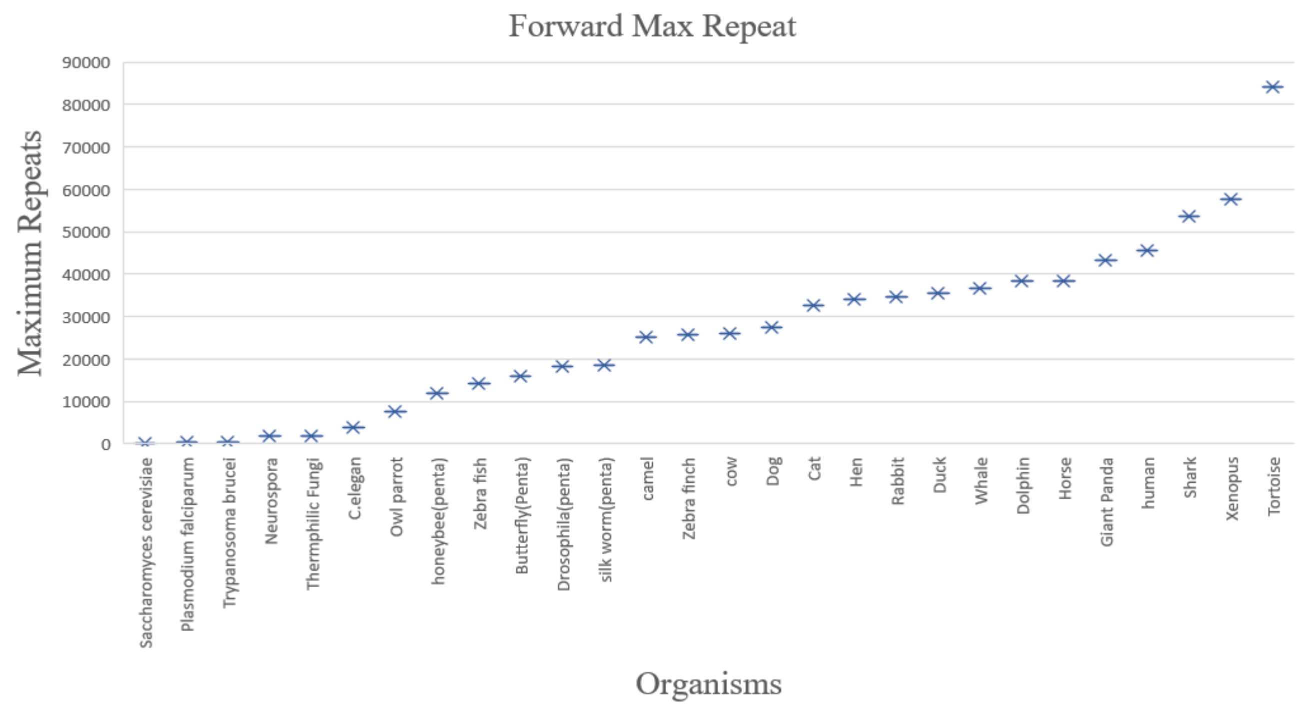

Fig 13: Shows that the Maximum repeats among all species in Forward repeat.

