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

**References**

1. Biscotti MA, Olmo E, Heslop-Harrison JS. Repetitive DNA in eukaryotic genomes. Chromosom. Res. 2015;23:415–420. doi: 10.1007/s10577-015-9499-z.
2. Xingyu Liao, Wufei Zhu, Juexiao Zhou, Haoyang Li, Xiaopeng Xu, Bin Zhang , Xin Gao. Repetitive DNA sequence detection and its role in the human genome. Commun Biol. 2023 Sep 19;6:954. doi: 10.1038/s42003-023-05322-y.
3. Mehrotra S, Goyal V. Repetitive Sequences in Plant Nuclear DNA: Types, Distribution, Evolution and Function. Genom. Proteom. Bioinform. 2014;12:164–171. doi: 10.1016/j.gpb.2014.07.003.
4. Hannan AJ. Tandem repeats mediating genetic plasticity in health and disease. Nat. Rev. Genet. 2018;19:286–298. doi: 10.1038/nrg.2017.115.
5. Shah NM, et al. Pan-cancer analysis identifies tumor-specific antigens derived from transposable elements. Nat. Genet. 2023;55:631–639. doi: 10.1038/s41588-023-01349-3.
6. Jurka J, Kapitonov VV, Kohany O, Jurka MV. Repetitive sequences in complex genomes: structure and evolution. Annu. Rev. Genom. Hum. Genet. 2007;8:241–259. doi:10.1146/annurev.genom.8.080706.092416.
7. Bernabe IB, et al. Genome-wide contribution of common short-tandem repeats to Parkinson’s disease genetic risk. Brain. 2023;146:65–74. doi: 10.1093/brain/awac301.
8. Alexander RP, Fang G, Rozowsky J, Snyder M, Gerstein MB. Annotating non-coding regions of the genome. Nat. Rev. Genet. 2010;11:559–571. doi: 10.1038/nrg2814.
9. Biemont C, Vieira C. What transposable elements tell us about genome organization and evolution: the case of Drosophila. Cytogenet Genome Res. 2005;110(1-4):25-34. doi: 10.1159/000084935.
10. Adele L Schmidt, Lucy M Anderson. Repetitive DNA elements as mediators of genomic change in response to environmental cues. Review Biol Rev Camb Philos Soc. 2006 Nov;81(4):531-43. doi: 10.1017/S146479310600710X.
11. Roman Hobza, Zdenek Kubat, Radim Cegan, Wojciech Jesionek, Boris Vyskot, Eduard Kejnovsky. Impact of repetitive DNA on sex chromosome evolution in plants. Chromosome Res. 2015 Sep;23(3):561-70. doi: 10.1007/s10577-015-9496-2.
12. Guillaume Bourque.Transposable elements in gene regulation and in the evolution of vertebrate genomes. Curr Opin Genet Dev. 2009 Dec;19(6): 607-12.doi: 10.1016/j.gde.2009.10.013.
13. Liehr, T. Repetitive elements in humans. Int. J. Mol. Sci. 22, 2072 (2021).
14. Youssef, N., Budd, A. & Bielawski, J. P. Introduction to Genome Biology and Diversity. *Methods Mol. Biol.* 1910, 3–31 (2019).
15. Hou, Z., Romero, R., Uddin, M., Than, N. G. & Wildman, D. E. Adaptive history of single copy genes highly expressed in the term human placenta. Genomics 93, 33–41 (2009).
16. Pavlicek A., Kapitonov V.V., & Jurka J. Human Repetitive DNA[M]. Encyclopedic Reference of Genomics and Proteomics in Molecular Medicine. (Springer, Berlin, Heidelberg, 2005).
17. Kojima, K. K. Structural and sequence diversity of eukaryotic transposable elements. *Genes Genet. Syst.* 94, 233–252 (2020).
18. Genovese, L. M. et al. A Census of Tandemly Repeated Polymorphic Loci in Genic Regions Through the Comparative Integration of Human Genome Assemblies. *Front. Genet.* 9, 155 (2018).
19. Richard, G. F., Kerrest, A. & Dujon, B. Comparative genomics and molecular dynamics of DNA repeats in eukaryotes. *Microbiol. Mol. Biol. Rev.* 72, 686–727 (2008).
20. Glennis A Logsdon, Craig W Gambogi, Mikhail A Liskovykh, Evelyne J Barrey, Vladimir Larionov, Karen H Miga, Patrick Heun, Ben E Black.Human Artificial Chromosomes that Bypass Centromeric DNA.Cell. 2019 Jul 25;178(3):624-639.e19. doi: 10.1016/j.cell.2019.06.006.
21. Sawaya, S. et al. Microsatellite tandem repeats are abundant in human promoters and are associated with regulatory elements. *PLoS ONE* 8, e54710 (2013).
22. Richard, G. F. & Paques, F. Mini- and microsatellite expansions: the recombination connection. *EMBO Rep.* 1, 122–126 (2000).
23. Li, H. Identifying centromeric satellites with dna-brnn. Bioinformatics 35, 4408–4410 (2019).
24. Alaguponniah, S. et al. Finding of novel telomeric repeats and their distribution in the human genome. *Genomics* 112, 3565–3570 (2020).
25. Riethman, H. Human subtelomeric copy number variations. *Cytogenet. Genome Res.* 123, 244–252 (2008).
26. Han, Y. & Wessler, S. R. MITE-Hunter: a program for discovering miniature inverted-repeat transposable elements from genomic sequences. Nucleic Acids Res. 38, e199 (2010).
27. Kojima, K. K. & Jurka, J. Crypton transposons: identification of new diverse families and ancient domestication events. Mobile DNA 2, 12 (2011).
28. Krupovic, M. & Koonin, E. V. Polintons: a hotbed of eukaryotic virus, transposon and plasmid evolution. Nat. Rev. Microbiol. 13, 105–115 (2015).
29. Lee, T. F. et al. RNA polymerase V-dependent small RNAs in Arabidopsis originate from small, intergenic loci including most SINE repeats. Epigenetics 7, 781–795 (2012).
30. Munoz-Lopez, M. & Garcla-Perez, J. L. DNA transposons: nature and applications in genomics. Curr. Genom. 11, 115–128 (2010).
31. Kojima, K. K. Human transposable elements in Repbase: genomic footprints from fish to humans. Mobile DNA 9, 2 (2018).
32. Pace, J. K. & Feschotte, C. The evolutionary history of human DNA transposons: evidence for intense activity in the primate lineage. Genome Res. 17, 422–432 (2007).
33. David, J. F. Retrotransposons. Curr. Biol. 22, R432–R437 (2012).
34. Muszewska, A., Hoffman-Sommer, M. & Grynberg, M. LTR retrotransposons in fungi. PLoS ONE 6, e29425 (2011).
35. Thompson, P. J., Macfarlan, T. S. & Lorincz, M. C. Long Terminal Repeats: From Parasitic Elements to Building Blocks of the Transcriptional Regulatory Repertoire. Mol. Cell 62, 766–76 (2016).
36. Ardeljan, D., Taylor, M. S., Ting, D. T. & Burns, K. H. The Human Long Interspersed Element-1 Retrotransposon: An Emerging Biomarker of Neoplasia. Clin. Chem. 63, 816–822 (2017).
37. Kramerov, D. A. & Vassetzky, N. S. Origin and evolution of SINEs in eukaryotic genomes. Heredity 107, 487–495 (2011).
38. Han, G. et al. Diversity of short interspersed nuclear elements (SINEs) in lepidopteran insects and evidence of horizontal SINE transfer between baculovirus and lepidopteran hosts. BMC Genom. 22, 226 (2021).
39. Malicki, M., Spaller, T., Winckler, T. & Hammann, C. DIRS retrotransposons amplify via linear, single-stranded cDNA intermediates. Nucleic Acids Res. 48, 4230–4243 (2020).
40. Wiegand, S. et al. The Dictyostelium discoideum RNA-dependent RNA polymerase RrpC silences the centromeric retrotransposon DIRS-1 post-transcriptionally and is required for the spreading of RNA silencing signals. Nucleic Acids Res. 42, 3330–3345 (2014).
41. Wang, Y., Gallagher-Jones, M., Suśac, L., Song, H. & Feigon, J. A structurally conserved human and Tetrahymena telomerase catalytic core. *Proc. Natl Acad. Sci. USA.* 117, 31078–31087 (2020).
42. Han, J. S. Non-long terminal repeat (non-LTR) retrotransposons: mechanisms, recent developments, and unanswered questions. Mobile DNA 1, 15 (2010).
43. Biscotti, M. A., Olmo, E. & Heslop-Harrison, J. S. (2015). Repetitive DNA in eukaryotic genomes. Chromosom. Res. 23, 415–420.
44. Erica, J., Polleys. & Nealia, C.M. (2017). Role of recombination and replication fork restart in repeat instability, DNA Repair, Volume 56, Pages 156-165, ISSN 1568-7864.<https://doi.org/10.1016/j.dnarep.2017.06.018>.
45. Ait Saada, A., Lambert, S. A. E., & Carr, A. M. (2018). Preserving replication fork integrity and competence via the homologous recombination pathway. DNA repair, 71, 135–147. <https://doi.org/10.1016/j.dnarep.2018.08.017>.
46. Molecular Biology of the Cell. 7th edition.Alberts B, Johnson A, Lewis J, et al. New York: Garland Science; 2024.
47. Casas-Delucchi, C.S., Daza-Martin, M. & Williams, S.L.(2022). The mechanism of replication stalling and recovery within repetitive DNA. Nat Commun 13, 3953. <https://doi.org/10.1038/s41467-022-31657-x>.
48. Petruska J, Hartenstine MJ, Goodman MF. Analysis of strand slippage in DNA polymerase expansions of CAG/CTG triplet repeats associated with neurodegenerative disease". J. Biol. Chem. 273 (9): 5204–10.1998 doi:10.1074/jbc.273.9.5204. PMID 9478975.
49. Kunkel, T. A. (1990). Misalignment-mediated DNA synthesis errors. Biochemistry 29. <https://doi.org/10.1021/bi00487a001>.
50. Khristich, A. N., & Mirkin, S. M. (2020). On the wrong DNA track: Molecular mechanisms of repeat-mediated genome instability. The Journal of biological chemistry, 295(13), 4134–4170.
51. Samadashwily, G. M., Raca, G., & Mirkin, S. M. (1997). Trinucleotide repeats affect DNA replication in vivo. Nature genetics, 17(3), 298–304. <https://doi.org/10.1038/ng1197-298>
52. Brown, R. E., & Freudenreich, C. H. (2021). Structure-forming repeats and their impact on genome stability. Current opinion in genetics & development, 67, 41–51. <https://doi.org/10.1016/j.gde.2020.10.006>.
53. Neil, A. J., Kim, J.C. & Mirkin, S.M. (2017). Precarious maintenance of simple DNA repeats in eukaryotes. BioEssays, 39:1–10.
54. Kim, J.C., Harris, S.T., Dinter, T., Shah, K.A. & Mirkin, S.M. (2017).The role of break-induced replication in large scale expansions of (CAG)n/(CTG)n repeats. Nat Struct Mol Biol, 24:55–60.
55. Polleys, E. J., House, N. C. M., & Freudenreich, C. H. (2017). Role of recombination and replication fork restart in repeat instability. DNA repair, 56, 156–165. https://doi.org/10.1016/j.dnarep.2017.06.018.
56. Ismail Iraqui,Yasmina Chekkal ,Nada Jmari ,Violena Pietrobon,Karine Fréon,Audrey Costes,Sarah A. E. Lambert Recovery of Arrested Replication Forks by Homologous Recombination Is Error-Prone. (2012)PLoS Genet 8(10): e1002976. <https://doi.org/10.1371/journal.pgen.1002976>.
57. Malkova, A. & Haber, J.E. (2012). Mutations arising during repair of chromosome breaks. Annu Rev Genet, 46:455-73.
58. Richard, G.F. & Paques, F. (2000). Mini- and microsatellite expansions: the recombination connection. EMBO Rep, 1(2):122-6.
59. Matthew M Parks, Charles E Lawrence & Benjamin J Raphael. (2015)Detecting non-allelic homologous recombination from high-throughput sequencing data.Genome Biology volume 16, Article number: 72.
60. Seoyoung Kim,Shaun E. Peterson,Maria Jasin,Scott Keeney.Mechanisms of germ line genome instability.Seminars in Cell & Developmental Biology

Volume 54, June 2016, Pages 177-187

62.Hui Pang, Xiaowei Yu, Young Mi Kim, Xianfu Wang, Jeremy K Jinkins, Jianing Yin, Shibo Li, Hongcang Gu.Disorders Associated With Diverse, Recurrent Deletions and Duplications at 1q21.1.Front Genet. 2020 Jun 23:11:577. doi: 10.3389/fgene.2020.00577. eCollection 2020.

63.Bruna Burssed, Malú Zamariolli, Fernanda Teixeira Bellucco & Maria Isabel Melaragno.Mechanisms of structural chromosomal rearrangement formation

Molecular Cytogenetics volume 15, Article number: 23 (2022).

64. Agnel Sfeir, Marcel Tijsterman, and Mitch McVey.Microhomology-Mediated

End-Joining Chronicles:Tracing the EvolutionaryFootprints of Genome

Protection Annu. Rev. Cell Dev. Biol. 2024. 40:195–218.

65. Diego Ottaviani,Magdalena LeCain, Denise Sheer.The role of microhomology in genomic structural variation.Trends in Genetics.Volume 30, Issue 3, March 2014, Pages 85-94.

66. Arora, U. P., & Dumont, B. L. (2024). Molecular evolution of the mammalian kinetochore complex. bioRxiv : the preprint server for biology, 2024.06.27.600994.

<https://doi.org/10.1101/2024.06.27.600994>.

67. Sundar Ram Sankaranarayanan, Giuseppe Ianiri , Marco A Coelho, Md Hashim Reza , Bhagya C Thimmappa , Promit Ganguly , Rakesh Netha Vadnala , Sheng Sun , Rahul Siddharthan , Christian Tellgren-Roth , Thomas L Dawson Jnr , Joseph Heitman, Kaustuv Sanyal. Loss of centromere function drives karyotype evolution in closely related Malassezia species Elife

. 2020 Jan 20:9:e53944. doi: 10.7554/eLife.53944.68.

68. Miroslav Plohl, Nevenka Meštrović, Brankica Mravinac.Centromere identity from the DNA point of view.Chromosoma. 2014 Aug;123(4):313-25. doi: 10.1007/s00412-014-0462-0. Epub 2014 Apr 25.

69. Neumann, P., Navrátilová, A., Schroeder-Reiter, E., Koblížková, A., Steinbauerová, V., Chocholová, E., Novák, P., Wanner, G., & Macas, J. (2012). Stretching the rules: monocentric chromosomes with multiple centromere domains. *PLoS genetics*, *8*(6), e1002777.

 <https://doi.org/10.1371/journal.pgen.1002777>.

70.Cappelletti, E., Piras, F. M., Sola, L., Santagostino, M., Abdelgadir, W. A., Raimondi, E., Lescai, F., Nergadze, S. G., & Giulotto, E. (2022). Robertsonian Fusion and Centromere Repositioning Contributed to the Formation of Satellite-free Centromeres During the Evolution of Zebras. Molecular biology and evolution, 39(8), msac162. <https://doi.org/10.1093/molbev/msac162>.

72.Okhovat, M., Nevonen, K. A., Davis, B. A., Michener, P., Ward, S., Milhaven, M., Harshman, L., Sohota, A., Fernandes, J. D., Salama, S. R., O'Neill, R. J., Ahituv, N., Veeramah, K. R., & Carbone, L. (2020). Co-option of the lineage-specific LAVA retrotransposon in the gibbon genome. Proceedings of the National Academy of Sciences of the United States of America, 117(32), 19328–19338.

 <https://doi.org/10.1073/pnas.2006038117>.

73. Chen, C. C., Bowers, S., Lipinszki, Z., Palladino, J., Trusiak, S., Bettini, E., Rosin, L., Przewloka, M. R., Glover, D. M., O'Neill, R. J., & Mellone, B. G. (2015). Establishment of Centromeric Chromatin by the CENP-A Assembly Factor CAL1 Requires FACT-Mediated Transcription. Developmental cell, 34(1), 73–84. <https://doi.org/10.1016/j.devcel.2015.05.012>

72. Chabot, B. J., Sun, R., Amjad, A., Hoyt, S. J., Ouyang, L., Courret, C., Drennan, R., Leo, L., Larracuente, A. M., Core, L. J., O'Neill, R. J., & Mellone, B. G. (2024). Transcription of a centromere-enriched retroelement and local retention of its RNA are significant features of the CENP-A chromatin landscape. Genome biology, 25(1), 295. <https://doi.org/10.1186/s13059-024-03433-1>.

