Review: **Ms\_BPR\_5976: Repetitive DNA and Its Roles in Diverse Facets of Biology**

REs exhibit an array of structural and evolutionary effects on genome evolution across species. Transposable elements (TEs) can be associated with genome rearrangement through various mechanisms, such as de novo TE insertion, TE insertion-mediated deletion, and homologous recombination between them.

**Epigenetic and roles of repetitive DNA in human diseases have been recognized as niche areas by researcher’s further the role of TE in gene regulation,sex chromosome**

STRs are essential for maintaining the structural integrity of genetic materials throughout the cell cycle.Further,

Numerous investigations have demonstrated a robust association between these repeats and a wide range of human disorders, including genetic abnormalities like hemophilia, neurological conditions like poly-Q diseases, and benign and malignant tumors such as endometrial, stomach, and colorectal tumors.

binding protein, which have been used to create synthetic human chromosomes (Logsdon et al., 2019)20.

sequence, gain or loss of repeat units can occur during both HR and EJ (Polleys et al., 2017)54. In addition, recombination is a primary mechanism used in restarting stalled or collapsed replication forks and in repairing gaps left behind the replication fork(Iraqui et al., 2102 )55.

Several disorders are associated with recurrent large-scale deletions and reciprocal duplications that arise via SD misalignment and NAHR in meiosis (Pang et al., 2020).

Recent high-resolution sequencing studies of germline and somatic rearrangement breakpoints have revealed molecular signatures that enable reconstruction of mutational mechanisms(Burssed et al., 2022).

~~These sequencing studies have also revealed short regions of DNA sequence homology, called ‘micro homology’. At certain germline and somatic breakpoint junctions. Although definitions of breakpoint micro homology vary with respect to the length of the homologous region, it can be defined as a series of nucleotides (<70) that are identical at the junctions of the two genomic segments that contribute to the rearrangement. Microhomology has also been reported in DNA sequences that are adjacent to, but do not overlap, breakpoint junctions.~~ MMEJ, or Microhomology-mediated end joining, is a DNA repair pathway that utilizes short stretches of microhomology to join broken DNA ends. It's often referred to as alternative end joining (aEJ) and is considered an error-prone repair mechanism. MMEJ is particularly important in cells lacking homologous recombination (HR) or during mitosis where HR and classical non-homologous end joining (NHEJ) are suppressed (Agnel Sfeir et al., 2024).

These sequencing studies have also revealed short regions of DNA sequence homology, called ‘microhomology’ at certain germline and somatic breakpoint junctions (Diego Ottaviani et al., 2014) 64. Although definitions of breakpoint microhomology vary with respect to the length of the homologous region, it can be defined as a series of nucleotides (<70) that are identical at the junctions of the two genomic segments that contribute to the rearrangement. Microhomology has also been reported in DNA sequences that are adjacent to, but do not overlap, breakpoint junctions. MMEJ, or Microhomology-mediated end joining, is a DNA repair pathway that utilizes short stretches of microhomology to join broken DNA ends. It's often referred to as alternative end joining (aEJ) and is considered an error-prone repair mechanism. MMEJ is particularly important in cells lacking homologous recombination (HR) or during mitosis where HR and classical non-homologous end joining (NHEJ) are suppressed (Agnel Sfeir et al., 2024). The figure-1 summarises the various mechanisms.

**Chapter-3.Role of Repetitive DNA in centromere organization, Histone kinetics, Epigenetics and Nuclear, cellular, and organismal functions.**

The functional conservation of the elements at the inner kinetochore interface and the faster evolution of centromeric DNA sequences have been found to be in contrast in comparative studies conducted across deep branches of eukaryotic lineages(Arora and Dumont 2024).

serve as the location for kinetochore assembly, which ensures proper chromosome inheritance; hence, chromosome loss occurs when the centromere is deleted or when essential kinetochore proteins are mutated(Sankaranarayanan et al., 2020). At the centromeres of the genomes of both plants and animals, tandem repeats, satellite DNA, and ~~transposable elements (~~TEs~~)~~ are common

putative centromere tandem repeats.Hence, tandem repeats are eventually acquired by neocentromeres ~~throughout~~ during evolution (Cappelletti et al., 2022).

