



GEN PHILIC



Department of Biotechnology
Fergusson College (Autonomous),Pune.

Issue 2 | August 2020
Human Genome | What? Why? & How?



Dr. Sonali Joshi
Head of The Department of Biotechnology



Dr. Gayatri Gurjar
Newsletter Coordinator

Sequencing Our Blueprint

The Human Genome Project

The very first question that comes to mind when reading the title is, “WHAT IS A GENOME?”. A genome is an organism’s complete set of DNA, including all the genes. Each genome contains all the information required in order to build and maintain the organism it belongs to. In humans, a copy of the entire genome—more than 3 billion DNA base pairs—is contained in all the cells that possess a nucleus.

The Human Genome Project (HGP) was an international research effort made in order to determine the nucleotide sequence of a human haploid reference genome [22 autosomes + (X + Y) sex chromosomes]. The Project was coordinated by the National Institutes of Health (NIH) and the U.S. Department of Energy (DOE) and was contributed to by universities in United States of America, United Kingdom, France, Germany, Japan and China.

The results of the Human Genome Project allowed researchers to understand the blueprint essential for building a human being.

The idea of sequencing the human genome first occurred to three scientists, Robert Sinsheimer (University of California at Santa Cruz), Rene Dulbecco (Salk Institute) and Charles DeLisi (DOE). These gentlemen’s idea, while garnering enthusiasm from a number of prominent molecular biologists like James D. Watson, Walter Gilbert, was also met with resistance from many, having concerns that this large project may drain funds which could otherwise be allocated to numerous smaller projects having concrete application of their results. It was a long and arduous journey to convince people of the significance of this project.

HGP officially began in October 1990 and it’s estimated date of completion was in 2005. The goals of the Human Genome Project at it’s beginning were:

- (i) To identify all genes of the human genome.
- (ii) To sequence the nucleotides of the human genome which were about approximately 3 billion in number (now we know its 3.2 billion base pairs).
- (iii) To develop databases in order to store the information which was obtained.
- (iv) To develop tools for data analysis.
- (v) To address the ethical, legal, and social issues.
- (vi) To sequence a number of “model organisms,” including the bacterium *Escherichia coli*, the yeast *Saccharomyces cerevisiae*, the roundworm *Caenorhabditis elegans*, the fruitfly *Drosophila melanogaster*, and the mouse *Mus musculus*.