73. Shu-Fen Li, Ting Su, Guang-Qian Cheng, Bing-Xiao Wang, Xu Li , Chuan-Liang Deng, Wu-Jun Gao.Chromosome Evolution in Connection with Repetitive Sequences and Epigenetics in Plants.Genes (Basel). 2017 Oct 24;8(10):290. doi: 10.3390/genes8100290.

74. Ravi, M., Shibata, F., Ramahi, J. S., Nagaki, K., Chen, C., Murata, M., & Chan, S. W. (2011). Meiosis-specific loading of the centromere-specific histone CENH3 in Arabidopsis thaliana. PLoS genetics, 7(6), e1002121. <https://doi.org/10.1371/journal.pgen.1002121>.

75. Yuan, J., Guo, X., Hu, J., Lv, Z., & Han, F. (2015). Characterization of two CENH3 genes and their roles in wheat evolution. The New phytologist, 206(2), 839–851.

<https://doi.org/10.1111/nph.13235>.

76. Kuo, Y. T., Schubert, V., Marques, A., Schubert, I., & Houben, A. (2024). Centromere diversity: How different repeat-based holocentromeres may have evolved. BioEssays: news and reviews in molecular, cellular and developmental biology, 46(6), e2400013.

<https://doi.org/10.1002/bies.202400013>.

77. Naish, M., & Henderson, I. R. (2024). The structure, function, and evolution of plant centromeres. Genome research, 34(2), 161–178.

 <https://doi.org/10.1101/gr.278409.123>.

78. Thakur, J., Packiaraj, J., & Henikoff, S. (2021). Sequence, Chromatin and Evolution of Satellite DNA. International journal of molecular sciences, 22(9), 4309.

<https://doi.org/10.3390/ijms22094309>.

79.Wlodzimierz, P., Rabanal, F. A., Burns, R., Naish, M., Primetis, E., Scott, A., Mandáková, T., Gorringe, N., Tock, A. J., Holland, D., Fritschi, K., Habring, A., Lanz, C., Patel, C., Schlegel, T., Collenberg, M., Mielke, M., Nordborg, M., Roux, F., Shirsekar, G., … Henderson, I. R. (2023). Cycles of satellite and transposon evolution in Arabidopsis centromeres. Nature, 618(7965), 557–565.https://doi.org/10.1038/s41586-023-06062-z.

80. Logsdon, G. A., Rozanski, A. N., Ryabov, F., Potapova, T., Shepelev, V. A., Mao, Y., Rautiainen, M., Koren, S., Nurk, S., Porubsky, D., Lucas, J. K., Hoekzema, K., Munson, K. M., Gerton, J. L., Phillippy, A. M., Alexandrov, I. A., & Eichler, E. E. (2023). The variation and evolution of complete human centromeres. bioRxiv : the preprint server for biology, 2023.05.30.542849.

<https://doi.org/10.1101/2023.05.30.542849>.

81.Dong, Xiao & Jiao, Wen-Biao & Campoy, Jose & Rabanal, Fernando & Ton, Jurriaan & Smith, Lisa & Weigel, Detlef & Schneeberger, Korbinian. (2025). The mutational dynamics of the Arabidopsis centromeres. 10.1101/2025.06.02.657473.

82.Neumann, P., Navrátilová, A., Koblížková, A., Kejnovský, E., Hřibová, E., Hobza, R., Widmer, A., Doležel, J., & Macas, J. (2011). Plant centromeric retrotransposons: a structural and cytogenetic perspective. Mobile DNA, 2(1), 4. <https://doi.org/10.1186/1759-8753-2-4>.

83. Renny-Byfield, S., & Baumgarten, A. (2020). Repetitive DNA content in the maize genome is uncoupled from population stratification at SNP loci. BMC genomics, 21(1), 9

<https://doi.org/10.1186/s12864-020-6517-0>.

84.Stroud, H., Do, T., Du, J., Zhong, X., Feng, S., Johnson, L., Patel, D. J., & Jacobsen, S. E. (2014). Non-CG methylation patterns shape the epigenetic landscape in Arabidopsis. Nature structural & molecular biology, 21(1), 64–72.

<https://doi.org/10.1038/nsmb.2735>.

85. Hofstatter, P. G., Thangavel, G., Lux, T., Neumann, P., Vondrak, T., Novak, P., Zhang, M., Costa, L., Castellani, M., Scott, A., Toegelová, H., Fuchs, J., Mata-Sucre, Y., Dias, Y., Vanzela, A. L. L., Huettel, B., Almeida, C. C. S., Šimková, H., Souza, G., Pedrosa-Harand, A., … Marques, A. (2022). Repeat-based holocentromeres influence genome architecture and karyotype evolution. Cell, 185(17), 3153–3168.e18.

 <https://doi.org/10.1016/j.cell.2022.06.045>.

86. Kuo, Y. T., Câmara, A. S., Schubert, V., Neumann, P., Macas, J., Melzer, M., Chen, J., Fuchs, J., Abel, S., Klocke, E., Huettel, B., Himmelbach, A., Demidov, D., Dunemann, F., Mascher, M., Ishii, T., Marques, A., & Houben, A. (2023). Holocentromeres can consist of merely a few megabase-sized satellite arrays. Nature communications, 14(1), 3502. <https://doi.org/10.1038/s41467-023-38922-7>.

87. Gutbrod, M. J., & Martienssen, R. A. (2020). Conserved chromosomal functions of RNA interference. Nature reviews. Genetics, 21(5), 311–331.

 <https://doi.org/10.1038/s41576-019-0203-6>.

88. Tsukahara, S., Bousios, A., Perez-Roman, E., Yamaguchi, S., Leduque, B., Nakano, A., Naish, M., Osakabe, A., Toyoda, A., Ito, H., Edera, A., Tominaga, S., Juliarni, Kato, K., Oda, S., Inagaki, S., Lorković, Z., Nagaki, K., Berger, F., Kawabe, A., … Kakutani, T. (2025). Centrophilic retrotransposon integration via CENH3 chromatin in Arabidopsis. Nature, 637(8046), 744–748.

 <https://doi.org/10.1038/s41586-024-08319-7>.

89. Leclerc, S., & Kitagawa, K. (2021). The Role of Human Centromeric RNA in Chromosome Stability. Frontiers in molecular biosciences, 8, 642732.

https://doi.org/10.3389/fmolb.2021.642732.

90.Yadav, V., Sun, S., Billmyre, R. B., Thimmappa, B. C., Shea, T., Lintner, R., Bakkeren, G., Cuomo, C. A., Heitman, J., & Sanyal, K. (2018). RNAi is a critical determinant of centromere evolution in closely related fungi. Proceedings of the National Academy of Sciences of the United States of America, 115(12), 3108–3113.

<https://doi.org/10.1073/pnas.1713725115>.

91. Ferreri, G. C., Marzelli, M., Rens, W., & O'Neill, R. J. (2004). A centromere-specific retroviral element associated with breaks of synteny in macropodine marsupials. Cytogenetic and genome research, 107(1-2), 115–118.

 <https://doi.org/10.1159/000079580>.

92.Courret, C., Hemmer, L. W., Wei, X., Patel, P. D., Chabot, B. J., Fuda, N. J., Geng, X., Chang, C. H., Mellone, B. G., & Larracuente, A. M. (2024). Turnover of retroelements and satellite DNA drives centromere reorganization over short evolutionary timescales in Drosophila. PLoS biology, 22(11), e3002911.

 <https://doi.org/10.1371/journal.pbio.3002911>.

93.Gonen, S., Akiyoshi, B., Iadanza, M. G., Shi, D., Duggan, N., Biggins, S., & Gonen, T. (2012). The structure of purified kinetochores reveals multiple microtubule-attachment sites. Nature structural & molecular biology, 19(9), 925–929.

 <https://doi.org/10.1038/nsmb.2358>.

94. Hofstatter, P. G., Thangavel, G., Lux, T., Neumann, P., Vondrak, T., Novak, P., Zhang, M., Costa, L., Castellani, M., Scott, A., Toegelová, H., Fuchs, J., Mata-Sucre, Y., Dias, Y., Vanzela, A. L. L., Huettel, B., Almeida, C. C. S., Šimková, H., Souza, G., Pedrosa-Harand, A., … Marques, A. (2022). Repeat-based holocentromeres influence genome architecture and karyotype evolution. Cell, 185(17), 3153–3168.e18.

 <https://doi.org/10.1016/j.cell.2022.06.045>.

95. Macas, J., Ávila Robledillo, L., Kreplak, J., Novák, P., Koblížková, A., Vrbová, I., Burstin, J., & Neumann, P. (2023). Assembly of the 81.6 Mb centromere of pea chromosome 6 elucidates the structure and evolution of metapolycentric chromosomes. PLoS genetics, 19(2), e1010633.

<https://doi.org/10.1371/journal.pgen.1010633>.

96. Toubiana, W., Dumas, Z., Van, P. T., Parker, D. J., Mérel, V., Schubert, V., Aury, J. M., Bournonville, L., Cruaud, C., Houben, A., Istace, B., Labadie, K., Noel, B., & Schwander, T. (2025). Functional monocentricity with holocentric characteristics and chromosome-specific centromeres in a stick insect. Science advances, 11(1), eads6459. <https://doi.org/10.1126/sciadv.ads6459>.

97. Ávila Robledillo, L., Neumann, P., Koblížková, A., Novák, P., Vrbová, I., & Macas, J. (2020). Extraordinary Sequence Diversity and Promiscuity of Centromeric Satellites in the Legume Tribe Fabeae. Molecular biology and evolution, 37(8), 2341–2356.

<https://doi.org/10.1093/molbev/msaa090>.

98. Hoyt, S. J., Storer, J. M., Hartley, G. A., Grady, P. G. S., Gershman, A., de Lima, L. G., Limouse, C., Halabian, R., Wojenski, L., Rodriguez, M., Altemose, N., Rhie, A., Core, L. J., Gerton, J. L., Makalowski, W., Olson, D., Rosen, J., Smit, A. F. A., Straight, A. F., Vollger, M. R. O'Neill, R. J. (2022). From telomere to telomere: The transcriptional and epigenetic state of human repeat elements. Science (New York, N.Y.), 376(6588), eabk3112.

<https://doi.org/10.1126/science.abk3112>.

100. Sosa, D., Miramontes, P., Li, W., Mireles, V., Bobadilla, J. R., & José, M. V. (2013). Periodic distribution of a putative nucleosome positioning motif in human, nonhuman primates, and archaea: mutual information analysis. International journal of genomics, 2013, 963956.

<https://doi.org/10.1155/2013/963956>.

101. Ma, H., Ding, W., Chen, Y., Zhou, J., Chen, W., Lan, C., Mao, H., Li, Q., Yan, W., & Su, H. (2023). Centromere Plasticity With Evolutionary Conservation and Divergence Uncovered by Wheat 10+ Genomes. Molecular biology and evolution, 40(8), msad176.

<https://doi.org/10.1093/molbev/msad176>.

102. Han, F., Gao, Z., & Birchler, J. A. (2009). Reactivation of an inactive centromere reveals epigenetic and structural components for centromere specification in maize. The Plant cell, 21(7), 1929–1939. <https://doi.org/10.1105/tpc.109.066662>.

103.Arora, U. P., & Dumont, B. L. (2022). Meiotic drive-in house mice: mechanisms, consequences, and insights for human biology. Chromosome research: an international journal on the molecular, supramolecular and evolutionary aspects of chromosome biology, 30(2-3), 165–186. <https://doi.org/10.1007/s10577-022-09697-2>.

104. Guirouilh-Barbat, J., Lambert, S., Bertrand, P., & Lopez, B. S. (2014). Is homologous recombination really an error-free process?. Frontiers in genetics, 5, 175.

 <https://doi.org/10.3389/fgene.2014.00175>.

104. Xiao-Shu Chen, Jia-Bi Chen. Dosage compensation of sex chromosomes in animals. Yi Chuan. 2025;47(2):200-210. doi: 10.16288/j.yczz.24-165.

105. Stacy Colaco, Deepak Modi. Genetics of the human Y chromosome and its association with male infertility. Reprod Biol Endocrinol. 2018;16(1):14. doi: 10.1186/s12958-018-0330-5.

106. Wen-Juan Ma, Paris Veltsos. The Diversity and Evolution of Sex Chromosomes in Frogs. Genes (Basel). 2021 Mar 26;12(4):483. doi: 10.3390/genes12040483.

107. Ezaz, Tariq , Srikulnath, Kornsorn , Graves, Jennifer. (2016). Origin of Amniote Sex Chromosomes: An Ancestral Super-Sex Chromosome, or Common Requirements?. Journal of Heredity. 2016. 1-12. 10.1093/jhered/esw053.

2024108.

108.Paul Jay, Daniel Jeffries, Fanny E Hartmann, Amandine Veber, Tatiana Giraud. Why do sex chromosomes progressively lose recombination?. Trends Genet. 2024;40(7):564-579. doi: 10.1016/j.tig.2024.03.005.

109.Ewa B Sliwinska, Rafal Martyka, Piotr Tryjanowski. Evolutionary interaction between W/Y chromosome and transposable elements. Genetica. 2016;144:267–278. doi: 10.1007/s10709-016-9895-0.

110. Joanna L Rifkin, Felix E G Beaudry, Zoe Humphries, Baharul I Choudhury, Spencer C H Barrett, Stephen I Wright. Widespread Recombination Suppression Facilitates Plant Sex Chromosome Evolution. Mol Biol Evol. 2021 Mar 9;38(3):1018-1030. doi: 10.1093/molbev/msaa271.

111. Jordi Paps, Maria Eleonora Rossi, Alexander M. C. Bowles, Marta Alvarez-Presas. Assembling animals: trees, genomes, cells, and contrast to plants. Front. Ecol. Evol.2023;11. doi:10.3389/fevo.2023.1185566.

112. Rodolfo Rey, Nathalie Josso, Chrystele Racine, Kenneth R Feingold, S. Faisal Ahmed, Bradley Anawalt, et al., Sexual Differentiation. In: Endotext [Internet]. South Dartmouth (MA): MDText.com, Inc.; 2000.

113. Mila Mirceta, Natalie Shum, Monika H M Schmidt, Christopher E Pearson. Fragile sites, chromosomal lesions, tandem repeats, and disease. Front Genet. 2022; 13:985975. doi: 10.3389/fgene.2022.985975.

114.Svetlana A Romanenko, Yulia E Fedorova, Natalya A Serdyukova, Marco Zaccaroni, Roscoe Stanyon, Alexander S Graphodatsky. Evolutionary rearrangements of X chromosomes in voles (Arvicolinae, Rodentia). Sci Rep. 2020;10(1):13235. doi: 10.1038/s41598-020-70226-4.

115. Yuan Fu, Xiaoxia Zhang, Tian Zhang, Wenjing Sun, Wenjun Yang, Yajing Shi,Jian Zhang Qiang He, Deborah Charlesworth, Yuannian Jiao,Zhiduan Chen, Bo Xu.Evidence for evolution of a new sex chromosome within the haploid‐dominant Marchantiales plant lineage.J Integr Plant Biol. 2025 Feb 21;67(6):1533–1550. doi: 10.1111/jipb.13867

116.Fanny E Hartmann, Marine Duhamel, Fantin Carpentier, Michael E Hood, Marie Foulongne-Oriol, Philippe Silar, Fabienne Malagnac, Pierre Grognet, Tatiana Giraud. Recombination suppression and evolutionary strata around mating-type loci in fungi: documenting patterns and understanding evolutionary and mechanistic causes. New Phytol. 2021;229(5):2470-2491. doi: 10.1111/nph.17039.

117.Francesc Piferrer. Epigenetic mechanisms in sex determination and in the evolutionary transitions between sexual systems. Philos Trans R Soc Lond B Biol Sci. 2021;376(1832):20200110. doi: 10.1098/rstb.2020.0110.

118.Ryan Bracewell, Doris Bachtrog. Complex Evolutionary History of the Y Chromosome in Flies of the Drosophila obscura Species Group. Genome Biol Evol. 2020;12(5):494-505. doi: 10.1093/gbe/evaa051.

119.Masafumi Nozawa, Yohei Minakuchi, Kazuhiro Satomura, Shu Kondo, Atsushi Toyoda, Koichiro Tamura. Shared evolutionary trajectories of three independent neo-sex chromosomes in *Drosophila*. Genome Res. 2021;31(11):2069-2079. doi: 10.1101/gr.275503.121.

120. Ming Li, Rui Zhang, Guangyi Fan, Wenteng Xu, Qian Zhou, Lei Wang, Wensheng Li, Zunfang Pang, Mengjun Yu, Qun Liu, Xin Liu, Manfred Schartl, Songlin Chen. Reconstruction of the Origin of a Neo-Y Sex Chromosome and Its Evolution in the Spotted Knifejaw, *Oplegnathus punctatus*. Mol Biol Evol. 2021;38(6):2615-2626. doi: 10.1093/molbev/msab056.