Retroelements of wide classes are preferentially bound by Centromere protein A (CENP-A ) nucleosomes and the DNA proteins that interface with the inner kinetochore in all gibbon genera(Chen et al., 2015)71.

by megabase distances, which is compatible with long-range recombination (Xiao et al., 2025)81.Long terminal-repeat (LTR) class retrotransposons are commonly linked to plant centromeres; some subfamilies of this class are referred to as centrophilic; examples include *A. thaliana* and ATHILA retrotransposons

Baumgarten 2020).Tandem repeats at the functional centromere have been found to have lower

maintenance at (peri)centromeric regions.This pattern is consistent with methylation within the

Furthermore, centromeric retroelements have been implicated in facilitating chromosome evolution through the introduction of large-scale genomic rearrangements, since they are enriched at evolutionary breakpoints (Hoyt ~~O’Neill~~ et al., 2022).

The orderly and non-random arrangement of nucleosomes along DNA, which results in a repeating pattern of nucleosome sites, is known as nucleosome phasing(Sosa et al., 2013). Even though it is a modest characteristic, histone sequence preferences cause phasing on every tandem repeat, and nucleosome phasing may be advantageous for centromeres. The centromere chromatin layout would promote the acquisition and accumulation of tandem repeat arrays in a phasing model(Ma et al., 2023).

may favor the rapid evolution that tandem repetitions promote(Arora, et al., 2022). In terms of mutations, replication fork collapse or unequal crossing over can both amplify and disperse mutations that occur in any copy of a tandem repeat throughout the array(Guirouilh-Barbat, et al.,

Sex chromosomes of birds (ZZ/ZW) and mammals (XX/XY) are highly differentiated, resulting from a long evolutionary process(Chen et al., 2025)105. It is estimated, for example, that the mammalian Y chromosome has been differentiated more than 150 million years ago (Stacy Colaco and Deepak Modi. 2018)106. In turn, sex chromosomes of amphibian and fish have a more recent origin, with less than 10 million years in some species (Wen-Juan Ma and Paris Veltsos 2021).Sex chromosomes are the most dynamic entity in any genome having unique morphology, gene content, and evolution evolved multiple times and independently throughout vertebrate evolution(Tariq et al., 2016)1. Sex chromosomes and their differentiation are among the most interesting topics in evolutionary genetics. However, although evolutionary processes shaping sex chromosomes are still not completely understood the cessation or the partial restriction of recombination within the sex chromosome pair is always observed(Jay, et al.,)109. Data from phylogenetically distinct organisms show that this phenomenon is frequently associated with the accumulation of repetitive DNAs in the sex chromosomes, indicating that this feature is an inherent property of sex chromosome differentiation(Sliwinska, et al., 2016).

important models for research in vertebrates independently throughout evolution(Paps, et al., 2023).

even sex-specific selection(Rey et al., 2000). These unique features provide unique opportunities

(e.g., histone modifications)(Mirceta, et al., 2022). Figure- 5.Processes of Y-chromosome degeneration in *D.Melanogaster.*However, this is certainly not the case in mammalian sex chromosomes, as the human X chromosome contains only three fragile sites, while the Y contains none. Nonetheless, the sex-determining gene SRY lies very close to the pseudo-autosomal region (PAR), which seems to be somewhat unstable(Romanenko et al., 2020)115.

throughout the genome, implying preferential amplification(Fu et al., 2025). Why repetitive sequences preferentially amplify on sex chromosomes is an ongoing investigation, and many theories have been put forward. One of the well-accepted theories is that the accumulation of repetitive sequences on one of the pair of sex chromosomes facilitates suppression of recombination between sex chromosome homologues, therefore protecting the sexually beneficial mutations(Hartmann et al., 2021).

On the other hand, it is equally plausible that chromosome rearrangements as well as repeat accumulation and amplification may occur near the sex-determining locus as a result of suppression of recombination(Piferrer 2021). 117.Mechanisms that initiate suppression of recombination near the sex-determining locus are yet to be elucidated. A plausible explanation is that heritable epimutation, such as a change in DNA methylation and not a genetic mutation in the sex-determining locus, may be the first step in sex chromosome evolution(Bracewell, et al., 2020) 118.