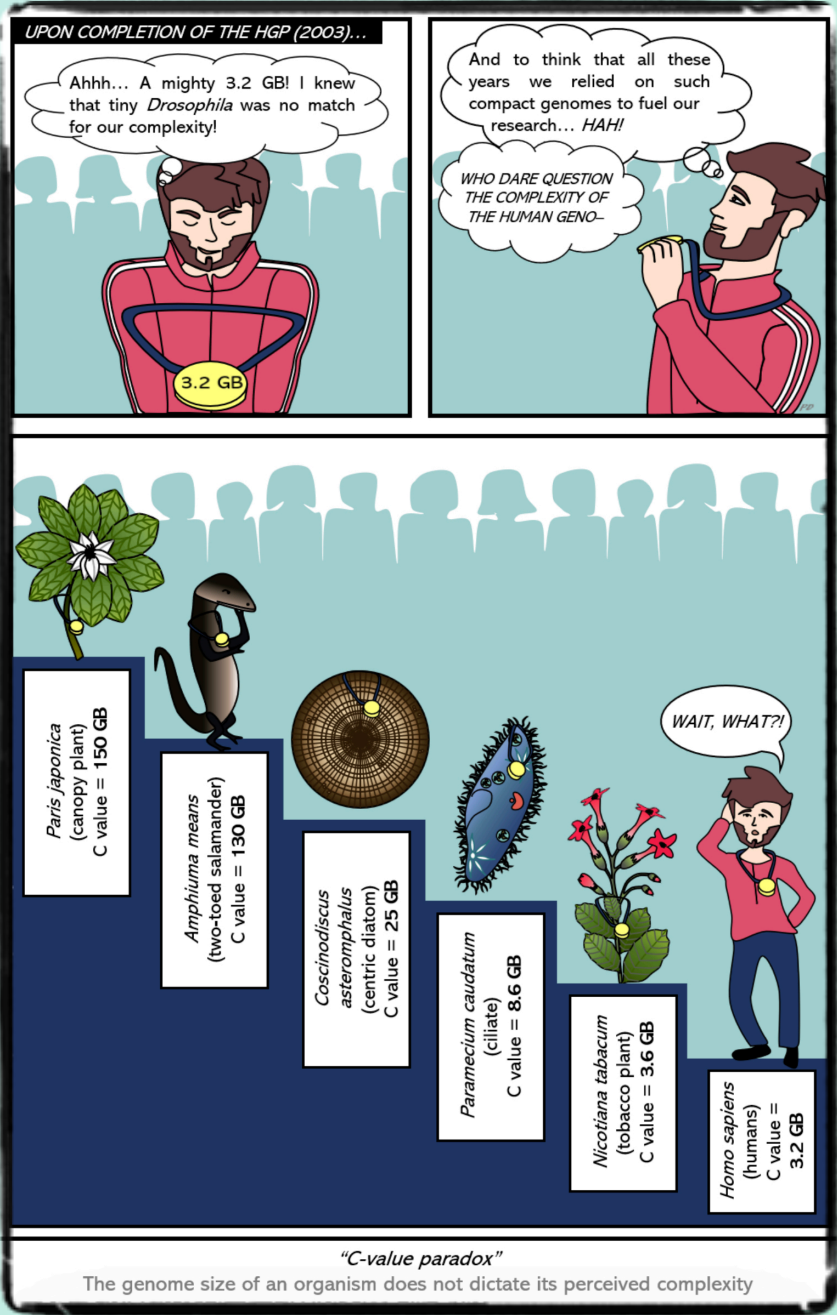


Illustration 1 : “C-value paradox”



Illustration : Priyanjali Dias
MSc II Biotechnology



Mudra Deshpande
S. Y. BSc Biotechnology
(Editor)

Divya Bhardwaj
S. Y. BSc Biotechnology
(Editor)





My genome, my health, my privacy!

In 1990, the Ethical, Legal, and Social Implications (ELSI) program was established as an integral part of the Human Genome Project. The mission of the ELSI program was to identify and address the issues raised by genomic research that would affect individuals, families, and the society.

The ELSI program focused on the possible consequences of genomic research in four main areas:

- Maintaining privacy and integrity in the use of genetic information, including the potential for genetic discrimination in employment and insurance.
- The incorporation of new genetic technologies, such as genetic testing, and practices of clinical medicine.
- Handle ethical issues surrounding the design and conduct of genetic research with the people involved, including the process of informed accord .
- The education of healthcare professionals, policy makers, students, and the public about genetics and the complex issues that result from genomic research.

It was recommended at the outset of the project that the focus be given to mapping rather than sequencing the human genome. The scientists sought to construct two kinds of maps:

- (i) Genetic maps which ordered the polymorphic markers to align linearly on chromosomes and the aim behind this was to have these markers densely situated so that relation between the linkage could be used to locate the chromosomal regions containing the genes of interest.
- (ii) Physical maps to order collections of cloned DNA fragments that covered an organism's genome and these fragments could then be replicated in quantity for sequencing.

By February 2003, 3.7 million human SNPs (Single nucleotide polymorphisms) were mapped. These regions are present between genes and can function as biological markers for scientists to identify disease- associated genes.

The finished sequence produced and released by the HGP in April 2003 covers 99% of the gene-containing regions (euchromatin) and has an accuracy of 99.99%. The remaining 1% is the heterochromatin and contains repetitive DNA sequences (includes almost no genes) which are a bit difficult to sequence. It is notably found in the centromeric and telomeric regions of a chromosome.

Scientists in HGP also surpassed their goal and finished the genome sequences of *E. coli*, *S. cerevisiae*, *C. elegans*, *D. melanogaster*, as well as the whole-genome drafts of several others, *C. briggsae* (nematode), *D. pseudoobscura* (a fruit fly specie), mouse and rat; all of which were model organisms.

The Human Genome Project (HGP) was declared complete in April 2003.



Article by : Akanksha Mahajan
S. Y. BSc Biotechnology

India joins the Race

India and its first Human Genome Database

As of November 2019, CSIR completed the sequencing of 1,008 Indians under the 'IndiGen' program providing the country with its first, very own genomic dataset.

While the same institute was instrumental in sequencing the first Indian genome back in 2009, it has been a decade of rigorous efforts to scale up the process in order to achieve this milestone. The driving force behind this program was to have a dataset of Indian genetic variations linked to diseases, thereby eliminating the dependency on international gene data banks from the US and UK to reach a reliable medical opinion and treatment strategy.