121.Sebastien Guizard, Benoit Piegu, Peter Arensburger, Florian Guillou,Yves Bigot. Deep landscape update of dispersed and tandem repeats in the genome model of the red jungle fowl, Gallus gallus, using a series of de novo investigating tools. BMC Genomics. 2016;17(1):659. doi: 10.1186/s12864-016-3015-5.

122. Roy N Platt, Michael W Vandewege, David A Ray. Mammalian transposable elements and their impacts on genome evolution. Chromosome Res. 2018;26(1-2):25-43. doi: 10.1007/s10577-017-9570-z.

123.Jing Sun, Yanfang Zhang, Minhui Wang, Qian Guan, Xiujia Yang, Jin Xia Ou, Mingchen Yan, Chengrui Wang, Yan Zhang, Zhi-Hao Li, Chunhong Lan, Chen Mao, Hong-Wei Zhou, Bingtao Hao, Zhenhai Zhang. The Biological Significance of Multi-copy Regions and Their Impact on Variant Discovery. Genomics Proteomics Bioinformatics. 2020;18(5):516-524. doi: 10.1016/j.gpb.2019.05.004.

124.Worapong Singchat, Syed Farhan Ahmad, Nararat Laopichienpong, Aorarat Suntronpong, Thitipong Panthum, Darren K Griffin, Kornsorn Srikulnath.Snake W Sex Chromosome: The Shadow of Ancestral Amniote Super-Sex Chromosome.Cells. 2020 Oct 31;9(11):2386. doi: 10.3390/cells9112386.

125.Celine Cosseau, Olaf Wolkenhauer, Gilda Padalino, Kathrin K Geyer, Karl F Hoffmann, Christoph Grunau. (Epi)genetic Inheritance in Schistosoma mansoni: A Systems Approach.Trends Parasitol. 2017;33(4):285-294. doi: 10.1016/j.pt.2016.12.002.

126. Thomas Liehr. Repetitive Elements in Humans. Int J Mol Sci. 2021;22(4):2072. doi: 10.3390/ijms22042072.

127.Emily J Brown, Alison H Nguyen, Doris Bachtrog. The Drosophila Y Chromosome Affects Heterochromatin Integrity Genome-Wide. Mol Biol Evol. 2020;37(10):2808-2824. doi: 10.1093/molbev/msaa082.

128. Laure K Case, Emma H Wall, Erin E Osmanski, Julie A Dragon, Naresha Saligrama, James F Zachary, Bernardo Lemos, Elizabeth P Blankenhorn, Cory Teuscher. Copy number variation in Y chromosome multicopy genes is linked to a paternal parent-of-origin effect on CNS autoimmune disease in female offspring. Genome Biol. 2015;16(1):28. doi: 10.1186/s13059-015-0591-7.

129. Rakesh Kumar Sahu, Sakshi Singh, Raghuvir Singh Tomar. The mechanisms of action of chromatin remodelers and implications in development and disease. Biochem Pharmacol. 2020;180:114200. doi: 10.1016/j.bcp.2020.114200.

130. Rebekah L Rogers, Julie M Cridland, Ling Shao, Tina T Hu, Peter Andolfatto, Kevin R Thornton. Landscape of standing variation for tandem duplications in *Drosophila yakuba* and *Drosophila simulans.* Mol Biol Evol. 2014;31(7):1750-66. doi: 10.1093/molbev/msu124.

131. Mahul Chakraborty, Ching-Ho Chang, Danielle E Khost, Jeffrey Vedanayagam, Jeffrey R Adrion, Yi Liao, Kristi L Montooth, Colin D Meiklejohn, Amanda M Larracuente, J J Emerson. Evolution of genome structure in the *Drosophila simulans* species complex. Genome Res. 2021;31(3):380-396. doi: 10.1101/gr.263442.120.

132. John S Sproul, Danielle E Khost, Danna G Eickbush, Sherif Negm, Xiaolu Wei, Isaac Wong, Amanda M Larracuente. Dynamic Evolution of Euchromatic Satellites on the X Chromosome in *Drosophila melanogaster* and the simulans Clade. Mol Biol Evol. 2020;37(8):2241-2256. doi: 10.1093/molbev/msaa078.

133.Alexander Belyayev, Jirina Josefiova, Michaela Jandova, Ruslan Kalendar, Vaclav Mahelka, Bohumil Mandak, Karol Krak. The structural diversity of CACTA transposons in genomes of Chenopodium (Amaranthaceae, Caryophyllales) species: specific traits and comparison with the similar elements of angiosperms. Mob DNA. 2022;13(1):8. doi: 10.1186/s13100-022-00265-3.

134. Melissa A Wilson Sayres. Genetic Diversity on the Sex Chromosomes. Genome Biol Evol. 2018; 10(4):1064-1078. doi: 10.1093/gbe/evy039.

135. Daniela Cecalev, Beatriz Viçoso, Rafael Galupa. Compensation of gene dosage on the mammalian X. Development. 2024;151(15):dev202891. doi: 10.1242/dev.202891.

136.Leila Elizabeth Rieder, William Thomas Jordan, Erica Nicole Larschan. Targeting of the Dosage-Compensated Male X-Chromosome during Early Drosophila Development. Cell Rep. 2019;29(13):4268-4275.e2. doi: 10.1016/j.celrep.2019.11.095.

137. Daniela Barro-Trastoy, Claudia Kohler. Helitrons: genomic parasites that generate developmental novelties. Trends Genet. 2024 May;40(5):437-448. doi:10.1016/j.tig.2024.02.002.

138.Daniel F Deegan, Nora Engel. Sexual Dimorphism in the Age of Genomics: How, When, Where. Front Cell Dev Biol. 2019;7:186. doi: 10.3389/fcell.2019.00186.

139. Gautier Richard, Fabrice Legeai, Nathalie Prunier-Leterme, Anthony Bretaudeau, Denis Tagu, Julie Jaquiéry & Gaël Le Trionnaire.Dosage compensation and sex-specific epigenetic landscape of the X chromosome in the pea aphid.Epigenetics & Chromatin volume 10, Article number: 30 (2017).

140.Nikita Deshpande, Victoria H Meller.Sex chromosome evolution: life, death and repetitive.Fly (Austin). 2015 Mar 9;8(4):197–199. doi: DNA.10.1080/19336934.2015.1024395.

141. Ryan Bracewell, Doris Bachtrog.Complex Evolutionary History of the Y Chromosome in Flies of the Drosophila obscura Species.Genome Biology and Evolution, Volume 12, Issue 5, May 2020, Pages 494–505, <https://doi.org/10.1093/gbe/evaa051>.

142.Zachary L Fuller , Spencer A Koury , Christopher J Leonard , Randee E Young , Kobe Ikegami , Jonathan Westlake , Stephen Richards , Stephen W Schaeffer , Nitin PhadnisExtensive Recombination Suppression and Epistatic Selection Causes Chromosome-Wide Differentiation of a Selfish Sex Chromosome in Drosophila pseudoobscura.Genetics, Volume 216, Issue 1, 1 September 2020, Pages 205–226, <https://doi.org/10.1534/genetics.120.303460>.

143.Frederic Zimmer,Annika Maria Fox,Qiaowei Pan,Frank Rühle, Peter Andersen,Ann-Kathrin Huylmans,Tanja Schwander,M. Felicia Basilicata,Claudia Isabelle Keller Valsecchi.Convergent Evolution of H4K16ac-mediated Dosage Compensation Shapes Sex-dependent Lifespan in a ZW Species.bioRxiv 2025.04.10.648168; doi: https://doi.org/10.1101/2025.04.10.648168

144.Miguel Gallach. 1.688 g/cm(3) satellite-related repeats: a missing link to dosage compensation and speciation. Mol Ecol. 2015;24(17):4340-7. doi: 10.1111/mec.13335.

145.Leonardo G. de Lima, Francisco J. Ruiz-Ruano.In-Depth Satellitome Analyses of 37 Drosophila Species Illuminate Repetitive DNA Evolution in the Drosophila Genus.Genome Biology and Evolution, Volume 14, Issue 5, May 2022, evac064, https://doi.org/10.1093/gbe/evac064

146.Kenneth S Ramos, Pasano Bojang, Emma Bowers.Role of long interspersed nuclear element-1 in the regulation of chromatin landscapes and genome dynamics.Exp Biol Med (Maywood). 2021 Jul 25;246(19):2082–2097. doi: 10.1177/15353702211031247.

147.John L. Goodier, Haig H. Kazazian Jr.Retrotransposons Revisited: The Restraint and Rehabilitation of Parasites.Cell Volume 135, Issue 1, 3 October 2008, Pages 23-35.

148.Homa Papoli Yazdi, Willian T A F Silva, Alexander Suh.Why Do Some Sex Chromosomes Degenerate More Slowly Than Others? The Odd Case of Ratite Sex Chromosomes.Genes (Basel). 2020 Sep 30;11(10):1153. doi: 10.3390/genes11101153.

149.Khanam Taslima, Kiyoshi Kikuchi, Sho Hosoya.Genomic architecture and sex chromosome systems of commercially important fish species in Asia – Current status, knowledge gaps and future prospects. reviewes in aquaculture.Volume16, Issue4.September 2024.

150.Marcelo de Bello Cioffi, Eduard Kejnovský, Vinicius Marquioni, Juliana Poltronieri, Wagner Franco Molina, Débora Diniz, Luiz Antonio Carlos Bertollo.The key role of repeated DNAs in sex chromosome evolution in two fish species with ZW sex chromosome system.Mol Cytogenet. 2012 Jun 1;5(1):28. doi: 10.1186/1755-8166-5-28.151.C F Yano, L A C Bertollo, T Ezaz, V Trifonov, A Sember, T Liehr, M B Cioffi. Highly conserved Z and molecularly diverged W chromosomes in the fish genus Triportheus (Characiformes, Triportheidae) Heredity (Edinb). 2017 Mar;118(3):276-283. doi: 10.1038/hdy.2016.83. Epub 2016 Dec 21.

152.Barcellos, Mariannah & Kretschmer, Rafael & Deon, Geize & Toma, Gustavo & Ezaz, Tariq & Goes, Caio & Porto-Foresti, Fábio & Liehr, Thomas & Utsunomia, Ricardo & Cioffi, Marcelo. (2023). Following the Pathway of W Chromosome Differentiation in Triportheus (Teleostei: Characiformes). Biology. 12. 1114. 10.3390/biology12081114.

153.Cassia Fernanda Yano, Luiz Antônio Carlos Bertollo, Thomas Liehr, Waldo Pinheiro Troy, Marcelo de Bello Cioffi.W Chromosome Dynamics in Triportheus Species (Characiformes, Triportheidae): An Ongoing Process Narrated by Repetitive Sequences.J Hered. 2016 Jul;107(4):342-8. doi: 10.1093/jhered/esw021. Epub 2016 Apr 1.

154.R F Artoni & L A C Bertollo.Evolutionary aspects of the ZZ/ZW sex chromosome system in the Characidae fish, genus Triportheus. A monophyletic state and NOR location on the W chromosome.Heredity volume 89, pages15–19 (2002).

155.Edson Lourenço da Silva, Rafael Splendore de Borba, Patrícia Pasquali Parise-Maltempi.Chromosome mapping of repetitive sequences in Anostomidae species: implications for genomic and sex chromosome evolution.Molecular Cytogenetics volume 5, Article number: 45 (2012)

155.Natália Lourenço de Freitas, Ahmed Basheer Hamid Al-Rikabi, Luiz Antonio Carlos Bertollo, Tariq Ezaz, Cassia Fernanda Yano, Ezequiel Aguiar de Oliveira, Terumi Hatanaka, Marcelo de Bello Cioffi.Early Stages of XY Sex Chromosomes Differentiation in the Fish Hoplias malabaricus (Characiformes, Erythrinidae) Revealed by DNA Repeats Accumulation.Curr Genomics. 2018 Apr;19(3):216-226. doi: 10.2174/1389202918666170711160528.

156.Victor Spangenberg, Marine Arakelyan, Marcelo de Bello Cioffi, Thomas Liehr, Ahmed Al-Rikabi, Elena Martynova, Felix Danielyan, Ilona Stepanyan, Eduard Galoyan, Oxana Kolomiets Cytogenetic mechanisms of unisexuality in rock lizards.Sci Rep. 2020 May 26;10(1):8697. doi: 10.1038/s41598-020-65686-7.

157.Václav Bačovský, Radim Čegan, Denisa Šimoníková,Eva Hřibová ,Roman Hobza.The Formation of Sex Chromosomes in Silene latifolia and S. dioica Was Accompanied by Multiple Chromosomal Rearrangements.Front Plant Sci. 2020 Feb 28:11:205. doi: 10.3389/fpls.2020.00205. eCollection 2020.

158.Roman Hobza, Radim Cegan, Wojciech Jesionek, Eduard Kejnovsky, Boris Vyskot, Zdenek Kubat.Impact of Repetitive Elements on the Y Chromosome Formation in Plants.Genes (Basel). 2017 Nov 1;8(11):302. doi: 10.3390/genes8110302.

159.Shivani Mahajan, Doris Bachtrog.Convergent evolution of Y chromosome gene content in flies.Nat Commun. 2017 Oct 4;8(1):785. doi: 10.1038/s41467-017-00653-x.

160. Liao, Daiqing. Concerted Evolution.2006. Encyclopedia of Life Sciences1-5.doi: 10.1038/npg.els.0005132.

161. Mehrotra S, Goyal V. Repetitive sequences in plant nuclear DNA: types, distribution, evolution and function. Genomics Proteomics Bioinformatics. 2014 Aug;12(4):164-71. doi: 10.1016/j.gpb.2014.07.003. Epub 2014 Aug 15.

162.Christmas MJ, Jones JC, Olsson A, Wallerman O, Bunikis I, Kierczak M, Peona V, Whitley KM, Larva T, Suh A, Miller-Struttmann NE, Geib JC, Webster MT. Genetic Barriers to Historical Gene Flow between Cryptic Species of Alpine Bumblebees Revealed by Comparative Population Genomics. Mol Biol Evol. 2021 Jul 29;38(8):3126-3143. doi: 10.1093/molbev/msab086.

163. Catlin NS, Josephs EB. The important contribution of transposable elements to phenotypic variation and evolution. Curr Opin Plant Biol. 2022 Feb;65:102140. doi: 10.1016/j.pbi.2021.102140. Epub 2021 Dec 6. PMID: 34883307.

164.Yushkova E, Moskalev A. Transposable elements and their role in aging. Ageing Res Rev. 2023 Apr;86:101881. doi: 10.1016/j.arr.2023.101881. Epub 2023 Feb 10. PMID: 36773759.

165. Erica J Polleys,Catherine H Freudenreich.Homologous recombination within repetitive DNA. Curr Opin Genet Dev. 2021 Aug 28;71:143–153. doi: 10.1016/j.gde.2021.08.005

166.Ma X, Fan L, Zhang Z, Yang X, Liu Y, Ma Y, Pan Y, Zhou G, Zhang M, Ning H, Kong F, Ma J, Liu S, Tian Z. Global dissection of the recombination landscape in soybean using a high-density 600K SoySNP array. Plant Biotechnol J. 2023 Mar;21(3):606-620. doi: 10.1111/pbi.13975. Epub 2022 Dec 19.

167.Palsson G, Hardarson MT, Jonsson H, Steinthorsdottir V, Stefansson OA, Eggertsson HP, Gudjonsson SA, Olason PI, Gylfason A, Masson G, Thorsteinsdottir U, Sulem P, Helgason A, Gudbjartsson DF, Halldorsson BV, Stefansson K. Complete human recombination maps. Nature. 2025 Mar;639(8055):700-707. doi: 10.1038/s41586-024-08450-5. Epub 2025 Jan 22.

168.Bonchev G, Willi Y. Accumulation of transposable elements in selfing populations of Arabidopsis lyrata supports the ectopic recombination model of transposon evolution. New Phytol. 2018 Jul;219(2):767-778. doi: 10.1111/nph.15201. Epub 2018 May 14.

169. Haley AL, Mueller RL. Transposable Element Diversity Remains High in Gigantic Genomes. J Mol Evol. 2022 Oct;90(5):332-341. doi: 10.1007/s00239-022-10063-3. Epub 2022 Jun 25. Rezvykh AP, Funikov SY, Protsenko LA, Kulikova DA, Zelentsova ES, Chuvakova LN, Blumenstiel JP, Evgen'ev MB. Evolutionary Dynamics of the Pericentromeric Heterochromatin in *Drosophila virilis* and Related Species. Genes (Basel). 2021 Jan 27;12(2):175. doi: 10.3390/genes12020175.

170. Saha P, Sowpati DT, Soujanya M, Srivastava I, Mishra RK. Interplay of pericentromeric genome organization and chromatin landscape regulates the expression of Drosophila melanogaster heterochromatic genes. Epigenetics Chromatin. 2020 Oct 7;13(1):41. doi: 10.1186/s13072-020-00358-4.