In *D. miranda*, neo-sex chromosomes were formed approximately 1 million years ago (MYA) from the fusion of the ancestral Y chromosome with an autosome (Nozawa et al., 2021)120. Nearly 50% of the neo-Y sequence consists of repeats, demonstrating the rapid changes that have occurred in the evolution of sex chromosomes in just 1 million years of evolution(Li et al., 2021) 121.

and micro), telomeric sequences (including megatelomeres in chickens)(Guizard et al., 2016), amplification of multigene families (rDNA and histones)(Platt et al., 2018), taxon-specific repeats, transposable elements (LINEs and SINEs), and multicopy genes as players(Sun, et al., 2020)123.

species(Singchat et al., 2020). When it comes to sex chromosomes, the idea of “junk DNA” is also

*mansoni*, a parasitic platyhelminth, with a ZW sex determination system(Cosseau, et al., 2017).

transposons(Liehr et al., 2021). Most Drosophila Y chromosome polymorphisms are not located in protein-coding genes but in the heterochromatic regions where repetitive sequences are abundant(Brown, et al., 2020).

may be widespread(Sahu, et al., 2020).

incompatibilities between species(Rogers et al.,2014). Genome assemblies allow direct comparison of repetitive sequences between ~~these four~~ species. Chakraborty et al., 2013 **report** 15% of the *D. simulans* complex species genomes fail to align uniquely to *D. melanogaster*

tRNA tandem arrays, and gene duplications(Belyayev et al., 2022). Divergence of Y-linked genes,

Dimorphic sex chromosomes create problems. Males of many species, including Drosophila, are heterogametic, with dissimilar X and Y chromosomes(Sayres 2018).

ratio of X to autosomal expression(Cecalev, et al., 2024). Figure-7 illustrates an overview of sex

is recruited to genes on the X chromosome and modifies chromatin to increase expression(Rieder

expanded across the X chromosome in at least one Drosophila species(Barro-Trastoy, et al.,

organisms that carry them(Deegan and Engel 2019). Recombination between the X and Y

neo-X chromosome is 1 million years old(Fuller et al., 2020)142. *D. Miranda* uses MREs to attract

and enrichment for H4K16Ac in males, but this process is near-complete on the XR. 1.15(Zimmer

is strikingly conserved in Drosophila species(de Lima and Ruiz-Ruano 2022). Furthermore, the

ZZ/ZW sex system but differ in respect to the size of the sex-specific chromosome(de Bello Cioffi et al., 2012). Both W chromosomes are almost fully heterochromatic, with accumulation of repeated DNAs in their heterochromatic regions(Yano et al., 2016). Microsatellites have strongly accumulated on the large W chromosome of *L. reinhardti* but not on the reduced-size W chromosome of *T. auritus* and are therefore important players in the W chromosome expansion(de Oliveira MPB ~~Mariannah~~ et al., 2023).

and W2(da Silva et al., 2012). The unique feature of Triportheus species W chromosomes is the

evolutionary stages of sex chromosome differentiation found among its populations(de Freitas 2018)155.

chromosomes may be both the cause and the consequence of the recombination suppression(Hobza et al., 2017).

Drosophila and in some plants are often larger than the X chromosomes(Mahajan and Bachtrog 2017).

evolution(Mehrotra and Goyal 2014). The possible importance of these evolutionary dynamics for

evolution of repeating DNA arrays(Christmas et al., 2021). Since these effects are known to

recombination rates is one of the most remarkable patterns of genome structure(Catlin, et al.,

evolutionary factors at play. Research indicates the negative association, albeit the trend can be

that TE control may affect local recombination rates(Yushkova and Moskalev 2023(184).

contributes to the spread of recombination suppression(Polleys and Freudenreich et al., 2022).

large accumulation of TEs in most eukaryotes studied to date(Ma et al., 2023).