To cover the State as well as ethnic diversity, the representatives were selected from all over India. While IndiGen will be India's first step, the Department of Biotechnology has much larger plans - the 'Genome India Project' aimed at sequencing more than 10,000 Indian genomes has been initiated.

The larger expanse of this project will allow researchers to understand horizontal diversity generated by population migrations as well as vertical diversity that occurs due to endogamy or inter-caste marriages practiced among distinct groups in India. With nearly seven crore Indians suffering from rare genetic disorders, such genomic data sets will be an important aid in diagnosing and delivering targeted medical services.

However, with this being said it becomes essential to secure patient's privacy data which could be used as a basis for genetic discrimination. Another challenge is the sequencing cost which accounted for about ₹ 1,00,000 for sequencing one sample in the IndiGene project.

Nevertheless, with the increase in the sequencing scale and multiple collaborators participating in the project this issue is likely to be resolved in the coming future.

Finally, once the complete dataset becomes available it will be an interdisciplinary effort to translate the collected information to be utilised to its full extent to benefit the masses. This emphasises the need for an all-inclusive team of well-trained doctors, geneticists, and social workers amongst others. Though the major role of regulating and publicising the information obtained from such projects will be done by the government, it will be the masses who will play a significant role in deciding the future directions of such projects.



Illustration 2 : Logo of Human Genome Project



Illustrator : Akanksha Mahajan
S. Y. BSc Biotechnology

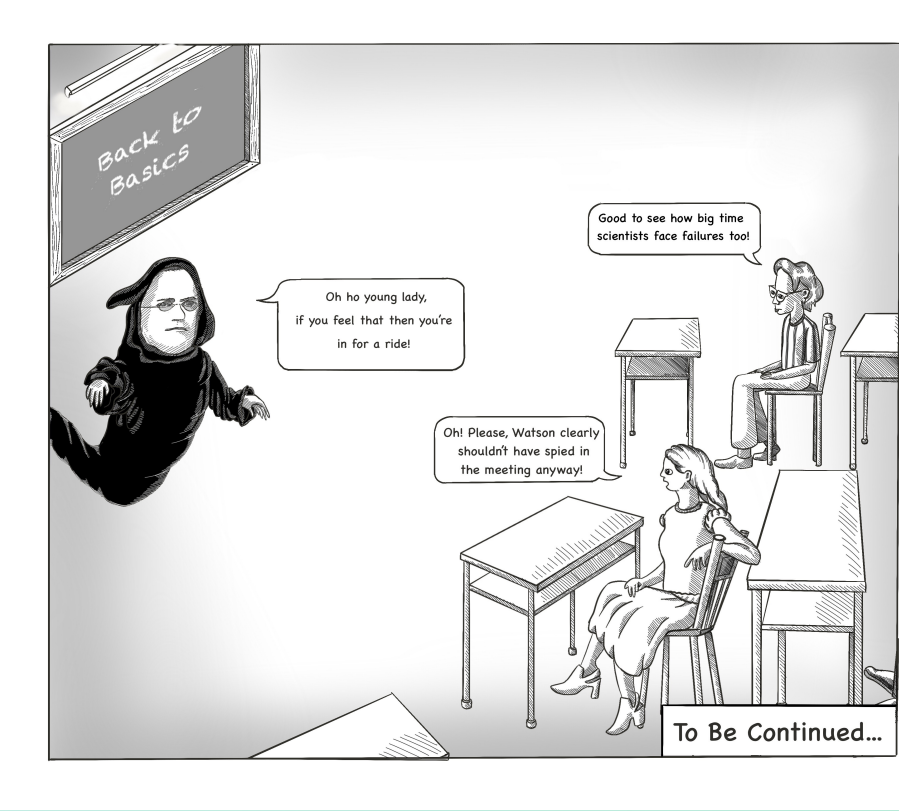
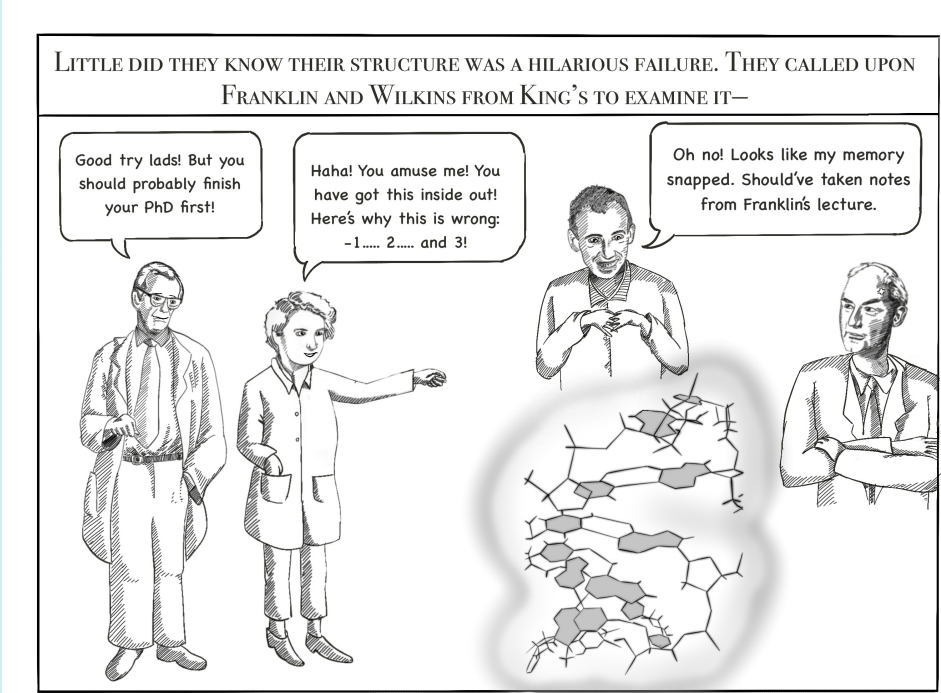
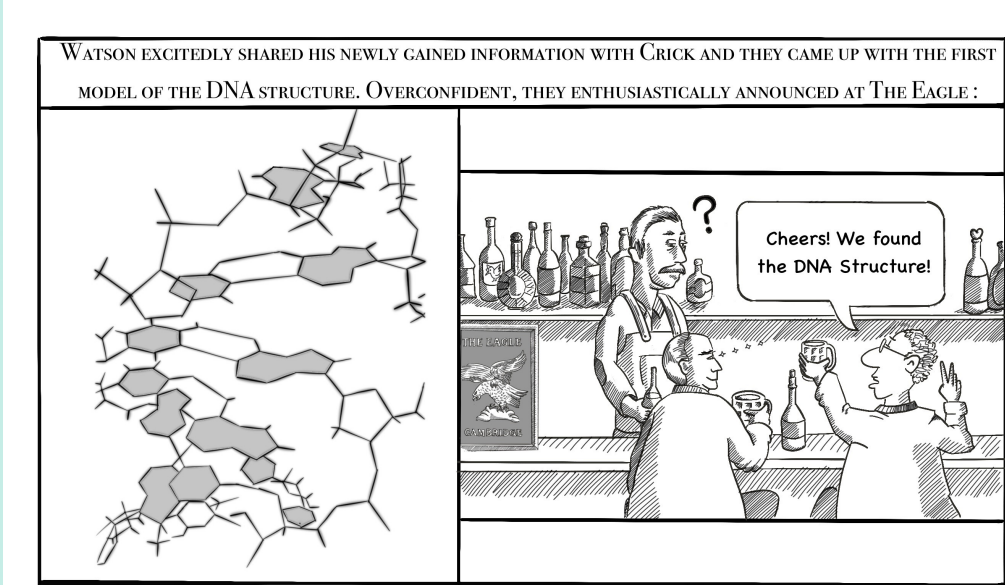
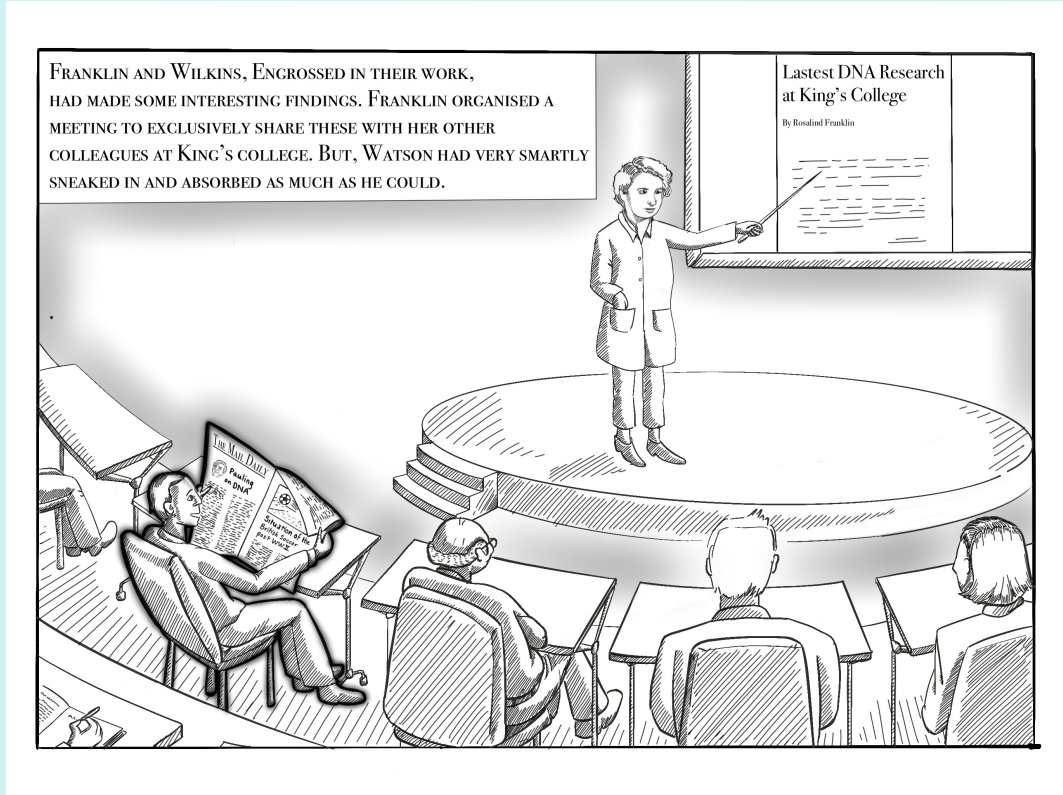
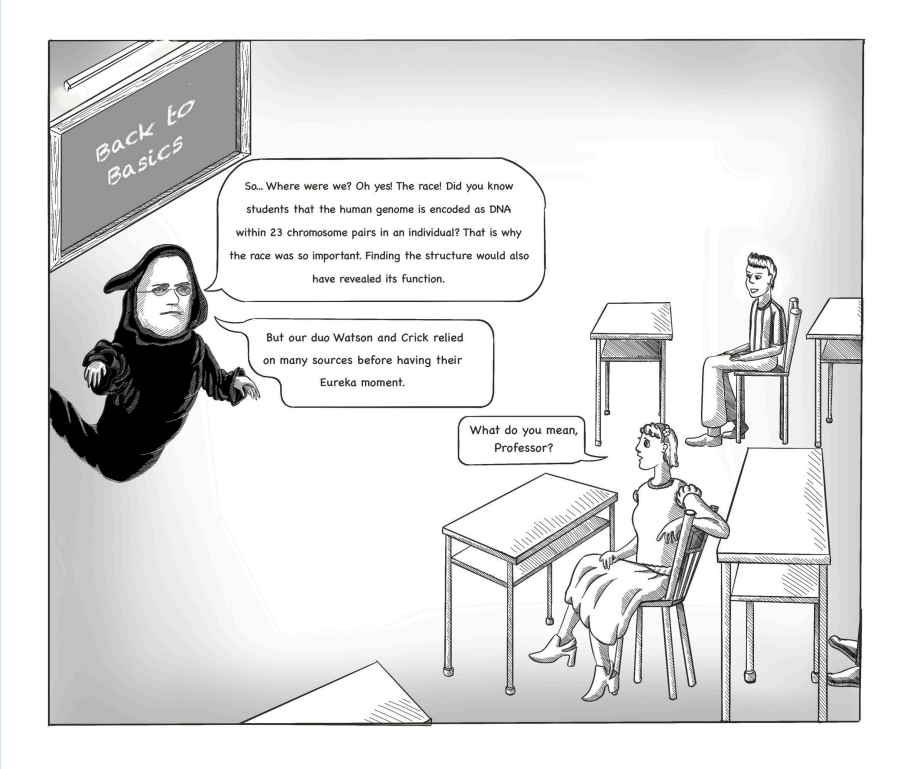
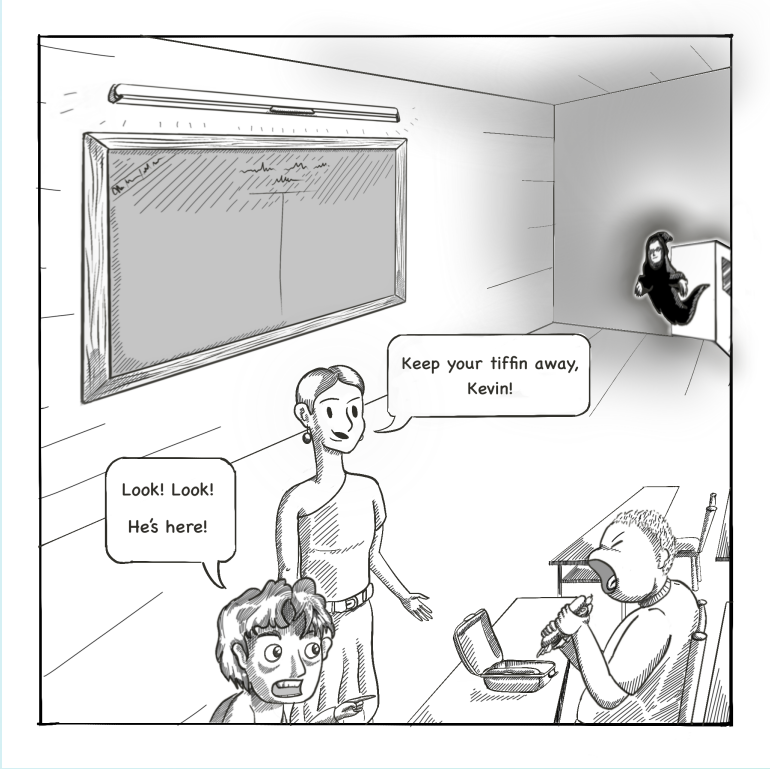