171. Simon L, Voisin M, Tatout C, Probst AV. Structure and Function of Centromeric and Pericentromeric Heterochromatin in Arabidopsis thaliana. Front Plant Sci. 2015 Nov 30;6:1049. doi: 10.3389/fpls.2015.01049.

172.Lee YCG, Ogiyama Y, Martins NMC, Beliveau BJ, Acevedo D, Wu CT, Cavalli G, Karpen GH. Pericentromeric heterochromatin is hierarchically organized and spatially contacts H3K9me2 islands in euchromatin. PLoS Genet. 2020 Mar 23;16(3):e1008673. doi: 10.1371/journal.pgen.1008673.

173.Makarevitch I, Eichten SR, Briskine R, Waters AJ, Danilevskaya ON, Meeley RB, Myers CL, Vaughn MW, Springer NM. Genomic distribution of maize facultative heterochromatin marked by trimethylation of H3K27. Plant Cell. 2013 Mar;25(3):780-93. doi: 10.1105/tpc.112.106427. Epub 2013 Mar 5.

174..Le Veve A, Genete M, Lepers-Blassiau C, Ponitzki C, Poux C, Vekemans X, Durand E, Castric V. The genetic architecture of the load linked to dominant and recessive self-incompatibility alleles in *Arabidopsis halleri* and *Arabidopsis lyrata*. Elife. 2024 Sep 2;13:RP94972. doi: 10.7554/eLife.94972.

175.Betancourt AJ, Wei KH, Huang Y, Lee YCG. Causes and Consequences of Varying Transposable Element Activity: An Evolutionary Perspective. Annu Rev Genomics Hum Genet. 2024 Aug;25(1):1-25. doi: 10.1146/annurev-genom-120822-105708. Epub 2024 Aug 6.

176. Teresi SJ, Teresi MB, Edger PP. TE Density: a tool to investigate the biology of transposable elements. Mob DNA. 2022 Apr 12;13(1):11. doi: 10.1186/s13100-022-00264-4.

177.Gu Z, Jin K, Crabbe MJC, Zhang Y, Liu X, Huang Y, Hua M, Nan P, Zhang Z, Zhong Y. Enrichment analysis of Alu elements with different spatial chromatin proximity in the human genome. Protein Cell. 2016 Apr;7(4):250-266. doi: 10.1007/s13238-015-0240-7. Epub 2016 Feb 10.

178. Daron J, Glover N, Pingault L, Theil S, Jamilloux V, Paux E, Barbe V, Mangenot S, Alberti A, Wincker P, Quesneville H, Feuillet C, Choulet F. Organization and evolution of transposable elements along the bread wheat chromosome 3B. Genome Biol. 2014;15(12):546. doi: 10.1186/s13059-014-0546-4.

179.Minami K, Semeigazin A, Nakazato K, Maeshima K. Euchromatin and Heterochromatin: Implications for DNA Accessibility and Transcription. J Mol Biol. 2025 Jun 6:169270. doi: 10.1016/j.jmb.2025.169270. Epub ahead of print.

199.

180. Lee YCG. Synergistic epistasis of the deleterious effects of transposable elements. Genetics. 2022 Feb 4;220(2):iyab211. doi: 10.1093/genetics/iyab211.

181.Stapley J, Feulner PGD, Johnston SE, Santure AW, Smadja CM. Variation in recombination frequency and distribution across eukaryotes: patterns and processes. Philos Trans R Soc Lond B Biol Sci. 2017 Dec 19;372(1736):20160455. doi: 10.1098/rstb.2016.0455. Erratum in: Philos Trans R Soc Lond B Biol Sci. 2018 Feb 5;373(1739):20170360. doi: 10.1098/rstb.2017.0360.

182. Iwasaki WM, Kijima TE, Innan H. Population Genetics and Molecular Evolution of DNA Sequences in Transposable Elements. II. Accumulation of Variation and Evolution of a New Subfamily. Mol Biol Evol. 2020 Feb 1;37(2):355-364. doi: 10.1093/molbev/msz220.

183.Cutter AD, Jovelin R. When natural selection gives gene function the cold shoulder. Bioessays. 2015 Nov;37(11):1169-73. doi: 10.1002/bies.201500083. Epub 2015 Sep 28.

184. Stapley J, Feulner PGD, Johnston SE, Santure AW, Smadja CM. Variation in recombination frequency and distribution across eukaryotes: patterns and processes. Philos Trans R Soc Lond B Biol Sci. 2017 Dec 19;372(1736):20160455. doi: 10.1098/rstb.2016.0455. Erratum in: Philos Trans R Soc Lond B Biol Sci. 2018 Feb 5;373(1739):20170360. doi: 10.1098/rstb.2017.0360.

185.Iwasaki WM, Kijima TE, Innan H. Population Genetics and Molecular Evolution of DNA Sequences in Transposable Elements. II. Accumulation of Variation and Evolution of a New Subfamily. Mol Biol Evol. 2020 Feb 1;37(2):355-364. doi: 10.1093/molbev/msz220.

186. Rachal M Allison, Dominic J Johnson, Matthew J Neale, Stephen Gray.Recombinase-independent chromosomal rearrangements between dispersed inverted repeats in Saccharomyces cerevisiae meiosis.Nucleic Acids Res. 2023 Aug 7;51(18):9703–9715. doi: 10.1093/nar/gkad650

187. Kent Tyler V., Uzunović Jasmina and Wright Stephen I. 2017.Coevolution between transposable elements and recombination.Phil. Trans. R. Soc. B37220160458

188. Asher D Cutter, Richard Jovelin.When natural selection gives gene function the cold shoulderBioessays. 2015 Sep 28;37(11):1169–1173. doi: 10.1002/bies.201500083.

189. Thomas Brazier, Sylvain Glémin.Diversity in Recombination Hotspot Characteristics and Gene Structure Shape Fine-Scale Recombination Patterns in Plant Genomes.Molecular Biology and Evolution, Volume 41, Issue 9, September 2024, msae183,

190. Becher H, Charlesworth B. A model of Hill-Robertson interference caused by purifying selection in a nonrecombining genome. Genetics. 2025 May 8;230(1):iyaf048. doi: 10.1093/genetics/iyaf048.

191. Shuping Zhang,Alejandra Macias-Garcia,Jacob C Ulirsch,Jason Velazquez,Vincent L Butty,Stuart S Levine,Vijay G Sankaran,Jane-Jane Chen (2019) HRI coordinates translation necessary for protein homeostasis and mitochondrial function in erythropoiesis eLife 8:e46976.

192. Hartmann FE, Duhamel M, Carpentier F, Hood ME, Foulongne-Oriol M, Silar P, Malagnac F, Grognet P, Giraud T. Recombination suppression and evolutionary strata around mating-type loci in fungi: documenting patterns and understanding evolutionary and mechanistic causes. New Phytol. 2021 Mar;229(5):2470-2491. doi: 10.1111/nph.17039. Epub 2020 Dec 1.

193. Song H, Giorgi EE, Ganusov VV, Cai F, Athreya G, Yoon H, Carja O, Hora B, Hraber P, Romero-Severson E, Jiang C, Li X, Wang S, Li H, Salazar-Gonzalez JF, Salazar MG, Goonetilleke N, Keele BF, Montefiori DC, Cohen MS, Shaw GM, Hahn BH, McMichael AJ, Haynes BF, Korber B, Bhattacharya T, Gao F. Tracking HIV-1 recombination to resolve its contribution to HIV-1 evolution in natural infection. Nat Commun. 2018 May 15;9(1):1928. doi: 10.1038/s41467-018-04217-5.

194. Liu G, Sun Y, Jia L, Li R, Zuo Y. Chromatin accessibility shapes meiotic recombination in mouse primordial germ cells through assisting double-strand breaks and loop formation. Biochim Biophys Acta Gene Regul Mech. 2022 Jul;1865(5):194844. doi: 10.1016/j.bbagrm.2022.194844. Epub 2022 Jul 20.

195. Choi J, Lyons DB, Kim MY, Moore JD, Zilberman D. DNA Methylation and Histone H1 Jointly Repress Transposable Elements and Aberrant Intragenic Transcripts. Mol Cell. 2020 Jan 16;77(2):310-323.e7. doi: 10.1016/j.molcel.2019.10.011. Epub 2019 Nov 12.

196. Gilbert Matthew, Mack Brian, Moore Geromy, Downey Darlene, Lebar Matthew Joardar, Vinita Losada, Liliana Yu, JiuJiang Nierman, William Bhatnagar, Deepak. (2018). Whole genome comparison of Aspergillus flavus L-morphotype strain NRRL 3357 (type) and S-morphotype strain AF70. PLOS ONE. 13. e0199169. 10.1371/journal.pone.0199169.

197.Jeffrey W Cary,Matthew K Gilbert, Matthew D Lebar, Rajtilak Majumdar, Ana M Calvo.Aspergillus flavus Secondary Metabolites: More than Just AflatoxinsFood Saf (Tokyo). 2018 Mar 30;6(1):7–32. doi: 10.14252/foodsafetyfscj.2017024.

198. Arthur J Lustig.Investigating the origin of subtelomeric and centromeric AT-rich elements in Aspergillus flavus.PLoS One. 2023 Feb 9;18(2):e0279148. doi: 10.1371/journal.pone.0279148199

.Mei Han, Matthew H Perkins, Leonardo Santana Novaes, Tao Xu, Hao Chang.Advances in transposable elements: from mechanisms to applications in mammalian genomics.Front Genet. 2023 Nov 30;14:1290146. doi: 10.3389/fgene.2023.1290146.

199.Tifenn Donnart, Mathieu Piednoël, Dominique Higuet & Éric Bonnivard.Filamentous ascomycete genomes provide insights into Copia retrotransposon diversity in fungi.BMC Genomics volume 18, Article number: 410 (2017).

200. Hironobu Ogasawara , Hiroshi Obata, Yoji Hata, Saori Takahashi, Katsuya Gomi.Crawler, a novel Tc1/mariner-type transposable element in Aspergillus oryzae transposes under stress conditions.Fungal Genet Bio. 2009 Jun-Jul;46(6-7):441-9. doi: 10.1016/j.fgb.2009.02.007. Epub 2009 Mar 6.

201. Marianne Yoth, Silke Jensen and Emilie Brasset.The Intricate Evolutionary Balance between Transposable Elements and Their Host: Who Will Kick at Goal and Convert the Next Try?. Biology 2022, 11(5), 710; <https://doi.org/10.3390/biology11050710>.

202. Kristina M Smith, Jonathan M Galazka, Pallavi A Phatale, Lanelle R Connolly, Michael Freitag.Centromeres of filamentous fungi. Chromosome Res. 2012 Jul;20(5):635–656. doi: 10.1007/s10577-012-9290-3

203. Savannah J Klein, Rachel J O’Neill.Transposable elements: genome innovation, chromosome diversity, and centromere conflict.Chromosome Res. 2018 Jan 13;26(1):5–23. doi: 10.1007/s10577-017-9569-5.

Klein SJ, O'Neill RJ. Transposable elements: genome innovation, chromosome diversity, and centromere conflict. Chromosome Res. 2018 Mar;26(1-2):5-23. doi: 10.1007/s10577-017-9569-5. Epub 2018 Jan 13.

204.William C Nierman, Jiujiang Yu, Natalie D Fedorova-Abrams, Liliana Losada, Thomas E Cleveland, Deepak Bhatnagar, Joan W Bennett, Ralph Dean, Gary A Payne. Genome Sequence of Aspergillus flavus NRRL 3357, a Strain That Causes Aflatoxin Contamination of Food and Feed Genome Announc. 2015 Apr 16;3(2):e00168-15. doi: 10.1128/genomeA.00168-15

205. John S Sproul, Scott Hotaling, Jacqueline Heckenhauer, Ashlyn Powell, Dez Marshall, Amanda M Larracuente, Joanna L Kelley, Steffen U Pauls, Paul B Frandsen.Analyses of 600+ insect genomes reveal repetitive element dynamics and highlight biodiversity-scale repeat annotation challenges.Genome Res. 2023 Oct;33(10):1708-1717. doi: 10.1101/gr.277387.122. Epub 2023 Sep 22.

206. Yuyang Cong, Xinhai Ye, Yang Mei, Kang He, Fei Li.Transposons and non-coding regions drive the intrafamily differences of genome size in insects.iScience. 2022 Aug 4;25(9):104873. doi: 10.1016/j.isci.2022.104873.

207. Henrik Kaessmann. Origins, evolution, and phenotypic impact of new genes Genome Res. 2010 Oct;20(10):1313–1326. doi: 10.1101/gr.101386.109.

208.Robin C Allshire, Hiten D Madhani.Ten principles of heterochromatin formation and function. Nat Rev Mol Cell Biol. 2017 Dec 13;19(4):229–244. doi: 10.1038/nrm.2017.119.

209. Lee YCG, Karpen GH Pervasive epigenetic effects of Drosophila euchromatic transposable elements impact their evolution. Elife. 2017 Jul 11;6:e25762. doi: 10.7554/eLife.25762.

210. Hao Yuan, Xiao-Jing Liu, Xuan-Zeng Liu, Li-Na Zhao, Shao-Li Mao & Yuan Huang The evolutionary dynamics of genome sizes and repetitive elements in Ensifera (Insecta: Orthoptera).BMC Genomics volume 25, Article number: 1041 (2024).

211.Heckenhauer J, Frandsen PB, Sproul JS, Li Z, Paule J, Larracuente AM, Maughan PJ, Barker MS, Schneider JV, Stewart RJ, Pauls SU.Genome size evolution in the diverse insect order Trichoptera. Gigascience. 2022 Feb 25;11:giac011. doi: 10.1093/gigascience/giac011.

212.Indranil Malik,Chase P Kelley,Eric Wang,Peter Todd.Molecular Mechanisms Underlying Nucleotide Repeat Expansion Disorders.Nat Rev Mol Cell Biol. 2021 Jun 17;22(9):589–607. doi: 10.1038/s41580-021-00382-6

213. Julieta Rivosecchi,Katarina Jurikova,Emilio Cusanelli.Telomere-specific regulation of TERRA and its impact on telomere stability.Seminars in Cell & Developmental Biology.Volume 157, April 2024, Pages 3-23.

214. Pratibha Siwach, Subramaniam Ganesh.Tandem repeats in human disorders: mechanisms and evolutionReview Front Biosci. 2008 May 1:13:4467-84. doi: 10.2741/3017.

215.Jingwei Zhou, Yang Liu, Xianrui Guo, James A Birchler, Fangpu Han, Handong Su..Centromeres: From chromosome biology to biotechnology applications and synthetic genomes in plants.Plant Biotechnol J. 2022 Jul 7;20(11):2051–2063. doi: 10.1111/pbi.13875.

216. Sharu Paul, Thomas PetersonComplex chromosomal rearrangements induced by transposons in maize.Genetics, Volume 223, Issue 2, February 2023, iyac124.

217. Diwash Jangam,Cédric Feschotte, Esther Betrán.Transposable element domestication as an adaptation to evolutionary conflicts.Trends Genet. 2017 Aug 24;33(11):817–831. doi: 10.1016/j.tig.2017.07.011

218. Beibei Liu,Meixia Zhao.How transposable elements are recognized and epigenetically silenced in plants?Current Opinion in Plant Biology.Volume 75, October 2023, 102428

220. Maria E Bernabéu-Herrero, Dilipkumar Patel, Adrianna Bielowka, JiaYi Zhu, Kinshuk Jain, Ian S Mackay, Patricia Chaves Guerrero, Giulia Emanuelli, Luca Jovine, Michela Noseda, Stefan J Marciniak, Micheala A Aldred, Claire L Shovlin.Mutations causing premature termination codons discriminate and generate cellular and clinical variability in HHT∗.Blood. 2024 Mar 19;143(22):2314–2331. doi: 10.1182/blood.2023021777.

221. Abramowicz Anna, Gos Monika.Splicing mutations in human genetic disorders: examples, detection, and confirmation.J Appl Genet. 2018 Apr 21;59(3):253–268. doi: 10.1007/s13353-018-0444-7.

222. David S M Lee, Joseph Park, Andrew Kromer, Aris Baras, Daniel J Rader, Marylyn D Ritchie, Louis R Ghanem, Yoseph Barash.Disrupting upstream translation in mRNAs is associated with human disease.Nat Commun. 2021 Mar 9;12(1):1515. doi: 10.1038/s41467-021-21812-1.

223. Zetao Bai, Jinfeng Chen, Yi Liao, Meijiao Wang, Rong Liu, Song Ge, Rod A. Wing & Mingsheng Chen.The impact and origin of copy number variations in the Oryza species.BMC Genomics volume 17, Article number: 261 (2016).

224. Troskie RL, Faulkner GJ, Cheetham SW.Processed pseudogenes: A substrate for evolutionary innovation: Retrotransposition contributes to genome evolution by propagating pseudogene sequences with rich regulatory potential throughout the genome. Bioessays. 2021 Nov;43(11):e2100186. doi: 10.1002/bies.202100186. Epub 2021 Sep 27.

