1. **LTR Retrotransposons.** The long direct repeating terminals of LTR retrotransposons range from ~100 Bp up to 5 Kb in the scale. Both LTR functional retrotransposons are necessary for replication to encode a minimum of two genes, gag and po. Gag encodes a capsid and nucleocapsid polyprotein. Gag protein in the cytoplasm, where reverse transcription occurs, forms virus-like spores. Pol genes contain a three protein spectrum of several hundred base pairs to 25 kb, like the retrotransposon of the ogre in the pea genome. It produces three protein forms of reverse transcriptase endowed with an RT and an RNAsH domain. The largest repetitive sequence class for plant genomes is LTR retrotransposons that, for example, can account for over 75 percent of the maize génome. Approx. 8% of the human genome and 10% of the mouse genome represent retrotransposons from LTR.
2. **DNA transposons.** DNA transposons are DNA sequences which can travel and fit into various positions within the genome, also known as "jumping genes." In comparison to class I TE, retrotransposons, they are transposable components of class II, which fly over an intermediate DNA. DNA transposons may be classified as autonomous as well as non-autonomous in relation to movement. DNA transposons are unable to synthesize DNA, but they can replicate with a host replicator. These three primary groups are then further categorized into 23 separate superfamilies with their composition, sequence and action mechanisms.
3. **Simple sequence repeats.** The basic sequence repeats are DNA tracts in which a small base pair motive is replicated many to several times together, often called the genetic 'stutter' one. SSRs are also present in promoters or in untranslated regions and even coding sequences; these mutations can potentially impact almost every part of gene activity. SSRs can affect the number of repeats. These sequences. The reciprocal expansion of such triplets triggers many inherited neurodegenerative diseases, but SSR alloys can also lead to normal brain and behavioral differences. Here we study research involving RSDs in circadian rhythm, socio-sexual activity, aggression, memory, and personality, as well as illnesses. Neuronal division, brain formation and behavioural evolution may also be influenced by SSR.
4. **Segmental duplications.** Segmental duplications (SDs) are long DNA sequences, which have exactly the same sequences (90-100 percent) and occur at many points as a result of duplicating events. SDs may be interspersed or tandem and may be intrachromosomal or interchromosomal. Since SDs are so broad and are sequentially identical, they may also lead to chromosomal rearrangements and genome instability.
5. **Miscellaneous Heterochromatin.** Miscellaneous Heterochromatin is a closely packaged, numerous types of DNA or concentrated DNA. The two ends of constituent heterochromatin and optionally heterochromatin lie on a continuum. In gene expression, both play a role. Since it's closely packed, polymerase was assumed to be unavailable, but not transcribed according to Volpe et al. and many other sources, as most DNA is currently transcribed, but is actively transcribed by RNA-induced transcriptional silencing. The thick packaging would not result from a chromatin in recent experiments using an electron microscopy and OSO4 staining.
6. **Miscellaneous unique sequences.** In the low portion of the distribution, the very short sequences contribute to simple stretches of different single, intrinsic sequences, intergenic segments and transposon remnants. They are almost free of any redistributive functions or energy recruiting functions. By numbers, they add to the entropy of the system; otherwise, matter flows mostly from the genome through them.
7. **SINEs.** SINEs feature their numerous modules, basically a portion of their chain. SINE may be non-autónomous, transposable elements of approximately 100 to 700 base pairs of length, but do not inherently have to have a head, leg, or tail. They are a type of retrotransposons, which amplify themselves in the eukaryotic genomes, often by RNA intermediates. Fundamentally, short nuclear elements are genetic parasites that have formed in the history of eukaryotes quite early in the history, so as to use protein machines within the organism and co-opt this machinery from similarly parasite genomic elements.
8. **LINEs.** Long interspersed nuclear elements (LINEs) (also known as long interspersed nucleotide elements or long interspersed elements) are a group of non-LTR (long terminal repeat) retrotransposons that are widespread in the genome of many eukaryotes. They make up around 21.1% of the human genome. LINEs make up a family of transposons, where each LINE is about 7,000 base pairs long. LINEs are transcribed into mRNA and translated into protein that acts as a reverse transcriptase. The reverse transcriptase makes a DNA copy of the LINE RNA that can be integrated into the genome at a new site.In the first human genome draft the fraction of LINE elements of the human genome was given as 21% and their copy number as 850,000.
9. **Protein coding genes.** The protein coding gene consists of a promoter and then a terminator, followed by the protein coding sequence. The promoter is a pair-base sequence defining where the transcription starts. The gene coding area (CDS) is the part of a gene that codes for the protein. The human gene coding genes is estimated at 20,000-25,000. As genome sequence accuracy and gene finding techniques have increased, it is estimated that the number of humans have been updated repeatedly from the original 100,000 estimates or higher, and will begin to decline more.
10. **Introns.** An intron consists of any series of nucleotides in a gene which is discarded when the finite RNA product is matured. The non-coding regions for the RNA transcription, or the DNA encoding, are introns that are deleted before the translation, meaning that introns range greatly across the continuum of biologic species. Intruder occurrence across various genomes. Introns, for example, are particularly common in the nuclear genome of mandibular vertebrates, whereby protein-coding genes nearly always produce several introns while introns in certain eukaryotic microorganisms are uncommon in their nuclear genes.

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Thank you

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