Article by : Anagha Bhagat
MSc II Biotechnology

Back to the Basics with Friendly Ghost Grandpa Mendel!

You know the legendary Gregor Mendel. You might not know the legends in the race to find secret of life! Come, discover the story with Mendel himself, and see where the journey takes you! (Note : Read from left to right)

Continued from Issue 1...



Author : Aarvi Jain
S. Y. BSc. Biotechnology

Illustrator : Hrishikesh Hardikar
S. Y. BSc. Biotechnology



Isn't it Junk? Why not just throw it away?

The Non-coding Genome

When we say that our genetic manual (DNA) is the blueprint of our being, it means that it holds the instructions for the proteins that keep our body up and functioning. However, less than 2% of our DNA actually codes for them. The rest 98-99% of DNA sequences that do not code for proteins have been coined the term 'junk DNA', in genetics.

Although, previously appraised 'junk' as the name suggests, many scientists now agree that this dark and mysterious non-coding part which was initially ignored, may play important roles in the cell such as, regulation of genes. As such, the misnomer has been largely replaced by the term, "non-coding".

A project named Encyclopaedia of DNA elements (ENCODE) launched in 2003, is an effort made by scientists to identify the functional regions of human genome. The project claims that 80% of the human genome has "biochemical function". However, the claim received criticisms that ENCODE used a basic definition of "function", i.e anything that was transcribed was functional. ENCODE's results are still an active area of debate for scientists.