225. Fatemeh Pourraj, Seyedhossein Hekmatimoghaddam.Transposable elements, contributors in the evolution of organisms (from an arms race to a source of raw materials).Heliyon.Volume 7, Issue 1, January 2021, e06029.

226. Sumadi Lukman Anwar, Wahyu Wulaningsih,Ulrich Lehmann Transposable Elements in Human Cancer: Causes and Consequences of Deregulation.Int J Mol Sci. 2017 May 4;18(5):974. doi: 10.3390/ijms18050974.

227. Xingyu Liao, Wufei Zhu, Juexiao Zhou, Haoyang Li, Xiaopeng Xu, Bin Zhang, Xin Gao.Repetitive DNA sequence detection and its role in the human genome.Commun Biol. 2023 Sep 19;6:954. doi: 10.1038/s42003-023-05322-y.

228. Alemu Gebrie.Transposable elements as essential elements in the control of gene expression.Mobile DNA volume 14, Article number: 9 (2023).

229. Jungnam Cho. Transposon-Derived Non-coding RNAs and Their Function in Plants.Front. Plant Sci., 03 May 2018 Sec. Plant Cell Biology.Volume 9 - 2018 | https://doi.org/10.3389/fpls.2018.00600

230. Xianwei Song, Xiaofeng Cao.Transposon-mediated epigenetic regulation contributes to phenotypic diversity and environmental adaptation in rice.Current Opinion in Plant Biology.Volume 36, April 2017, Pages 111-118.

231. Xiaolei Li,Zhiqiang Wu, Xiaobing Fu, Weidong Han.lncRNAs: Insights into their function and mechanics in underlying disorders.Mutation Research/Reviews in Mutation Research.Volume 762, October–December 2014, Pages 1-21 251.Anil Panigrahi, Bert W. O’Malley Mechanisms of enhancer action: the known and the unknown.Genome Biology volume 22, Article number: 108 (2021).

232. Victoria P Belancio, Prescott L Deininger, Astrid M Roy-Engel.LINE dancing in the human genome: transposable elements and disease.Genome Med. 2009 Oct 27;1(10):97. doi: 10.1186/gm97.

233. Gymrek, M. (2017) A genomic view of short tandem repeats. Curr. Opin. Genet. Dev. 44, 9–16 10.1016/j.gde.2017.01.012.

234.Arne Nedergaard Kousholt, Tobias Menzel, Claus Storgaard Sørensen.Pathways for Genome Integrity in G2 Phase of the Cell Cycle Biomolecules. 2012 Nov 30;2(4):579–607. doi: 10.3390/biom2040579.

235. Ellen R. Edenberg,Michael Downey,David Toczyski.Polymerase Stalling during Replication, Transcription and Translation.Current Biology.Volume 24, Issue 10, 19 May 2014, Pages R445-R452.

236. Thomas JY Kono, Alex B Brohammer,Suzanne E McGaugh,Candice N Hirsch.Tandem Duplicate Genes in Maize Are Abundant and Date to Two Distinct Periods of Time.G3 (Bethesda). 2018 Jul 20;8(9):3049–3058. doi: 10.1534/g3.118.200580.

237. Akihiro Ezoe , Kazumasa Shirai , Kousuke Hanada STRs.numerous disorders, such as cancer, various ataxias, and fragile X syndrome.Molecular Biology and Evolution, Volume 38, Issue 4, April 2021, Pages 1447–1459, <https://doi.org/10.1093/molbev/msaa302>

238. S Panzer, D P Kuhl, C T Caskey.Unstable triplet repeat sequences: a source of cancer mutations?.Review Stem Cells 1995 Mar;13(2):146-57. doi: 10.1002/stem.5530130206.

## 239. Adam MP, Feldman J, Mirzaa GM, et al., editors.Seattle (WA): University of Washington, Seattle; 1993-2025. GeneReviews® [Internet].

240. Deborah A Hall, Elizabeth Berry-Kravis.Fragile X syndrome and fragile X-associated tremor ataxia syndrome.Handb Clin Neurol. 2018:147:377-391. doi: 10.1016/B978-0-444-63233-3.00025-7.

242.Thomas W , Heidrun G, Manuel S, Cristobal U, Philippa B, Ricardo H R, Romain De O, Klaus F X M, Etienne P, Frédéric C. Impact of transposable elements on genome structure and evolution in bread wheat. Genome Biol. 2018 Aug17;19(1):103.

doi: 10.1186/s13059-018-1479-0.

245.András F, Eszter G, László I, Nicolas B, Mahmoud S, Kateřina H, Kitti Szőke-P, Tamás S, Péter M, Edina T, Klaudia K, Péter K, Éva D, Éva S, Jan B, Jaroslav D, István M. Chromosome genomics facilitates the marker development and selection of wheat-Aegilops biuncialis addition, substitution and translocation lines. Sci Rep. 2023 Nov 22;13(1):20499. doi: 10.1038/s41598-023-47845-8.

246. Pradeep K P, Muthusamy R, Sileesh M, Ruslan K, Qiang W, Long H, Zishan A, Kunnummal K V, Ping Y, Mingbing Z. Retrotransposons: How the continuous evolutionary front shapes plant genomes for response to heat stress. Front Plant Sci. 2022 Dec 9:13:1064847. doi: 10.3389/fpls.2022.1064847.

247. Qing L, Xiaoyu L, Xiangying Z, Mingzhi L, F Zhang , Trude Ss, John S H-H. The repetitive DNA landscape in Avena (Poaceae): chromosome and genome evolution defined by major repeat classes in whole-genome sequence reads. BMC Plant Biol. 2019 May 30;19(1):226. doi: 10.1186/s12870-019-1769-z.

248.Alexander A G, Nikolai N N, Igor G L, Elena V B, Viktoria S S, Nina S P, Alexander V R. New Insights into the Genomic Structure of Avena L.: Comparison of the Divergence of A-Genome and One C-Genome Oat Species. Plants (Basel). 2022 Apr 19;11(9):1103. doi: 10.3390/plants11091103.

249.Leonardo G G, Corinne M, Marie-A G, Michael K D. Ty1-copia elements reveal diverse insertion sites linked to polymorphisms among flax (Linum usitatissimum L.) accessions. BMC Genomics. 2016 Dec 7;17(1):1002. doi: 10.1186/s12864-016-3337-3.

6. 7.

250.Sean W, Liangliang G, Cecile M, Georg H, Mulualem T K, Jemima B, Ricardo H R-G, Markus C K, et al., Multiple wheat genomes reveal global variation in modern breeding. Nature. 2020 Dec;588(7837):277-283. doi: 10.1038/s41586-020-2961-x.

251.Paulina T, Trude S, J S Pat H-H. Oat chromosome and genome evolution defined by widespread terminal intergenomic translocations in polyploids. Front Plant Sci.2022 Nov 22:13:1026364. doi: 10.3389/fpls.2022.1026364.

252.Qiang He, Wei Li, Yuqing Miao, Yu Wang, Ningkun Liu, Jianan Liu, Tao Li, Yao Xiao, Hongyu Zhang, Yaru Wang, Hanfei Liang, Yange Yun, Shuhui Wang, Qingbin Sun, Hongru Wang, Zhizhong Gong, Huilong D. The near-complete genome assembly of hexaploid wild oat reveals its genome evolution and divergence with cultivated oats. Nat Plants. 2024 Dec;10(12):2062-2078. doi: 10.1038/s41477-024-01866-x.

253. Brankica Mravinac, Miroslav Plohl. Parallelism in evolution of highly repetitive DNAs in sibling species. Mol Biol Evol . 2010 Aug;27(8):1857-67. doi: 10.1093/molbev/msq068.

254. R F Park, W H P Boshoff, A L Cabral, J Chong, J A Martinelli, M S McMullen, J W M F, E Paczos-Grzęda , E Prats, J Roake, S Sowa, L Ziems, D Singh. Breeding oat for resistance to the crown rust pathogen Puccinia coronata f. sp. avenae: achievements and prospects. Theor Appl Genet. 2022 Nov;135(11):3709-3734. doi: 10.1007/s00122-022-04121-z. Epub 2022 Jun 4.

255.Yves Van de Peer, Tia-Lynn Ashman, Pamela S Soltis, Douglas E Soltis. Polyploidy: an evolutionary and ecological force in stressful times.Plant Cell. 2021;33(1):11-26. doi: 10.1093/plcell/koaa015.

256.Itay M, Martin A L. The Evolution of Chromosome Numbers: Mechanistic Models and Experimental Approaches. Genome Biol Evol. 2021 Feb 3;13(2). doi: 10.1093/gbe/evaa220.

275.

257.Frese L, Ford-Lloyd B. Taxonomy, phylogeny, and the genepool. In book: Beta maritima. Springer, Cham. 2020; 121-151.doi:10.1007/978-3-030-28748-1\_6.

258.Juliane C Dohm, Andre E Minoche, Daniela Holtgrawe, Salvador Capella-Gutierrez, Falk Zakrzewski, Hakim Tafer, Oliver Rupp, Thomas Rosleff Sorensen, et al. The genome of the recently domesticated crop plant sugar beet (Beta vulgaris). Nature. 2014;505(7484):546-9. doi: 10.1038/nature12817.

259. Schmidt, N., Sielemann, K., Breitenbach, S., Fuchs, J., Pucker, B., Weisshaar, B., Holtgräwe, D. and Heitkam, T. (2024), Repeat turnover meets stable chromosomes: repetitive DNA sequences mark speciation and gene pool boundaries in sugar beet and wild beets. Plant J, 118: 171-190. <https://doi.org/10.1111/tpj.16599>.

260. Paul Galewski, J Mitchell McGrath.Genetic diversity among cultivated beets (Beta vulgaris) assessed via population-based whole genome sequencesBMC Genomics. 2020 Mar 2;21:189. doi: 10.1186/s12864-020-6451-1

261.Sophie Maiwald, Beatrice Weber, Kathrin M Seibt, Thomas Schmidt, Tony Heitkam. The Cassandra retrotransposon landscape in sugar beet (Beta vulgaris) and related Amaranthaceae: recombination and re-shuffling lead to a high structural variability. Ann Bot. 2021 Jan 1;127(1):91-109. doi: 10.1093/aob/mcaa176.

262.Falk Zakrzewski, Martin Schmidt, Mieke Van Lijsebettens, Thomas Schmidt. DNA methylation of retrotransposons, DNA transposons and genes in sugar beet (Beta vulgaris L.). Plant J. 2017;90(6):1156-1175. doi: 10.1111/tpj.13526.

263.Tony Heitkam, Beatrice Weber, Ines Walter, Susan Liedtke, Charlotte Ost, Thomas Schmidt. Satellite DNA landscapes after allotetraploidization of quinoa (Chenopodium quinoa) reveal unique A and B subgenomes. Plant J. 2020;103(1):32-52. doi: 10.1111/tpj.14705.

264. Xiaofeng Cai, Xuepeng Sun, Chenxi Xu, Honghe Sun, Xiaoli Wang, Chenhui Ge, Zhonghua Zhang, Quanxi Wang, Zhangjun Fei, Chen Jiao, Quanhua Wang. Genomic analyses provide insights into spinach domestication and the genetic basis of agronomic traits. Nat Commun. 2021;12(1):7246. doi: 10.1038/s41467-021-27432-z.

265. Wang, Wencai ,Zhang, Xianzhi, Garcia, Sònia, Leitch, Andrew Kovarik, Ales. (2023). Intragenomic rDNA variation - the product of concerted evolution, mutation, or something in between? Heredity. 131. 10.1038/s41437-023-00634-5.

266. Bruno Rafael Ribeiro de Almeida, Luciano Farias Souza, Thyana Ayres Alves, Adauto Lima Cardoso, Juliana Amorim de Oliveira, Talita Fernanda Augusto Ribas, Carlos Eduardo Vasconcelos Dos Santos, Luís Adriano Santos do Nascimento, Leandro Melo Sousa, Maria Iracilda da Cunha Sampaio, Cesar Martins, Cleusa Yoshiko Nagamachi, Julio Cesar Pieczarka, Renata Coelho Rodrigues Noronha. Chromosomal organization of multigene families and meiotic analysis in species of Loricariidae (Siluriformes) from Brazilian Amazon, with description of a new cytotype for genus Spatuloricaria. Biol Open. 2023 Nov 15;12(11): bio060029. doi: 10.1242/bio.060029. Epub 2023 Nov 9.

Almeida BRR, Farias Souza L, Alves TA, Cardoso AL, de Oliveira JA, Augusto Ribas TF, Dos Santos CEV, do Nascimento LAS, Sousa LM, da Cunha Sampaio MI, Martins C, Nagamachi CY, Pieczarka JC, Noronha RCR. Chromosomal organization of multigene families and meiotic analysis in species of Loricariidae (Siluriformes) from Brazilian Amazon, with description of a new cytotype for genus Spatuloricaria. Biol Open. 2023 Nov 15;12(11):bio060029. doi: 10.1242/bio.060029.

267.D Liao. Concerted evolution: molecular mechanism and biological implications. Am J Hum Genet. 1999 Jan;64(1):24-30. doi: 10.1086/302221.

268.T Pavelitz, L Rusché, A G Matera, J M Scharf, A M Weiner. Concerted evolution of the tandem array encoding primate U2 snRNA occurs in situ, without changing the cytological context of the RNU2 locus. EMBO J. 1995 Jan 3;14(1):169-77. doi: 10.1002/j.1460-2075. 1995.tb06987.x.

269. Bo Xu, Xiao-Mao Zeng, Xin-Fen Gao, Dong-Pil Jin, Li-Bing Zhang. ITS non-concerted evolution and rampant hybridization in the legume genus Lespedeza (Fabaceae). Sci Rep. 2017 Jan 4:7:40057. doi: 10.1038/srep40057.

270.Emiliano Martí, Diogo Milani, Vanessa B Bardella, Lucas Albuquerque, Hojun Song, Octavio M Palacios-Gimenez, Diogo C Cabral-de-Mello. Cytogenomic analysis unveils mixed molecular evolution and recurrent chromosomal rearrangements shaping the multigene families on Schistocerca grasshopper genomes. Evolution. 2021 Aug;75(8):2027-2041. doi: 10.1111/evo.14287. Epub 2021 Jul 5.

271. András Tóth, Lóránt Székvölgyi, Tibor Vellai. The genome loading model for the origin and maintenance of sex in eukaryotes. Biol Futur. 2022 Dec;73(4):345-357. doi: 10.1007/s42977-022-00148-x. Epub 2022 Dec 19.

272. Lunerová, S. Renny-Byfield, R. Matyášek, A. Leitch & A. Kovařík.Concerted evolution rapidly eliminates sequence variation in rDNA coding regions but not in intergenic spacers in Nicotiana tabacum allotetraploid. Plant Syst Evol. 2017;303:1043–1060.

273.Moritz Otto, Yichen Zheng, Thomas Wiehe. Recombination, selection, and the evolution of tandem gene arrays. Genetics. 2022 Jul 4;221(3):iyac052. doi: 10.1093/genetics/iyac052.

274. Meiyuan Ji, Huyen Bui, Ricardo A Ramirez, Richard M Clark. Concerted cis and trans effects underpin heightened defense gene expression in multi-herbivore-resistant maize lines. Plant J. 2022 Jul;111(2):508-528. doi: 10.1111/tpj.15812. Epub 2022 Jun 5.

275. James A. Birchler and Gernot G. Presting.Retrotransposon insertion targeting:a mechanism for homogenization of centromere sequences on nonhomologous chromosomes.GENES & DEVELOPMENT 26:638–640 2012.

Birchler JA, Presting GG. Retrotransposon insertion targeting: a mechanism for homogenization of centromere sequences on nonhomologous chromosomes. Genes Dev. 2012;26(7):638-40. doi: 10.1101/gad.191049.112.

276. Tsuneo Sasanuma, Deepmala Sehgal, Tetsuo Sasakuma, and Soom Nath Raina Phylogenetic analysis of Carthamus species based on the nucleotide sequence of the nuclear SACPD gene and chloroplast trnL–trnF IGS region.Genome.Volume 51, Number 9.September 2008

277. [Federico G Hoffmann](https://pubmed.ncbi.nlm.nih.gov/?term=Hoffmann+FG&cauthor_id=34480557), [Jay F Storz](https://pubmed.ncbi.nlm.nih.gov/?term=Storz+JF&cauthor_id=34480557), [Shigehiro Kuraku](https://pubmed.ncbi.nlm.nih.gov/?term=Kuraku+S&cauthor_id=34480557), [Michael W Vandewege](https://pubmed.ncbi.nlm.nih.gov/?term=Vandewege+MW&cauthor_id=34480557), [Juan C Opazo](https://pubmed.ncbi.nlm.nih.gov/?term=Opazo+JC&cauthor_id=34480557). Whole-Genome Duplications and the Diversification of the Globin-X Genes of Vertebrates. Genome Biol Evol. 2021 Oct 1;13(10):evab205. doi: 10.1093/gbe/evab205.