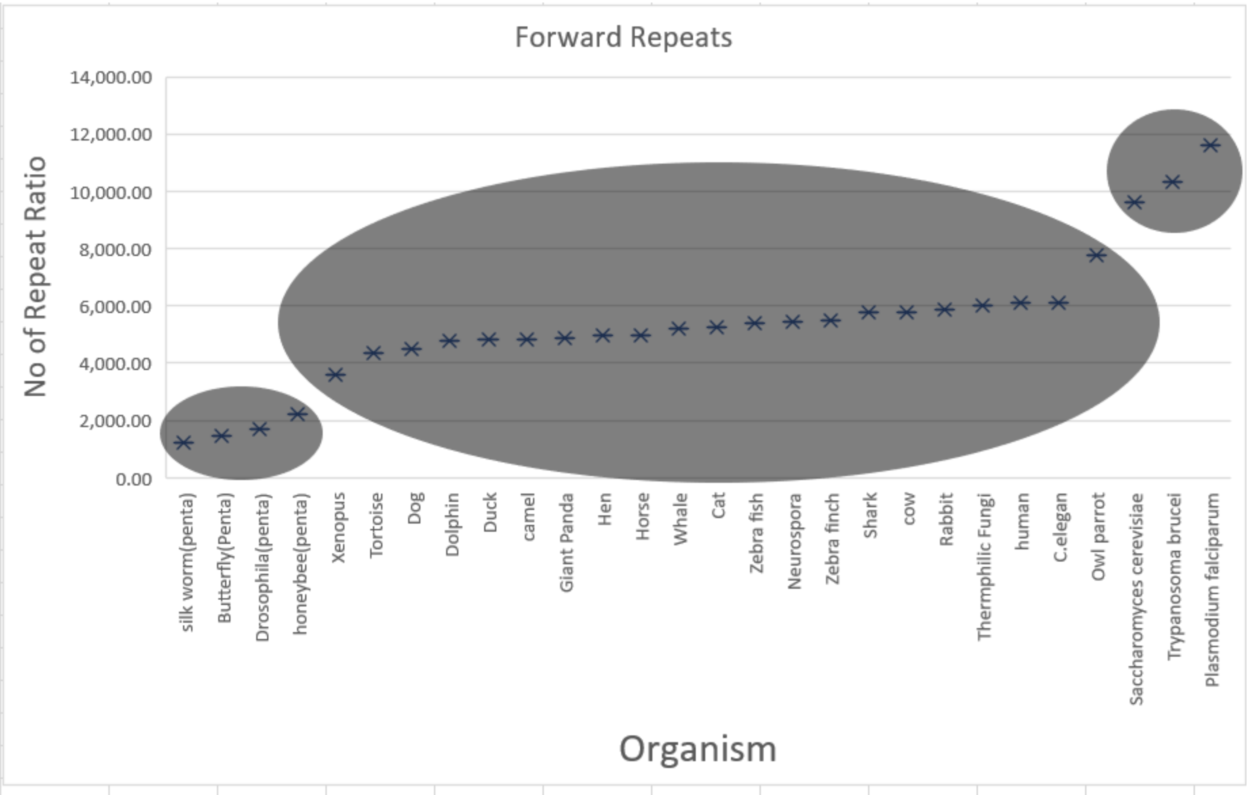

Fig 14: The data shows all Arthropod (Insects) genome has one repeat per 2000 bases. The Chordate (Vertebrates) genome has one repeat per every 4000 bases. In Ascomycota (Fungi) has one repeat every 6000 bases.

Thus, organisms coming under similar groups has its own signature value within a range and these values could have a resemblance with those organisms' lifespan, habitat and lifestyle as organisms having similar lifestyle and environment have similar values with each other. These repeat ratio values could prove to be a key to finding out the reason behind diversity and similarities in between organisms in all aspects of life.

Protozoans Repeats and Protozoans are eternal organisms:

From the results, both the protozoan which has the telomere repeat of TTAGGG are low because of that the average ratio is high. So that's why protozoans live is noticeably short.

Caenorhabditis elegans is a nematode which has the telomere sequence of TTAGGC. From the result, the telomere repeats are low with the average of 6452 which are like the vertebrate average ratio. But their lifespan is eternal (5)(32).

Comparison between Forward Repeat and Reverse Complementary Repeat:

From the result, the occurrence of both the average ratio and average repeat are similar in forward and reverse complementary repeat, and the average ratio and average repeat are also similar in both reverse and forward complementary repeat. Which as been shown in organisms like Neurospora crass, Hen, Duck, Dolphin, Dog (33).

Table 7: The comparison among the average ratio of varies telomeric repeats.