reversed, such as recombination hotspot enrichment in specific TE families in humans(Palsson et

these enlarged repetitive regions(Haley et al., 2022). The genetic and evolutionary processes

varies according to the size of the genome; in compact genomes like those of Drosophila(Saha et al.,2020) and Arabidopsis(Simon et al., 2015), the pericentromeric regions and other heterochromatin contain the highest density of TEs, whereas in genomes like those of humans(Lee et al., 2020)

also extensive variation across species and TE families (Betancourt et al., ~~2017~~ 2024) (194). For example, many plant species contain centromere-specific LTR retrotransposons interspersed with other centromeric satellite DNA(Teresi et al., ~~2017~~ 2022), although some TEs are enriched in euchromatic(Gu et al., 2016), gene-dense recombining regions(Daron et al., 2014)(197).TEs show positive correlations with recombination rates as seen in humans, where contrasting evidence depending on TE type; L1 LINEs are negatively correlated with recombination rate(Minami et al., 2025), while Alu elements tend to accumulate in gene-rich, highly recombining regions(Lee 2022).

but low abundance in euchromatin(Iwasaki et al., 2020). TE families in the genome are frequently

association between TEs and recombination(Cutter and Jovelin 2015).

recombination, is one way that selection can work against TEs(Allison et al., 2023)205.

of the inversions between humans and chimpanzees(Tyler et al., 2017).

(ii) Selection to prevent disruption of genes-Selection can also affect genes negatively, which results in alterations in the distribution of TE(Cutter and Jovelin 2017).

located immediately upstream of genes in many species(Brazier et al., 2024).

small(Zhang, et al., 2019). Retrotransposons, which do not excise, frequently have a larger

marks linked to open chromatin are strongly enriched in recombination hotspots(Liu et al., 2022), whereas densities of DNA methylation and repressive chromatin marks linked to the silencing of TEs and other repeats are frequently negatively connected with recombination rates with the exception of *C. elegans*(Choi et al., 2020).

**Chapter-6.Role of TE in genome regulation, genome stability, instability, and disease evolution and diversity.**

DNA)(Gilbert et al., 2018). However, the genome is uniquely organized into gene clusters

metabolites(Cary et al., 2018). With patterns in line with the ancestral action of repeat-induced

exhibiting polarity towards telomere make up the second category(Lustig 2023). Each centromere

examples of TEs found in filamentous fungi(Mei Han et al., 2023). TEs aid in the reorganization and non-allelic genomic rearrangement of filamentous fungus. Additionally, ectopic recombination may be encouraged by these transposable elements as evidenced by the LINE element and gypsy related in *A. flavus*(Donnart, et al., 2017).

ancestral transposition(Yoth et al., 2022). Neurospora centromeres and satellite sequences have an increased A+T bias as a result of transitions on either strand of the repeat(Smith et al., 2012).

there were notable differences in their duration, distribution, and recurrence(Nierman et al., 2015).

were noticeably rare in Lepidoptera but typically prevalent in most insect groups(Cong, et al.,

areas, which could have wide-ranging effects on the evolution of phenotypes(Kaessmann et al., 2010). Through the epigenetic suppression of repetitive sequences (e.g., heterochromatin formation), genomes inhibit RE activity(Allshire and Madhani2017).

genomic loci can have an immediate impact on the expression of nearby genes(Lee and Karpen 2017). Non-model insects tend to have larger, more repeat-rich genomes than the model species that seeded much of our present knowledge of RE dynamics(Yuan et al., 2024).

neurological conditions (including poly Q diseases), and genetic abnormalities (like hemophilia)( Siwach et al., 2008).

such chromosome segregation, genome organization, and chromosome end protection(Zhou, et al., 2022)237.

candidates for promoting gene adaptation(Jangam et al., 2017). Additionally, because of their mobility, TEs can translocate close to the genes they target and, depending on the situation, regulate the expression levels of those genes, demonstrating how TEs can have a direct or indirect impact on the genome(Liu and Zhao 2023).