278.J Blommaert, S Riss, B Hecox-Lea, D B Mark Welch, C P Stelzer.Small, but surprisingly repetitive genomes: transposon expansion and not polyploidy has driven a doubling in genome size in a metazoan species complex.BMC Genomics. 2019 Jun 7;20(1):466. doi: 10.1186/s12864-019-5859-y.

279.Claus-Peter Stelzer, Simone Riss, Peter Stadler.Genome size evolution at the speciation level: the cryptic species complex Brachionus plicatilis (Rotifera)BMC Evol Biol. 2011 Apr 7:11:90. doi: 10.1186/1471-2148-11-90.

280. Jonathon E Mohl, Patrick D Brown, Aaron J Robbins, Philip Lavretsky, Rick Hochberg, Robert L Wallace, Elizabeth J Walsh.Comparing Small and Large Genomes Within Monogonont Rotifers.Genome Biol Evol. 2025 Mar 6;17(3):evaf041. doi: 10.1093/gbe/evaf041.

281. Yimeng Nie, Xuanzeng Liu, Lina Zhao, Yuan Huang.Repetitive element expansions contribute to genome size gigantism in Pamphagidae: A comparative study (Orthoptera, Acridoidea).Genomics. 2024 Sep;116(5):110896. doi: 10.1016/j.ygeno.2024.110896. Epub 2024 Jul 19.

282. Yu-Fei Yang, Tao Zhu, Deng-Ke Niu.Association of intron loss with high mutation rate in Arabidopsis: implications for genome size evolution.Genome Biol Evol. 2013;5(4):723-33. doi: 10.1093/gbe/evt043.

283.Aurélie Kapusta, Alexander Suh, Cédric Feschotte.Dynamics of genome size evolution in birds and mammals.Proc Natl Acad Sci U S A

. 2017 Feb 21;114(8):E1460-E1469. doi: 10.1073/pnas.1616702114. Epub 2017 Feb 8.

284. Simone Riss, Wolfgang Arthofer, Florian M Steiner, Birgit C Schlick-Steiner, Maria Pichler, Peter Stadler, Claus-Peter Stelzer. Do genome size differences within Brachionus asplanchnoidis (Rotifera, Monogononta) cause reproductive barriers among geographic populations?Hydrobiologia. 2017 Jul;796(1):59-75. doi: 10.1007/s10750-016-2872-x. Epub 2016 Jun 30.

285. Robin A Weiss.On the concept and elucidation of endogenous retroviruses.

Philos Trans R Soc Lond B Biol Sci. 2013 Aug 12;368(1626):20120494. doi: 10.1098/rstb.2012.0494. Print 2013 Sep 19.

286. Alexander Hayward, Charlie K Cornwallis, Patric Jern.Pan-vertebrate comparative genomics unmasks retrovirus macroevolutionProc Natl Acad Sci U S A. 2015 Jan 13;112(2):464-9. doi: 10.1073/pnas.1414980112. Epub 2014 Dec 22.

287. Salvador Daniel Rivas-Carrillo, Mats E Pettersson, Carl-Johan Rubin, Patric Jern.Whole-genome comparison of endogenous retrovirus segregation across wild and domestic host species populations.Proc Natl Acad Sci U S A. 2018 Oct 23;115(43):11012-11017. doi: 10.1073/pnas.1815056115. Epub 2018 Oct 8.

288.Alex D Greenwood, Yasuko Ishida, Sean P O'Brien, Alfred L Roca, Maribeth V Eiden.Transmission, Evolution, and Endogenization: Lessons Learned from Recent Retroviral Invasions Microbiol Mol Biol Rev. 2017 Dec 13;82(1):e00044-17. doi: 10.1128/MMBR.00044-17. Print 2018 Mar.

289. Farid Benachenhou, Göran O Sperber, Erik Bongcam-Rudloff, Göran Andersson, Jef D Boeke & Jonas Blomberg.Conserved structure and inferred evolutionary history of long terminal repeats (LTRs).Mobile DNA volume 4, Article number: 5 (2013)

290. Yicong Chen, Xiaojing Wang, Meng-En Liao, Yuhe Song, Yu-Yi Zhang, Jie Cui.Evolution and Genetic Diversity of the Retroviral Envelope in Anamniotes.J Virol. 2022 Apr 7;96(8):e02072-21. doi: 10.1128/jvi.02072-21.

291.Xiaoyu Zhuo, Cédric Feschotte.Cross-Species Transmission and Differential Fate of an Endogenous Retrovirus in Three Mammal Lineages.PLoS Pathog

. 2015 Nov 12;11(11):e1005279. doi: 10.1371/journal.ppat.1005279. eCollection 2015.

292.Selene Ingusci, Bonnie L Hall 1, William F Goins, Justus B Cohen, Joseph C Glorioso.Viral vectors for gene delivery to the central nervous system.Handb Clin Neurol. 2024:205:59-81. doi: 10.1016/B978-0-323-90120-8.00001-0.

293. Savannah J Klein, Rachel J O'Neill.Transposable elements: genome innovation, chromosome diversity, and centromere conflict.Chromosome Res. 2018 Mar;26(1-2):5-23. doi: 10.1007/s10577-017-9569-5. Epub 2018 Jan 13.

294.Changcheng Wu, Jian Lu. Diversification of Transposable Elements in Arthropods and Its Impact on Genome Evolution.Genes (Basel) 2019 May; 10(5): 338. Published online 2019 May 6. doi: 10.3390/genes10050338.

295.Aurélie Kapusta, Alexander Suh, Cédric Feschotte. Dynamics of genome size evolution in birds and mammals.Proc Natl Acad Sci U S A. 2017 Feb 21;114(8):E1460-E1469. doi: 10.1073/pnas.1616702114. Epub 2017 Feb 8.

296.Changcheng Wu, Jian Lu.Diversification of Transposable Elements in Arthropods and Its Impact on Genome Evolution.Genes (Basel). 2019 May 6;10(5):338. doi: 10.3390/genes10050338.

297.Jie Wang, Guangpu Zhang, Cheng Sun, Liming Chang, Yingyong Wang, Xin Yang, Guiying Chen, Michael W Itgen, Ava Haley , Jiaxing Tang, Rachel Lockridge Mueller.DNA gains and losses in gigantic genomes do not track differences in transposable element-host silencing interactions.Commun Biol. 2025 May 6;8:704. doi: 10.1038/s42003-025-08127-3

298.Alexander Nater, Reto Burri, Takeshi Kawakami, Linnéa Smeds, Hans Ellegren.Resolving Evolutionary Relationships in Closely Related Species with Whole-Genome Sequencing Data. Syst Biol. 2015 Nov;64(6):1000-17. doi: 10.1093/sysbio/syv045. Epub 2015 Jul 17.

299.Antonio Serrato-Capuchina, Daniel R Matute.The Role of Transposable Elements in SpeciationGenes (Basel). 2018 May 15;9(5):254. doi: 10.3390/genes9050254.

300.Jacqueline Robinson, Christopher C Kyriazis, Stella C Yuan, Kirk E Lohmueller.Deleterious Variation in Natural Populations and Implications for Conservation Genetics.Annu Rev Anim Biosci. 2022 Nov 4;11:93–114. doi: 10.1146/annurev-animal-080522-093311.

301.R Wambui Mbichi, Qing-Feng Wang, Tao Wan.RNA directed DNA methylation and seed plant genome evolution.Plant Cell Rep. 2020 Aug;39(8):983-996. doi: 10.1007/s00299-020-02558-4..

302. Chunhui Zhang, Lei Wang, Liang Dou, Bisong Yue, Jinchuan Xing, Jing Li.Transposable Elements Shape the Genome Diversity and the Evolution of Noctuidae Species.Genes (Basel). 2023 Jun 10;14(6):1244. doi: 10.3390/genes14061244.

303.Justin P Blumenstiel.From the cauldron of conflict: Endogenous gene regulation by piRNA and other modes of adaptation enabled by selfish transposable elements

Semin Cell Dev Biol. 2025 Jan 1:164:1-12. doi: 10.1016/j.semcdb.2024.05.001. Epub 2024 May 31.

304.Christopher D Todd, Özgen Deniz, Darren Taylor, Miguel R Branco.

Functional evaluation of transposable elements as enhancers in mouse embryonic and trophoblast stem cellsElife.2019 Apr 23:8:e44344. doi: 10.7554/eLife.44344.

305.Erica Gasparotto, Filippo Vittorio Burattin, Valeria Di Gioia, Michele Panepuccia, Valeria Ranzani, Federica Marasca, Beatrice Bodega.Transposable Elements Co-Option in Genome Evolution and Gene Regulation Int J Mol Sci

. 2023 Jan 30;24(3):2610. doi: 10.3390/ijms24032610.

306.Bing Chen, Martin E Feder, Le Kang.Evolution of heat-shock protein expression underlying adaptive responses to environmental stress Mol Ecol

. 2018 Aug;27(15):3040-3054. doi: 10.1111/mec.14769. Epub 2018 Jul 2.

307. Jaume Pellicer, Oriane Hidalgo, Steven Dodsworth, Ilia J Leitch.Genome Size Diversity and Its Impact on the Evolution of Land Plants Genes (Basel)

. 2018 Feb 14;9(2):88. doi: 10.3390/genes9020088.

308.Flavia Mascagni, Tommaso Giordani, Marilena Ceccarelli, Andrea Cavallini, Lucia Natali.Genome-wide analysis of LTR-retrotransposon diversity and its impact on the evolution of the genus Helianthus (L.).BMC Genomics. 2017 Aug 18;18(1):634. doi: 10.1186/s12864-017-4050-6.

309.Mikhail Kazancev, Pavel Merkulov, Kirill Tiurin, Yakov Demurin, Alexander Soloviev, Ilya Kirov.Comparative Analysis of Active LTR Retrotransposons in Sunflower (Helianthus annuus L.): From Extrachromosomal Circular DNA Detection to Protein Structure Prediction.Int J Mol Sci. 2024 Dec 19;25(24):13615. doi: 10.3390/ijms252413615.

310. Maria Ventimiglia, Marco Castellacci, Gabriele Usai, Alberto Vangelisti, Samuel Simoni, Lucia Natali, Andrea Cavallini, Flavia Mascagni, Tommaso Giordani.Discovering the Repeatome of Five Species Belonging to the Asteraceae Family: A Computational Study.Plants (Basel).2023 Mar 22;12(6):1405. doi: 10.3390/plants12061405.

311.Ungerer, Mark, Strakosh, Suzanne, Stimpson, Kaitlin. (2009). Proliferation of Ty3/gypsy-like retrotransposons in hybrid sunflower taxa inferred from phylogenetic data. BMC biology. 7. 40. 10.1186/1741-7007-7-40.

312.Guillaume Bourque, Kathleen H Burns, Mary Gehring, Vera Gorbunova, Andrei Seluanov, Molly Hammell, Michaël Imbeault,Zsuzsanna Izsvák, Henry L Levin , Todd S Macfarlan, Dixie L Mager, Cédric Feschotte.Ten things you should know about transposable elements.Genome Biol. 2018 Nov 19;19(1):199. doi: 10.1186/s13059-018-1577-z.

Bourque G, Burns KH, Gehring M, Gorbunova V, Seluanov A, Hammell M, Imbeault M, Izsvák Z, Levin HL, Macfarlan TS, Mager DL, Feschotte C. Ten things you should know about transposable elements. Genome Biol. 2018 Nov 19;19(1):199. doi: 10.1186/s13059-018-1577-z.

313. Gabriele Usai, Flavia Mascagni, Alberto Vangelisti, Tommaso Giordani, Marilena Ceccarelli, Andrea Cavallini, Lucia Natali.Interspecific hybridisation and LTR-retrotransposon mobilisation-related structural variation in plants: A case study.Genomics. 2020 Mar;112(2):1611-1621. doi: 10.1016/j.ygeno.2019.09.010. Epub 2019 Oct 9.

314.L Natali, A Cavallini, G Cionini, O Sassoli, P G Cionini, M Durante.Nuclear DNA changes within Helianthus annum L.: changes within single progenies and their relationships with plant development.Theor Appl Genet. 1993 Jan;85(5):506-12. doi: 10.1007/BF00220906.

315.Petra Hloušková, Terezie Mandáková, Milan Pouch, Pavel Trávníček, Martin A Lysak.The large genome size variation in the Hesperis clade was shaped by the prevalent proliferation of DNA repeats and rarer genome downsizing. Ann Bot. 2019 Aug 2;124(1):103-120. doi: 10.1093/aob/mcz036.

316. Stephen L Brusatte, Jingmai K O Connor, Erich D Jarvis. The Origin and Diversification of Birds. Curr Biol. 2015;25(19): R888-98. doi: 10.1016/j.cub.2015.08.003.

317. Rafael Kretschmer, Malcolm A Ferguson-Smith, Edivaldo Herculano Correa de Oliveira. Karyotype Evolution in Birds: From Conventional Staining to Chromosome Painting. Genes (Basel). 2018;9(4):181. doi: 10.3390/genes9040181.

318.Natalie A Wright, T Ryan Gregory, Christopher C Witt. Metabolic 'engines' of flight drive genome size reduction in birds. Proc Biol Sci. 2014;281(1779):20132780. doi: 10.1098/rspb.2013.2780.

319.Marcelo de Bello Cioffi, Eduard Kejnovsky, Vinicius Marquioni, Juliana Poltronieri, Wagner Franco Molina, Débora Diniz, Luiz Antonio Carlos Bertollo.The key role of repeated DNAs in sex chromosome evolution in two fish species with ZW sex chromosome system. Mol Cytogenet. 2012;5(1):28. doi: 10.1186/1755-8166-5-28.

320.Kaize Feng, Chuang Zhou, Lei Wang, Chunhui Zhang, Zhixiong Yang, Zhengrui Hu, Bisong Yue, Yongjie Wu. Comprehensive Comparative Analysis Sheds Light on the Patterns of Microsatellite Distribution across Birds Based on the Chromosome-Level Genomes. Animals (Basel). 2023;13(4):655. doi: 10.3390/ani13040655.

321.Yun Xia, Hanrou Huang, Yulin Liang, Douyue Li, Tingyi Chen, Ruixue Shi, Saichao Pan, Fei Xu, Shaoliang Peng, Zhongyang Tan. Maps of high-density microsatellites accumulation in human genome. BMC Genomics.2022. doi: 10.1186/s12864-024-10843-9.

322. Surabhi Srivastava, Akshay Kumar Avvaru, Divya Tej Sowpati & Rakesh K. Mishra. Patterns of microsatellite distribution across eukaryotic genomes. BMC Genomics.2019;20(153). doi:10.1186/s12864-019-5516-5.

323. Manee M. Manee, Abdulmalek T. Algarni, Sultan N. Alharbi, Badr M. Al-Shomrani, Mohanad A. Ibrahim, Sarah A. Binghadir & Mohamed B. Al-Fageeh. Genome-wide characterization and analysis of microsatellite sequences in camelid species. Mammal Research. 2020; 65(16). doi:10.1007/s13364-019-00458-x.

324. Xuhao Song, Tingbang Yang, Xinyi Zhang, Ying Yuan, Xianghui Yan, Yi Wei, Jun Zhang, Caiquan Zhou. Comparison of the Microsatellite Distribution Patterns in the Genomes of Euarchontoglires at the Taxonomic Level. Front Genet.2021:12:622724. doi: 10.3389/fgene.2021.622724.

325.Anna S Trigos, Richard B Pearson, Anthony T Papenfuss, David L Goode. Somatic mutations in early metazoan genes disrupt regulatory links between unicellular and multicellular genes in cancer. Elife. 2019:8:e40947. doi: 10.7554/eLife.40947.

326.Michael S Neuberger. Antibody diversification by somatic mutation: from Burnet onwards.
Immunol Cell Biol.2008;86(2):124-32. doi: 10.1038/sj.icb.7100160.

327. John R Bracht, Wenwen Fang, Aaron David Goldman, Egor Dolzhenko, Elizabeth M Stein, Laura F Landweber. Genomes on the edge: programmed genome instability in ciliates. Cell. 2013;152(3):406-16. doi: 10.1016/j.cell.2013.01.005.

328. Andrey Grishanin. ﻿Chromatin diminution as a tool to study some biological problems. Comp Cytogenet. 2024:18:27-49. doi: 10.3897/compcytogen.17.112152.

329. Yuanyuan Kang, Jianbin Wang, Ashley Neff, Stella Kratzer, Hiroshi Kimura, Richard E Davis. Differential Chromosomal Localization of Centromeric Histone CENP-A Contributes to Nematode Programmed DNA Elimination. Cell Rep.2016;16(9):2308-16. doi: 10.1016/j.celrep.2016.07.079.

330. Maxim V Zagoskin, Jianbin Wang. Programmed DNA elimination: silencing genes and repetitive sequences in somatic cells. Biochem Soc Trans. 2021;49(5):1891-1903. doi: 10.1042/BST20190951.