Organisms	FR	RR	FCR	RCR
Drosophila	1691.7	1045.8	1061.9	1707
Silkworm	1238.36	1321.72	1317.84	1233.07
Honeybee	2207.21	1090.56	1061.3	2626.88
Butterfly	1446.92	1401.27	1385.89	1575.57
Zebrafish	5419	6778.1	6745	5371.1
Rabbit	5864.5	4995.3	5033.3	5848.1
Duck	4826	4074	4107.7	4927
Whale	5215.9	4063	4086.2	5194.6
Xenopus	3608.74	4765.31	4719.19	3684.4
Cow	5797.97	3279.13	2533.21	5868.18
Camel	4835.6	4249.73	4257.07	4953.56
Zebra finch	5496.35	2919.2	2953.2	5553.14
Dog	4513.22	3723.69	3743.55	4616.91
Hen	4970.3	3310.92	3339.89	5563.33
Parrot	7785	3962.73	3965.55	5871.6
Tortoise	4333.05	3659.46	3627.52	4226.88
Dolphin	4799.02	4093.252	3951.105	4548.06
Shark	5794.2	2657.575	2667.77	5640.17
Panda	4872.19	4249.607	4244.28	4898.63
Human	6088.79	2928.126	3364.46	6160.25
Horse	4979.3	4702.47	4689.029	4995.283
Cat	5260.9	3955.93	3951.24	5145.065
C.elegan	6452	7104.39	13098.12	7020.48
Neurospora	5440.5	4371.45	4698.64	5502.05
Thermophilic fungi	6028.19	6443.13	6685.56	5473.83
Saccharomyces cerevisiae	9613.5	8125.7	5685.3	8157.16
Plasmodium falciparum	11585.6	17778.18	17978.71	11039.8
Trypanosoma brucei	10334	5317.24	5730.85	8874.5

CONCLUSION

Conclusion:

The organism belonging to similar phylum had a characteristic repeat ratio value, which shows each phylum has a signature value which mostly common to the organisms coming under that phylum. The importance of telomeric repeats in the interstitial region and the abundance in which they occur was found out which shows telomere repeat has an important role to play in the internal region of the genome too. The values and the pattern of repeat occurrence had a similarity in Forward Repeat (TTAGGG) and Reverse Complementary Repeat (CCCTAA). Which helps us in understanding the genome organization and the way sequences occur in a genome. The data obtained in this work has a lot of valuable information which can have a significant application in genome organization and making it comprehensible in some respects. In the field of synthetic biology which involves redesigning organisms for useful purposes by engineering them to have new abilities, this data can prove to be remarkable for redesigning organism’s genome and ultimately harnessing the power of nature to solve problems in medicine, manufacturing and agriculture. Then it also throws light on understanding the lifespan and ageing process of organism which has been an enigma over the years in the field of science, but the current data shows some correlation which can become a real key behind discovering and ultimately completely understanding these phenomena. All the above information is used for genome organization, synthetic biology, ageing and lifespan.

SUMMARY

Summary:

The data, which was collected had high species diversity, totally 28 species were collected which belong to 6 different phyla. The richness in diversity played a key role in differentiating between organisms and correlating the organisms in a category.

(i) Most of the organisms belong were clustered into 3 groups which are insects, vertebrates and microorganisms and among these organisms some had exceptions like *C.elegans* which are eternal in nature comes under the vertebrate group, *Neurospora crassa* deviated from the usual pattern which microorganisms showed and *Saccharomyces cerevisiae* didn't had a specific telomeric repeat but it had TTAGGG repeat was present.

(ii) Forward repeat and reverse complementary occurrence pattern were inversely proportional to each other and average ratio was pretty similar and reverse repeat and forward complementary repeat also showed this similar pattern in occurrence and in values. This might have a huge role in genome organization and might hold the key to solve mystery behind the process of ageing and understanding lifespan.

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