codons(Bernabéu-Herrero et al., 2024), changing splicing patterns(Anna et al., 2018), or disrupting the reading frame when they insert into protein-coding areas(Lee et al., 2021). These insertional mutations can lead to phenotypic variety and genetic variants. Copy number variations may arise from the duplication of TEs and nearby genomic sequences as a result of this process(Bai, et al., 2016). Additionally, processed pseudogenes—gene copies that are not functional—can result from retrotransposition(Troskie et al., 2021).

and 4000 full-length L1 elements, making up roughly 17% of the total genome(Liao et al., 2023).

the TE transposition, which is a crucial component in gene expression variation. First,through genome's alterations properties for their expression, through cis-regulatory sequences make them potential regulators of host gene expression(Gebrie 2023). Secondly, regulatory RNAs(miRNAs and long noncoding RNAs lncRNAs can be encoded by TEs(Cho et al., 2018)251.

including histone modifications and DNA methylation(Song and Cao. 2017). By blocking

alter gene expression, TEs can operate as transcriptional starting sites(Li et al., 2014). Furthermore, TEs have the ability to be converted into siRNAs, which can direct RNA-induced gene silencing complex into in germline and somatic cells, transposable elements can function as insertional mutagens(Panigrahi and O’Malley 2021).

Alu, SVA, and HERV-K(Belancio et al., 2009). Satellite DNA, which can be further classified

new traits(Gymrek, 2017). STRs might be essential for maintaining the structural integrity of genetic materials throughout the cell cycle(Kousholt, et al., 2012). Because TRs are repeated, DNA

DNA replication(Edenberg, et al., 2014). Specialized TRs called telomeres, which are found at the

repeats(Kono et al., 2018). Variations, including point mutations or insertions/deletions, frequently

distinct roles or exhibit varying patterns of expression, may result from these alterations(Ezoe , et

STRs.numerous disorders, such as cancer(Panzer et al., 1995), various ataxias (Adam et al., 2025), and fragile X syndrome(Hall and Berry-Kravis. 2018).

other species groups(Thomas et al., 2018). Used as a source of DNA markers or chromosomal probes, retroelements have utility in crop breeding and tracking chromosomes in hybrids and translocation lines(András et al., 2023; Pradeep et al.,2022).

20 families making up 20% of the total(Qing et al., 2019). Retroelements represent the major component, with Ty3/Gypsy elements representing more than 40% of all the DNA, nearly three times more abundant than Ty1/Copia elements(Alexander AG et al., 2022)266. DNA transposons are about 5% of the total, while tandemly repeated; satellite DNA sequences fit into 55 families and represent about 2% of the genome. The Avena species are monophyletic, but both bioinformatic comparisons of repeats in the different genomes(Leonardo et al., 2016), and *in situ* hybridization to metaphase chromosomes from the hexaploid species, shows that some repeat families are specific to individual genomes, or the A and D genomes together(Sean et al., 2020).

used widely in bread wheat(Paulina et al., 2022). It is clear that repeat amplification and turnover

turnover events, have led to the rapid evolution seen in the hexaploids(Qiang et al.,2024).

agronomic traits(~~Brankica~~ Mravinac and Miroslav Plohl 2010). Many evolutionary models suggest that polyploid formation should be associated with a selective advantage, favouring parental genome divergence(Park et al., 2022).

rearrangements in plants(Yves et al., 2021). Beta and Patellifolia as examples of plant taxa that

chromosomes(Itay and Martin 2021). The genera Beta and Patellifolia comprise at least eleven

of domestication(Galewski and McGrath 2020). This has led to very low genetic diversity and a

quinoa (Heitkam et al., 2020); approx. 51% in spinach(Cai et al., 2021284). The abundance of a

maintenance of specific genomic regions.The satDNAs contribute to the wild beets

evolution(~~Rafael and~~ Almeida BRR et al., 2023). Concerted evolution is reported in species

chimpanzees) and humans have a 6-kb repeat unit(Lia et al., 1999). Subsequently, it had been

Repeats is under Concerted evolution(Martí et al., 2021) and Repetitive elements determine

between similar sequences, in which exchange of flanking DNA is not involved(Tóth et

in close proximity, this organization should allow for efficient homogenization(Otto et al.,

non-homologous chromosomes(Birchler and Presting ~~2022~~ 2012). Thus, to understand the

undergo concerted evolution(Li, et al., 2016). Conversely, if there is no sequence