331. Adrian Streit, Jianbin Wang, Yuanyuan Kang, Richard E Davis. Gene Silencing and Sex Determination by Programmed DNA Elimination in Parasitic Nematodes. Curr Opin Microbiol. 2016;32:120–127. doi: 10.1016/j.mib.2016.05.012.

332. Jianbin Wang, Giovana M B Veronezi, Yuanyuan Kang, Maxim Zagoskin, Eileen T O'Toole, Richard E Davis. Comprehensive Chromosome End Remodeling during Programmed DNA Elimination. Curr Biol. 2020;30(17):3397-3413.e4. doi: 10.1016/j.cub.2020.06.058.

333.Malgorzata Kloc, Jacek Z Kubiak, Rafik M Ghobrial. Natural genetic engineering: A programmed chromosome/DNA elimination. Dev Biol. 2022:486:15-25. doi: 10.1016/j.ydbio.2022.03.008.

334. Leon Perrie, Remy Amice, Lara D. Shepherd, & P.J. Brownsey.(2023) Tmesipteris alticola (Psilotaceae), a new fern species endemic to New Caledonia. New Zealand Journal of Botany 63(1):1-13. doi:10.1080/0028825X.2023.2240737.

335. Pol Fernández, Rémy Amice, David Bruy, Maarten J M Christenhusz, Ilia J Leitch, Andrew L Leitch, Lisa Pokorny, Oriane Hidalgo, Jaume Pellicer. A 160 Gbp fork fern genome shatters size record for eukaryotes. iScience.2024;27(6):109889. doi: 10.1016/j.isci.2024.109889.

336. Jaume Pellicer, Laura J Kelly, Ilia J Leitch, Wendy B Zomlefer, Michael F Fay. A universe of dwarfs and giants: genome size and chromosome evolution in the monocot family Melanthiaceae. New Phytol.2014;201(4):1484-1497. doi: 10.1111/nph.12617.

337. Hong-Mei Liu, Libor Ekrt, Petr Koutecky, Jaume Pellicer, Oriane Hidalgo, Jeannine Marquardt, Fatima Pustahija, Atsushi Ebihara, Sonja Siljak-Yakovlev, Mary Gibby, Ilia Leitch, Harald Schneider. Polyploidy does not control all: Lineage-specific average chromosome length constrains genome size evolution in ferns. Journal of Systematics and Evolution.2019;57(4): 418-430. doi:10.1111/jse.12525.

338. Pol Fernández, Ilia J Leitch, Andrew R Leitch, Oriane Hidalgo, Maarten J M Christenhusz, Lisa Pokorny, Jaume Pellicer. Giant Fern Genomes Show Complex Evolution Patterns: A Comparative Analysis in Two Species of Tmesipteris (Psilotaceae). Int J Mol Sci.2023;24(3):2708. doi: 10.3390/ijms24032708.

340.Giovanni Pascarella, Martin Frith, Piero Carninci. Challenges in Detecting Somatic Recombination of Repeat Elements: Insights from Short and Long Read Datasets.Biorxiv.2024. doi:10.1101/2024.08.25.609631.

341.Jerome Savocco, Aurele Piazza. Recombination-mediated genome rearrangements. Curr Opin Genet Dev. 2021:71:63-71. doi: 10.1016/j.gde.2021.06.008.

342. Kalpana Mujoo, Raj K Pandita, Anjana Tiwari, Vijay Charaka, Sharmistha Chakraborty, Dharmendra Kumar Singh, Shashank Hambarde, Walter N Hittelman, Nobuo Horikoshi, Clayton R Hunt, Kum Kum Khanna, Alexander Y Kots, E Brian Butler, Ferid Murad, Tej K Pandita. Differentiation of Human Induced Pluripotent or Embryonic Stem Cells Decreases the DNA Damage Repair by Homologous Recombination. Stem Cell Reports.2017;9(5):1660-1674. doi: 10.1016/j.stemcr.2017.10.002.

343. Paolo Mita, Jef D Boeke. How retrotransposons shape genome regulation. Curr Opin Genet Dev. 2016:37:90-100. doi: 10.1016/j.gde.2016.01.001.

344. Shen Gu, Bo Yuan, Ian M Campbell, Christine R Beck, Claudia M B Carvalho, Sandesh C S Nagamani, Ayelet Erez, Ankita Patel, Carlos A Bacino, Chad A Shaw, Paweł Stankiewicz, Sau Wai Cheung, Weimin Bi, James R Lupski. Alu-mediated diverse and complex pathogenic copy-number variants within human chromosome 17 at p13.3. Hum Mol Genet. 2015;24(14):4061-77. doi: 10.1093/hmg/ddv146.

345. Marit W Vermunt, Di Zhang, Gerd A Blobel. The interdependence of gene-regulatory elements and the 3D genome. J Cell Biol. 2019;218(1):12-26. doi: 10.1083/jcb.201809040.

346. Giovanni Pascarella, Chung Chau Hon, Kosuke Hashimoto, Annika Busch, Joachim Luginbuhl, Callum Parr, Wing Hin Yip, Kazumi Abe, Anton Kratz, Alessandro Bonetti, Federico Agostini, Jessica Severin, Shigeo Murayama, Yutaka Suzuki, Stefano Gustincich, Martin Frith, Piero Carninci. Recombination of repeat elements generates somatic complexity in human genomes. Cell. 2022;185(16):3025-3040.e6. doi: 10.1016/j.cell.2022.06.032.

347.Tyler D P Brunet, W Ford Doolittle.Multilevel Selection Theory and the Evolutionary Functions of Transposable Elements Genome Biol Evol. 2015 Aug 6;7(8):2445-57. doi: 10.1093/gbe/evv152.

348. Tyler D P Brunet, W Ford Doolittle. Multilevel Selection Theory and the Evolutionary Functions of Transposable Elements. Genome Biol Evol. 2015;7(8):2445-57. doi: 10.1093/gbe/evv152.

349. Lei Wu, Xiaolu Jiao, Dezhi Zhang, Yalin Cheng, Gang Song, Yanhua Qu, Fumin Lei. Comparative Genomics and Evolution of Avian Specialized Traits. Curr Genomics. 2021;22(7):496-511. doi: 10.2174/1389202923666211227143952.

350. Fidel Botero-Castro, Emeric Figuet, Marie-Ka Tilak, Benoit Nabholz, Nicolas Galtier. Avian Genomes Revisited: Hidden Genes Uncovered and the Rates versus Traits Paradox in Birds. Mol Biol Evol. 2017;34(12):3123-3131. doi: 10.1093/molbev/msx236.

351.Thays Duarte de Oliveira, Rafael Kretschmer, Natasha Avila Bertocchi, Tiago Marafiga Degrandi, Edivaldo Herculano Correa de Oliveira, Marcelo de Bello Cioffi, Analia Del Valle Garnero, Ricardo Jose Gunski. Genomic Organization of Repetitive DNA in Woodpeckers (Aves, Piciformes): Implications for Karyotype and ZW Sex Chromosome Differentiation. PLoS One. 2017;12(1): e0169987. doi: 10.1371/journal.pone.0169987.

352.Thomas Forest, Guillaume Achaz, Martial Marbouty, Amaury Bignaud, Agnes Thierry, Romain Koszul, Marine Milhes, Joanna Lledo, Jean-Marc Pons, Jerome Fuchs. Chromosome-level genome assembly of the European green woodpecker Picus viridis. G3 (Bethesda). 2024;14(5):jkae042. doi: 10.1093/g3journal/jkae042.

353. Joseph D Manthey, Robert G Moyle, Stephane Boissinot. Multiple and Independent Phases of Transposable Element Amplification in the Genomes of Piciformes (Woodpeckers and Allies). Genome Biol Evol. 2018;10(6):1445-1456. doi: 10.1093/gbe/evy105.

354. Guilherme Mota Souza, Jhon Alex Dziechciarz Vidal, Ricardo Utsunomia, Geize Aparecida Deon, Edivaldo Herculano Correa de Oliveira, Raqueli Teresinha Franca, Fabio Porto-Foresti, Thomas Liehr, Fernando Henrique Santos de Souza, Rafael Kretschmer, Marcelo de Bello Cioffi. Cytogenomic analysis in Seriemas (Cariamidae): Insights into an Atypical Avian Karyotype. J Hered. 2025:esaf012. doi: 10.1093/jhered/esaf012.

355.Marcelo Santos de Souza, Rafael Kretschmer, Suziane Alves Barcellos, Alice Lemos Costa, Marcelo de Bello Cioffi, Edivaldo Herculano Correa de Oliveira, Analía Del Valle Garnero, Ricardo Jose Gunski.Repeat Sequence Mapping Shows Different W Chromosome Evolutionary Pathways in Two Caprimulgiformes Families. Birds. 2020; 1(1): 19-34. doi:10.3390/birds1010004.

356. Alexandr Sember, Luiz A C Bertollo, Petr Rab, Cassia F Yano, Terumi Hatanaka, Ezequiel A de Oliveira, Marcelo de Bello Cioffi. Sex Chromosome Evolution and Genomic Divergence in the Fish Hoplias malabaricus (Characiformes, Erythrinidae). Front Genet.2018:9:71. doi: 10.3389/fgene.2018.00071.

357. Syed Farhan Ahmad, Worapong Singchat, Thitipong Panthum, Kornsorn Srikulnath. Impact of Repetitive DNA Elements on Snake Genome Biology and Evolution. Cells. 2021;10(7):1707. doi: 10.3390/cells10071707.

358.Patrik F Viana, Tariq Ezaz, Marcelo de Bello Cioffi, Thomas Liehr, Ahmed Al-Rikabi, Leonardo G Goll, Anderson M Rocha, Eliana Feldberg. Landscape of snake' sex chromosomes evolution spanning 85 MYR reveals ancestry of sequences despite distinct evolutionary trajectories. Sci Rep. 2020;10(1):12499. doi: 10.1038/s41598-020-69349-5.

359. Kyle J Shaney, Daren C. Card, Drew R Schield, Robert P Ruggiero. Squamate Reptile Genomics and Evolution. Toxinology. 2014:1-18. doi:10.1007/978-94-007-6649-5\_34-2.

360.Giulia I M Pasquesi, Richard H Adams, Daren C Card, Drew R Schield, Andrew B Corbin, Blair W Perry, Jacobo Reyes-Velasco, Robert P Ruggiero, Michael W Vandewege, Jonathan A Shortt, Todd A Castoe. Squamate reptiles challenge paradigms of genomic repeat element evolution set by birds and mammals. Nat Commun. 2018;9(1):2774. doi: 10.1038/s41467-018-05279-1.

361.Jin Sun, Chong Chen, Norio Miyamoto, Runsheng Li, Julia D Sigwart, Ting Xu, Yanan Sun, Wai Chuen Wong, Jack C H Ip, Weipeng Zhang, Yi Lan, Dass Bissessur, Tomo-O Watsuji, Hiromi Kayama Watanabe, Yoshihiro Takaki, Kazuho Ikeo, Nobuyuki Fujii, Kazutoshi Yoshitake, Jian-Wen Qiu, Ken Takai, Pei-Yuan Qian. The Scaly-foot Snail genome and implications for the origins of biomineralised armour. Nat Commun.2020;11(1):1657. doi: 10.1038/s41467-020-15522-3.

362.Jiabi Chen, Menghan Wang, Xionglei He, Jian-Rong Yang, Xiaoshu Chen. The evolution of sex chromosome dosage compensation in animals. J Genet Genomics. 2020;47(11):681-693. doi: 10.1016/j.jgg.2020.10.005.

363.Barbora Augstenová, Martina Johnson Pokorná, Marie Altmanová, Daniel Frynta, Michail Rovatsos, Lukáš Kratochví .ZW, XY, and yet ZW: Sex chromosome evolution in snakes even more complicated.Evolution. 2018 Jul 4. doi: 10.1111/evo.13543. Online ahead of print.

364. Drew R Schield, Daren C Card, Nicole R Hales, Blair W Perry, Giulia M Pasquesi, Heath Blackmon, Richard H Adams, Andrew B Corbin, Cara F Smith. et al., The origins and evolution of chromosomes, dosage compensation, and mechanisms underlying venom regulation in snakes.Genome Res. 2019 Apr;29(4):590–601. doi: 10.1101/gr.240952.118

365.Pedro G Nachtigall, Brett R Hamilton, Taline D Kazandjian, Paolo Stincone, Daniel Petras, Nicholas R Casewell, Eivind A B Undheim. The gene regulatory mechanisms shaping the heterogeneity of venom production in the Cape coral snake. Genome Biol. 2025;26(1):130. doi: 10.1186/s13059-025-03602-w.

366.Lisanework E Ayalew, Zelalem H Mekuria, Beatrice Despres, Matthew E Saab, Shivani Ojha.Genome Sequence Comparisons between Small and Large Colony Phenotypes of Equine Clinical Isolates of Arcanobacterium hippocoleae.Animals (Basel). 2024 May 29;14(11):1609. doi: 10.3390/ani14111609.

367.Juan A Subirana, Xavier Messeguer.Unique Features of Tandem Repeats in Bacteria.J Bacteriol. 2020 Oct 8;202(21):e00229-20. doi: 10.1128/JB.00229-20. Print 2020 Oct 8.

368.Junhua Zhao, Albino Bacolla, Guliang Wang, Karen M VasquezNon-B DNA structure-induced genetic instability and evolution.Review Cell Mol Life Sci. 2010 Jan;67(1):43-62. doi: 10.1007/s00018-009-0131-2. Epub 2009 Sep 1.

369.Karl A Dunne, Roy R Chaudhuri, Amanda E Rossiter, Irene Beriotto, Douglas F Browning, Derrick Squire, Adam F Cunningham , Jeffrey A Cole, Nicholas Loman, Ian R Henderson. Sequencing a piece of history: complete genome sequence of the original Escherichia coli strain.Microb Genom. 2017 Mar 23;3(3):mgen000106. doi: 10.1099/mgen.0.000106. eCollection 2017 Mar.

370Louis-Marie Bobay , Howard Ochman.The Evolution of Bacterial Genome Architecture.Front Genet. 2017 May 30:8:72. doi: 10.3389/fgene.2017.00072. eCollection 2017.

371.Zhan Li, Xiong Liu, Nianzhi Ning , Tao Li , Hui Wang.Diversity, Distribution, and Chromosomal Rearrangements of TRIP1 Repeat Sequences in Escherichia coli.Genes (Basel). 2024 Feb 13;15(2):236. doi: 10.3390/genes15020236.

372.Kai Zhou, Abram Aertsen, Chris W MichielsThe role of variable DNA tandem repeats in bacterial adaptation.FEMS Microbiol Rev. 2014 Jan;38(1):119-41. doi: 10.1111/1574-6976.12036. Epub 2013 Aug 28.

373.Li Xiao, Travis Ptacek, John D Osborne, Donna M Crabb, Warren L Simmons, Elliot J Lefkowitz, Ken B Waites, T Prescott Atkinson, Kevin Dybvig. Comparative genome analysis of Mycoplasma pneumoniae BMC Genomics. 2015 Aug 16;16(1):610. doi: 10.1186/s12864-015-1801-0.

374.Vaclav Brazda, Miroslav Fojta,Richard P. Bowater.Structures and stability of simple DNA repeats from bacteria.Biochemical Journal Volume 477, Issue 2, 22 January 2020, Pages 325-339.

375.Sung Ho Yoon, Mee-Jung Han, Haeyoung Jeong, Choong Hoon Lee, Xiao-Xia Xia, Dae-Hee Lee, Ji Hoon Shim, Sang Yup Lee, Tae Kwang Oh, Jihyun F Kim.Comparative multi-omics systems analysis of Escherichia coli strains B and K-12.Genome Biol. 2012 May 25;13(5):R37. doi: 10.1186/gb-2012-13-5-r37.

376.Karoline Marisch, Karl Bayer, Theresa Schar, Juergen Mairhofer, Peter M Krempl, Karin Hummel, Ebrahim Razzazi-Fazeli, Gerald StriednerA comparative analysis of industrial Escherichia coli K-12 and B strains in high-glucose batch cultivations on process-, transcriptome- and proteome level.PLoS One. 2013 Aug 8;8(8):e70516. doi: 10.1371/journal.pone.0070516. eCollection 2013.

377.Sandra R Richardson, Aurélien J Doucet, Huira C Kopera, John B Moldovan, José Luis Garcia-Perez, John V Moran.The Influence of LINE-1 and SINE Retrotransposons on Mammalian GenomesReview Microbiol Spectr. 2015 Apr;3(2):MDNA3-0061-2014. doi: 10.1128/microbiolspec.MDNA3-0061-2014.

378.Peters, Joseph. (2019). Targeted transposition with Tn7 elements: Safe sites, mobile plasmids, CRISPR/Cas and beyond. Molecular Microbiology. 112. 10.1111/mmi.14383.