Phylogeny of the Genus Carthamus L(Sasanuma, et al., 2008)297. In addition, some Alu

longer efficient and that genes therefore evolve independently (Hoffmann 2021)300.

of magnitude, have been hotly debated since before the advent of genome sequencing(Blommaert,

timescale(Stelzer et al., 2011)302. Even though the genome sizes of these species are at the low end of the metazoan spectrum, their genomes contain substantial amounts of repetitive elements(Mohl, et al., 2025).*Brachionus plicatilis*

polyploidy, while smaller changes are caused by repetitive element acquisition and loss(Nie et

transposons(Yang et al 2013, Kapusta, et al., 2017).Across the Brachionus genus and the *B.*

the host's genome, and spread vertically to the host's progeny(Weiss. Et al., 2013). As a result,

microevolutionary dynamics(Hayward et al., 2015). By employing a large-scale phylogenomic method with ~~endogenous retroviruses (~~ERVs~~)~~, recent technology advancements have made it possible to infer broad trends in retroviral diversity, evolution, and host–virus relationships(Rivas-Carrillo et al., 2018).

through the host lineage and serve as a record of previous host viral interactions(Greenwood, et al., 2017).

research into the evolution of host strategies to limit pathogens(Ingusci, et al., 2024).

Genome divergence by mobile elements activity and recombination is a continuous process that plays a key role in the evolution of species(Savannah J Klein et al., 2018)316.

reproductive isolation(Changcheng et al., 2019). Several researchers have investigated this

diversification are the leading driver of long terminal repeat (LTR) dynamics in Lepidoptera(Wu and Lu. 2019).

Drosophila(Wang, et al., 2025). The question is Why Does the TE load is so different across

different even between closely related species(Nater, et al.,2015). Unlike the protein-coding genes

different even between closely related species(Nater, et al.,2015). Unlike the protein-coding genes

constraints because TEs are in general deleterious and selected against in most species(Robinson et al., 2022).

pathway also suppress TE activities (Mbichi, et al., 2020)325. Therefore, the vast difference in TE

by vectors(Zhang, et al., 2023)326. In eukaryotes, TEs are repressed either by suppressing TE

between the two species(Blumenstiel. et al., 2025)327. TEs are important for providing raw materials of the regulatory elements and proteomes for the hosts. TEs could be domesticated as promotors or enhancers to regulate gene expression(Todd et al., 2019).

heat-shocked flies (Chen et al., 2018).Cumulatively, all these studies indicate that the beneficial

small- or medium sized genomes(Pellicer et al., 2018). In angiosperms, large sized genomes have been studied especially in monocotyledonous species such as maize (2.3 gigabase pairs) and barley (5.1 gigabase pairs). ~~332~~Mascagni, et al., 2017

differentiation(Kazancev et al., 2024). The extent of interspecific repetitive DNA variation related

Helianthus species was affected by the annual or perennial habit of that species(Ventimiglia, et al.,

2.3 times more represented than those belonging to the Copia superfamily(Mark et al., 2009).

evolution(Guillaume Bourque, et al., 2018)~~336~~ 312. Further analyses of Helianthus species have

evolution(Guillaume Bourque, et al., 2018)312. Further analyses of Helianthus species have

Helianthus species previously provided(Natali et al., 1993). Southern blot hybridization analyses

lineage(Hloušková et al., 2019). Such huge expansion is similar to others reported in different

physiological diversity(Brusatte et al., 2015). Despite the vast phenotypic diversity of birds, birds have an extremely compact genome with a small amount of repetitive DNA (4–10%)compared to other vertebrates, birds have the lowest average SSR density with very little variance. These genome characteristics are thought to be related to the selective pressure from flight adaptation that required a high rate of oxidative metabolism(Kretschmer, et al., 2018).Due to their high levels

differentiation of sex chromosomes and evolution of a karyotype(Wright et al.,2014). Studying the

**2.24%(**Cioffi et al., 2012**).** Imperfect SSRs were caused by substitutions, insertions, and deletions of perfect SSRs, and the higher abundance of I-SSRs is common in the genomes of different lineages, including beetles, Euarchontoglires, and in human genome(result of disrupting mutation

relative difficulty of strand separation for GC compared to AT(Manee, et al.,2020)336. The relatively high GC content of P-SSRs in the coding regions may affect the genome structure, methylation pattern, and gene expression(Song, et al., 2021).

inconsistent patterns with shorter P-SSRs(Trigos et al., 2019). Thus, the distribution of P-SSRs in

genome in somatic cells(Kang et al., 2016). **Report** that 43 Mb (13%) of genome sequence is eliminated in A. suum somatic cells(Zagoskin et al., 2021).

lineages(Kloc et al., 2022). During the Ascaris diminution process, chromosomes are broken, and

Tmesipteris (Psilotaceae) is a relatively understudied small genus made up of 15 species, 12 of which are mainly epiphytic ferns occurring in Oceania and several Pacific Islands(Perrie, et al., 2023).

these estimates by 7%(Fernández et al., 2024). Overall, this exceptional discovery extends the

Liliales(Pellicer et al., 2014).Therefore, the prospect of identifying larger monocot genomes within

consequence of the numerous rounds of whole genome multiplication (WGM)(Pellicer, et al.,

expression(Li et al., 2019). *Tmesipteris oblanceolata* subsp. linearifolia has been reported, like *P.*

*oblanceolata* were octoploid (i.e., 2n = 8x = 416)( Fernández et al., 2023).Its massive genome is

hallmarks(Pascarella et al., 2024). Centromeres and cancer-associated genes are enriched for retroelements that may act as recombination hotspots(Savocco and Piazza 2021).

**link between retroelement recombination and genomic instability in neurodegeneration(**Mujoo, et al., 2017**).**

events associated with cancer and other genetic disorders (Gu et al.,~~2015~~ 2016). Reports of somatic

higher proportion, DNA repetitive sequences(Wu et al., 2021). Recently, published results of genome sequences from 48 bird species showed that their amount of repetitive sequences is much smaller than other groups of tetrapods, corresponding to 4±10%, while in mammals the percentage of these sequences can reach up to 52% of the genome(Castro et al.,2017).

order, such as woodpeckers, show a relatively higher amount of these sequences(de Oliveira et

macrochromosomes(Manthey et al., 2018). However, some sequences produced patterns of

important components(Mota Souza et al., 2025). In addition, karyotype analyses showed that

karyotype(Santos de Souza et al., 2020). Repetitive sequences play an important role in the

with the Y(Sember et al., 2018). Thus, taking into account that the suppression of recombination

extra-long bodies(Ahmad et al., 2021). Snakes constitute two major recognized groups at the

phenotypic-level evolution(Viana, et al., 2020). Similar to other eukaryotic genomes, large proportions of snake genomes contain repetitive DNA(25 to 73%,), including transposable elements (TEs) and satellite repeats(Shaney et al., 2014).

(23-fold greater levels of TE-related transcripts) and python(Chen et al., 2020). Snake genomes

*cerastes* and *Coniophanes fissiden*(Chen et al.,2020). Low abundance of CR1 and LTRs, is

genus and within allopatric populations of the same species(Augstenová, et al., 2018). In addition,

**Chapter-10.Prokaryotic repetitive DNA and their role in Biochemistry and metabolism and evolution, virulence and pathogenicity.**

present in their genomes(Ayalew et al.,2024). Short, basic DNA repeats vary in frequency among a wide variety of bacteria with various genomes(Subirana and Messeguer 2020). All microbial genomes contain levels of DNA repetitive sequences that are greater than would be predicted for a random distribution of bases(Zhao et al., 2010).

characterized bacterial genomes(Dunne et al.,2017). Majority of bacterial genomes are round and

metabolism(Li et al., 2024). Negative selection is less likely to affect repetitions in bacteria(Zhou et al.,2014). As seen in mycoplasma, there are notable variations in the quantities of simple DNA repeats even among closely related species(Xiao et al.,2015). Several basic DNA repeats are overrepresented in microbial whole genome sequences, according to computer-based analysis. Thousands of tandem simple sequences

repeats contain transposable genetic elements in addition to basic microsatellites(Brazda et al.,2020).