379.Amit Kumar Gaurav, Jitender Kumar, Mridula Agrahari, Alok Bhattacharya, Vijay Pal Yadav, Sudha Bhattacharya.Functionally conserved RNA-binding and protein-protein interaction properties of LINE-ORF1p in an ancient clade of non-LTR retrotransposons of Entamoeba histolytica.Mol Biochem Parasitol. 2017 Jan:211:84-93. doi: 10.1016/j.molbiopara.2016.11.004. Epub 2016 Nov 25.

340.Fatemeh Pourrajab, Seyedhossein Hekmatimoghaddam.Transposable elements, contributors in the evolution of organisms (from an arms race to a source of raw materials)Review Heliyon. 2021 Jan 21;7(1):e06029. doi: 10.1016/j.heliyon.2021.e06029. eCollection 2021 Jan.

341.Jun Xia, Li-Ya Chiu, Ralf B Nehring, María Angélica Bravo Núñez, Qian Mei, Mercedes Perez, Yin Zhai, Devon M Fitzgerald, John P Pribis, Yumeng Wang, Chenyue W Hu, Reid T Powell, Sandra A LaBonte, et al.,Bacteria-to-Human Protein Networks Reveal Origins of Endogenous DNA Damage.Cell. 2019 Jan 10;176(1-2):127-143.e24. doi: 10.1016/j.cell.2018.12.008.

342.Ekaterina Avershina, Knut Rudi.Dominant short repeated sequences in bacterial genomes.Genomics. 2015 Mar;105(3):175-81. doi: 10.1016/j.ygeno.2014.12.009. Epub 2015 Jan 3.

343.M. Jamil Al-Obaidi, Zarizal Suhaili and Mohd Nasir Mohd Desa. Ibrokhim Y. Abdurakhmonov Genotyping Approaches for Identification and Characterization of Staphylococcus aureus.Mazen.intech open books.Genotyping.2018

344.Aparna Bansal, Shikha Kaushik, Shrikant Kukreti.Non-canonical DNA structures: Diversity and disease association.Front Genet. 2022 Sep 5:13:959258. doi: 10.3389/fgene.2022.959258. eCollection 2022.

345.Brázda, Václav & Fojta, Miroslav & Bowater, Richard. (2020). Structures and stability of simple DNA repeats from bacteria. Biochemical Journal. 477. 325-339. 10.1042/BCJ20190703.

346.Dawit Nigatu, Werner Henkel, Patrick Sobetzko, Georgi Muskhelishvili .Relationship between digital information and thermodynamic stability in bacterial genomes.EURASIP J Bioinform Syst Biol. 2016 Feb 2;2016(1):4. doi: 10.1186/s13637-016-0037-x. eCollection 2016 Dec.

347.Otília Porubiaková, Jan Havlík, Indu, Michal Šedý, Veronika Přepechalová, Martin Bartas, Stefan Bidula, Jiří Šťastný, Miroslav Fojta, Václav Brázda.Variability of Inverted Repeats in All Available Genomes of Bacteria.Microbiol Spectr. 2023 Aug 17;11(4):e0164823. doi: 10.1128/spectrum.01648-23. Epub 2023 Jun 26.

348.Corella S Casas-Delucchi, Manuel Daza-Martin, Sophie L Williams,Gideon Coster. The mechanism of replication stalling and recovery within repetitive DNA.Nat Commun. 2022 Jul 19;13(1):3953. doi: 10.1038/s41467-022-31657-x.

349.J Yuyang Lu, Wen Shao, Lei Chang, Yafei Yin, Tong Li, Hui Zhang, Yantao Hong, Michelle Percharde, Lerui Guo, Zhongyang Wu, Lichao Liu, Wei Liu, Pixi Yan, Miguel Ramalho-Santos, Yujie Sun, Xiaohua Shen.Genomic Repeats Categorize Genes with Distinct Functions for Orchestrated Regulation.Cell Rep. 2020 Mar 10;30(10):3296-3311.e5. doi: 10.1016/j.celrep.2020.02.048.

350.Isabelle T Holder, Stefanie Wagner, Peiwen Xiong, Malte Sinn, Tancred Frickey, Axel Meyer, Jörg S Hartig. Intrastrand triplex DNA repeats in bacteria: a source of genomic instability.Nucleic Acids Res. 2015 Dec 2;43(21):10126-42. doi: 10.1093/nar/gkv1017. Epub 2015 Oct 7.

351.https://ngdc.cncb.ac.cn/databasecommons/database/id/4765

352.Isabelle T Holder, Stefanie Wagner, Peiwen Xiong, Malte Sinn, Tancred Frickey, Axel Meyer, Jörg S Hartig.Intrastrand triplex DNA repeats in bacteria: a source of genomic instability.Nucleic Acids Res. 2015 Dec 2;43(21):10126-42. doi: 10.1093/nar/gkv1017. Epub 2015 Oct 7.

353.Houra Merrikh, Yan Zhang, Alan D Grossman, Jue D Wang.Replication-transcription conflicts in bacteria.Nat Rev Microbiol. 2012 Jun 6;10(7):449-58. doi: 10.1038/nrmicro2800.

354.Vaclav Brazda, Miroslav Fojta, Richard P Bowater.Structures and stability of simple DNA repeats from bacteria.Biochem J. 2020 Jan 31;477(2):325-339. doi: 10.1042/BCJ20190703.

355.Anurag Kumar Sinha, Anders Løbner-Olesen, Leise Riber. Bacterial Chromosome Replication and DNA Repair During the Stringent Response.Front Microbiol. 2020 Aug 28:11:582113. doi: 10.3389/fmicb.2020.582113. eCollection 2020.

356.Jamie McCann, Jiří Macas, Petr Novák, Tod F Stuessy, Jose L Villaseñor, Hanna Weiss-Schneeweiss.Differential Genome Size and Repetitive DNA Evolution in Diploid Species of Melampodium sect. Melampodium (Asteraceae).Front Plant Sci. 2020 Mar 31:11:362. doi: 10.3389/fpls.2020.00362. eCollection 2020.

357.Emma V Waters, Sarah K Cameron, Gemma C Langridge, Andrew Preston. Bacterial genome structural variation: prevalence, mechanisms, and consequences.Trends Microbiol. 2025 Apr 28:S0966-842X(25)00115-5. doi: 10.1016/j.tim.2025.04.004.

358.Nahikari López-López, Celia Gil-Campillo, Roberto Díez-Martínez, Junkal Garmendia.Learning from -omics strategies applied to uncover Haemophilus influenzae host-pathogen interactions: Current status and perspectives.Comput Struct Biotechnol J. 2021 May 15:19:3042-3050. doi: 10.1016/j.csbj.2021.05.026. eCollection 2021.

359.Andrew P Jackson. Preface. The evolution of parasite genomes and the origins of parasitismParasitology. 2015 Feb;142 Suppl 1(Suppl 1):S1-5. doi: 10.1017/S0031182014001516.

360.Sylvain Raffaele, Sophien Kamoun.Genome evolution in filamentous plant pathogens: why bigger can be better.Nat Rev Microbiol. 2012 May 8;10(6):417-30. doi: 10.1038/nrmicro2790.

361.David E. Torres,Ursula Oggenfuss,Daniel Croll,Michael F. Seidl.Genome evolution in fungal plant pathogens: looking beyond the two-speed genome model.Fungal Biology Reviews.Volume 34, Issue 3, September 2020, Pages 136-143.

362.J.C. Sauters,Antonis Rokas.Patterns and mechanisms of fungal genome plasticity.Thomas Current Biology.Volume 35, Issue 11, 9 June 2025, Pages R527-R544.

363.Alemu Gebrie.Transposable elements as essential elements in the control of gene expression. Mob DNA. 2023 Aug 18;14(1):9. doi: 10.1186/s13100-023-00297-3.

364.Toby E Newman, Mark C Derbyshire.The Evolutionary and Molecular Features of Broad Host-Range Necrotrophy in Plant Pathogenic Fungi.Review Front Plant Sci. 2020 Nov 12:11:591733. doi: 10.3389/fpls.2020.591733. eCollection 2020..

365.Shakhinur Islam Mondal, Arzuba Akter, Ryuichi Koga, Takahiro Hosokawa, Mehmet Dayi, Kazunori Murase, Ryusei Tanaka, Shuji Shigenobu, Takema Fukatsu, Taisei Kikuchi.Reduced Genome of the Gut Symbiotic Bacterium " Candidatus Benitsuchiphilus tojoi" Provides Insight Into Its Possible Roles in Ecology and Adaptation of the Host Insect.Front Microbiol. 2020 May 6:11:840. doi: 10.3389/fmicb.2020.00840. eCollection 2020.

366.Wesley Morovic, Charles R Budinoff.Epigenetics: A New Frontier in Probiotic Research. Trends Microbiol. 2021 Feb;29(2):117-126. doi: 10.1016/j.tim.2020.04.008. Epub 2020 May 11.

367.Giulia Oliva, Tobias Sahr, Carmen Buchrieser.Small RNAs, 5' UTR elements and RNA-binding proteins in intracellular bacteria: impact on metabolism and virulence.FEMS Microbiol Rev. 2015 May;39(3):331-49. doi: 10.1093/femsre/fuv022.

366.Victor E Reyes.Helicobacter pylori and Its Role in Gastric Cancer.Review Microorganisms. 2023 May 17;11(5):1312. doi: 10.3390/microorganisms11051312.

367.Rita Matos, Irina Amorim, Ana Magalhães, Freddy Haesebrouck, Fátima Gärtner, Celso A Reis. Adhesion of Helicobacter Species to the Human Gastric Mucosa: A Deep Look Into Glycans Role.Front Mol Biosci. 2021 May 7:8:656439. doi: 10.3389/fmolb.2021.656439. eCollection 2021.

368.Jeanna A Bugaytsova, Oscar Björnham, Yevgen A Chernov, Pär Gideonsson, Sara Henriksson, Melissa Mendez, Rolf Sjöström, Jafar Mahdavi, Anna Shevtsova, Dag Ilver, Kristof Moonens.Helicobacter pylori Adapts to Chronic Infection and Gastric Disease via pH-Responsive BabA-Mediated Adherence.Cell Host Microbe. 2017 Mar 8;21(3):376-389. doi: 10.1016/j.chom.2017.02.013.

369.Dalla Doohan, Yudith Annisa Ayu Rezkitha, Langgeng Agung Waskito, Yoshio Yamaoka, Muhammad MiftahussururHelicobacter pylori BabA-SabA Key Roles in the Adherence Phase: The Synergic Mechanism for Successful Colonization and Disease Development.Toxins (Basel). 2021 Jul 13;13(7):485. doi: 10.3390/toxins13070485.

370.Kao, Cheng-Yen ,Sheu Shew-Meei, Sheu, Bor-Shyang, Wu, Jiunn-Jong. (2012). Length of Thymidine Homopolymeric Repeats Modulates Promoter Activity of sabA in Helicobacter pylori. Helicobacter. 17. 203-9. 10.1111/j.1523-5378.2012.00936.x.

371.Anna Åberg, Pär Gideonsson, Abhayprasad Bhat, Prachetash Ghosh, Anna Arnqvist.Molecular insights into the fine-tuning of pH-dependent ArsR-mediated regulation of the SabA adhesin in Helicobacter pylori.Nucleic Acids Res. 2024 Jun 10;52(10):5572-5595. doi: 10.1093/nar/gkae188.

372Arthur Chou; Richard L. Austin.Entamoeba histolytica Infection.StatPearls [Internet].Treasure Island (FL): StatPearls Publishing; 2025.

373.Koushik Das, Sandipan Ganguly. Evolutionary genomics and population structure of Entamoeba histolytica.Comput Struct Biotechnol J. 2014 Oct 31;12(20-21):26-33. doi: 10.1016/j.csbj.2014.10.001. eCollection 2014 Nov.

374.Yasuaki Yanagawa, Manu Sharma, Shinji Izumiyama, Upinder Singh.Exploring virulence and stress response in Entamoeba histolytica: insights from clinical strains.Microbiol Spectr. 2025 Jul;13(7):e0050625. doi: 10.1128/spectrum.00506-25. Epub 2025 Jun 9.

375.Sanjib K Sardar, Ajanta Ghosal, Tapas Haldar, Akash Prasad, Sweety MalYumiko Saito-Nakano, Seiki Kobayashi, Shanta Dutta, Tomoyoshi Nozaki,Sandipan Ganguly.Genetic characterization of the Entamoeba moshkovskii population based on different potential genetic markers.Parasitology. 2024 Apr;151(4):429-439. doi: 10.1017/S003118202400026X. Epub 2024 Mar 11.

376.Carol A Gilchrist.The E. histolytica Genome Structure and Virulence.Curr Trop Med Rep. 2016 Dec;3(4):158-163. doi: 10.1007/s40475-016-0088-9. Epub 2016 Oct 3.

377.Francisco Javier Rendón-Gandarilla, Víctor Álvarez-Hernández, Elizabeth J Castañeda-Ortiz, Helios Cárdenas-Hernández, Rosa Elena Cárdenas-Guerra, Jesús Valdés, Abigail Betanzos, Bibiana Chávez-Munguía, Anel Lagunes-Guillen, Esther Orozco, Lilia López-Canovas, Elisa Azuara-Liceaga.Telomeric Repeat-Binding Factor Homologs in Entamoeba histolytica: New Clues for Telomeric Research.Front Cell Infect Microbiol. 2018 Oct 2:8:341. doi: 10.3389/fcimb.2018.00341. eCollection 2018.

378.Ehsan Nazemal hosseini Mojarad, Masoumeh Azimirad, Mansour Bayat, Abdollah Hellaly, Hamid Asadzadeh Aghdaei, Hamid Mohaghegh Shalmani.Polymorphism in two short tandem repeat loci (R-R and S-Q) linked to tRNA genes in Entamoeba dispar isolates.Gastroenterol Hepatol Bed Bench. 2012 Fall;5(4):202-8.

379.Escueta-De Cadiz, Aleyla & Kobayashi, Seiki & Takeuchi, Tsutomu & Tachibana, Hiroshi & Nozaki, Tomoyoshi. (2009). Identification of an avirulent Entamoeba histolytica strain with unique tRNA-linked short tandem repeat markers. Parasitology international. 59. 75-81. 10.1016/j.parint.2009.10.010.

380.Zonghui Jian, Li Zeng, Taojie Xu, Shuai Sun, Shixiong Yan, Lan Yang, Ying Huang, Junjing Jia, Tengfei Dou.Antibiotic resistance genes in bacteria: Occurrence, spread, and control.J Basic Microbiol. 2021 Dec;61(12):1049-1070. doi: 10.1002/jobm.202100201. Epub 2021 Oct 14.

381.Francisco Javier Rendón-Gandarilla, Víctor Álvarez-Hernández, Elizabeth J Castañeda-Ortiz, Helios Cárdenas-Hernández, Rosa Elena Cárdenas-Guerra 1, Jesús Valdés, Abigail Betanzos, Bibiana Chávez-Munguía, Anel Lagunes-Guillen, Esther Orozco, Lilia López-Canovas, Elisa Azuara-Liceaga.

382. Francisco Javier Rendón-Gandarilla, Víctor Álvarez-Hernández, Elizabeth J Castañeda-Ortiz, Helios Cárdenas-Hernández, Rosa Elena Cárdenas-Guerra, Jesús Valdés , Abigail Betanzos, Bibiana Chávez-Munguía, Anel Lagunes-Guillen , Esther Orozco, Lilia López-Canovas, Elisa Azuara-Liceaga.Telomeric Repeat-Binding Factor Homologs in Entamoeba histolytica: New Clues for Telomeric Research.Front Cell Infect Microbiol. 2018 Oct 2:8:341. doi: 10.3389/fcimb.2018.00341. eCollection 2018.

383.Daniela M. Faust,Nancy Guillen.Virulence and virulence factors in Entamoeba histolytica, the agent of human amoebiasis.Microbes and Infection.Volume 14, Issue 15, December 2012, Pages 1428-1441.

384.Sean Benler, Guilhem Faure, Han Altae-Tran, Sergey Shmakov, Feng Zheng, Eugene Koonin.Cargo Genes of Tn 7-Like Transposons Comprise an Enormous Diversity of Defense Systems, Mobile Genetic Elements, and Antibiotic Resistance Genes.mBio. 2021 Dec 21;12(6):e0293821. doi: 10.1128/mBio.02938-21. Epub 2021 Dec 7.

385.Antonio Serrato-Capuchina, Daniel R Matute.The Role of Transposable Elements in Speciation.Genes (Basel). 2018 May 15;9(5):254. doi: 10.3390/genes9050254.

386.Matthew A Lawlor, Christopher E Ellison.Evolutionary dynamics between transposable elements and their host genomes: mechanisms of suppression and escape.Curr Opin Genet Dev. 2023 Oct:82:102092. doi: 10.1016/j.gde.2023.102092. Epub 2023 Jul 28.