according to analyses of these repeats(Marisch 2013).

al., 2015). Bacterial Tn7-like elements are a well-known example(Joseph. 2019). Representatives

protozoans(Gaurav et al., 2017). Genomic rearrangement might be responsible for variation in the number of transposable elements in different lineages.

investigations of their biological impacts and functions(Pourrajab and Hekmatimoghaddam 2021).

bacterial strains, enabling the identification of those that may be harmful(Al-Obaidi, 2018). DNA repeats create right-handed helical B-form structures essential for basic biological functions that store, duplicate, and transcribe genetic information(Bansal, et al., 2022).

that repeating DNA sequences adopt as well as their thermodynamic stabilities(Václav et al., 2020). It has long been suggested that these kinds of non-B-DNA patterns are biologically significant for recombination, replication, and controlling gene expression(Nigatu, et al.,2023). Additionally, a number of investigations have shown how crucial non-B-DNA structures are to the control of bacterial genes. Cruciforms expandable repeats, for instance, have been demonstrated

genes(Porubiaková, et al.,2023). A wide variety of basic repeats can create three-stranded triplex structures, and numerous forms of these structures have been described(Casas-Delucchi, et al., 2022). As shown in some Enterobacteria and Cyanobacteria species, genomic loci with triplex-forming motifs are far more likely to experience genome rearrangement than control sites(Holder et al., 2015). The ITxF database contains genomes and plasmids for intra-strand triplex motif variation(ngdc.cncb.ac.cn/).

transcription of DNA mononucleotide repeats inhibits replication(Holder et al.,2015). These

repeats(Merrikh 2012). Understanding how DNA repair systems affect the genetic stability of

organisms through their effects on DNA metabolism(Sinha 2020). The evolution of genomic

changes(McCann et al.,2020). Simple DNA repeats in bacteria, however, are obviously hypermutable loci linked to reversible variations in the ~~amount~~ number of repetitions(Waters, et al., 2025).

that allow environmental adaptation(López-López et al., 2021). Variation in the overall size of the

The evolution of parasitism and symbiosis is usually linked to genome reduction(Jackson 2015).

sequenced(Raffaele et al., 2012). There is a noticeable variation in the repetition and gene load of

pathogens from various lineages, repeat-rich areas varied in size and location(Torres 2020). The

influences the formation of virulence(Newman 2020). Numerous oomycetes and fungal species

develops or the host population declines(Mondal et al., 2020). The genomes of a number of

mechanisms(Oliva et al., 2015).Human stomach infections caused by *Helicobacter pylori* can result in chronic gastritis, which can lead to peptic ulcer disease and gastric cancer if treatment is not received(Victor E Reyes et al., 2023).

inflammatory mucosa(Matos et al., 2021). Through the blood group antigen-binding adhesin BabA, *H. pylori* contacts the ABO/Leb receptors, and through the sialic acid-binding adhesion SabA, it binds the sLex/sLea receptors(Bugaytsova et al., 2017). Because the glycosylation pattern

thymine dinucleotide (CT) repeat tract in the 5'-end of the sabA coding sequence (CDS)( Doohan,

sabA(Cheng-Yen et al., 2012). The length affects RNA polymerase binding, which in turn

UP-like regions(Åberg et al.,2024). These alterations need to be accompanied by changes in BabA

annum.The parasite has an interchangeable two-stage life cycle consisting of an infective cyst form

outcomes. 90% of infected individuals remain asymptomatic, while only 10% develop symptoms of invasive amoebiasis(Chou 2025).

with disease outcome, motivates a substantial area of Entamoeba research(Das et al.,2014). To

correspond to species-level differences(Yanagawa, et al., 2025). Some peculiar aspects of the

copies—roughly ten times the human genome—tRNA genes are remarkably prevalent(Sardar et

five different types of tRNA acceptors(Gilchrist 2016). Short tandemly repeated sequences

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