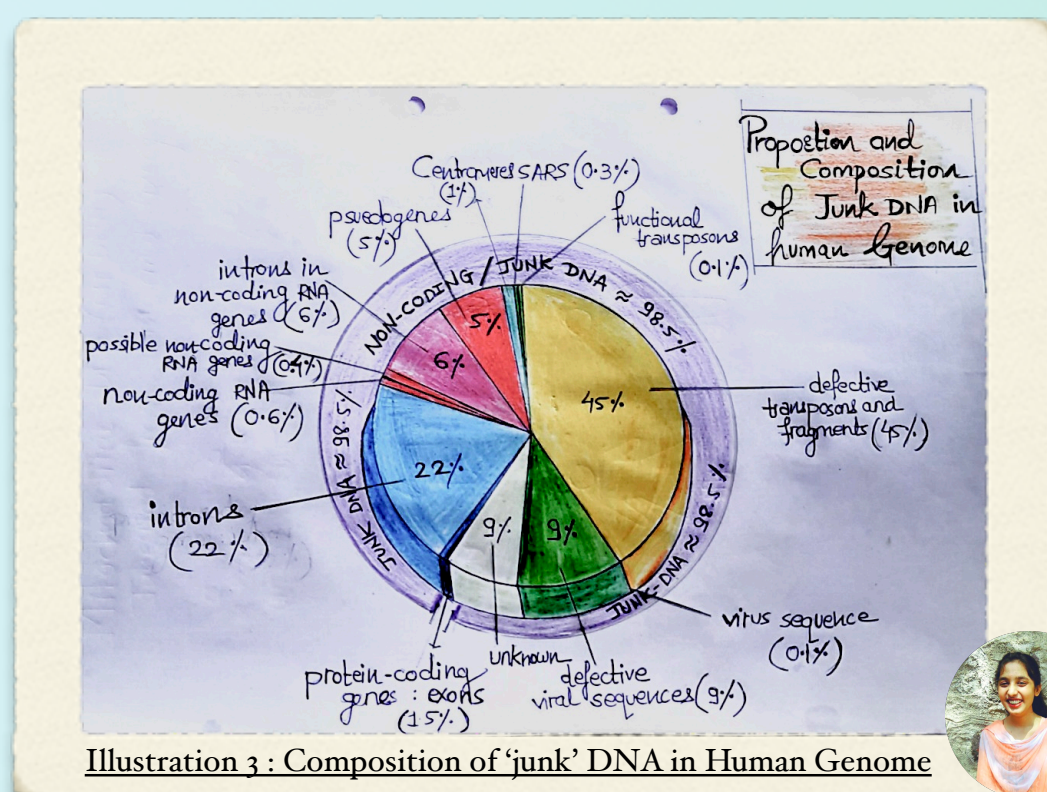


Illustration 3 : Composition of 'junk' DNA in Human Genome



Illustrator : Aqsareha Mujawar
S. Y. BSc. Biotechnology

We called the 'Junk' DNA important, why is that so?

Some of it's types which come under the umbrella term, 'Junk DNA' and their functions are given below:

I. **Functional non-coding RNAs** : For example, transfer RNA and ribosomal RNA, while not coding directly into proteins, aid in the process.

II. **Regulatory elements** : Sometimes also known as "gene switches", they include sequences such as enhancers, promoters and silencers, which control and regulate the expression of a gene, by 'switching' it on and off in specific cells in response to specific intracellular or extracellular signals.

III. **Introns** : Non-coding DNA incorporated into gene sequences. They have been known to play a role in regulation as well as 'alternate splicing' (a process by which different proteins are formed from the same gene). However, most are not functional.

IV. **Pseudogenes** : Once known as "genomic fossils", they are non-functional DNA sequences which resemble a gene. Many are transcribed and may form small interfering RNA. They have also been known to regulate tumour suppressors and oncogenes.

V. **Transposable elements** : Comprising nearly 50% of the human genome, these mobile genetic elements can 'travel' through the genome. By changing their location, they may correct a mutation or induce one.

VI. **Centromeres and telomeres** : Essential parts of a chromosomal structure which ensure it's structural integrity and play an important part in DNA replication.

VII. Some stretches of DNA are left in the genome by either our evolutionary past or the retroviruses which had once infected a cell. These stretches most of the time are truly 'junk' and do not perform any known task.

Our genome also has conserved non-coding sequences (CNSs), which perhaps due to their functional importance are evolutionarily conserved, especially the ones located near protein-coding genes (generally associated with

Don't know about you, but evolution likes 'Junk'!

After studying the DNA sequences of more than 100 vertebrate species it was found that 'Junk DNA' is highly conserved, sometimes over hundreds of millions of years, which suggests that these non-coding regions have undergone positive selection throughout evolution and confer an advantage in terms of preserving certain biological traits and suggesting its importance for survival.

Did you know?

- Recent estimates suggest that human non-coding genome contains over 5 times more information critical to health than the coding genome.
- The non-coding sequences are responsible for development of uterus and also of our opposable thumbs.
- During starvation, non-coding genome has been found to be crucial for yeast survival.
- Non-coding DNA is pivotal in variable response of the cells to drugs and other environmental cues.

Curious? Find Out.

- Why does an onion need a genome that is about five times larger than ours?
- Is there any relation between alcohol intake and junk DNA?
- What estimates of the non-coding DNA is responsible for gene regulation?

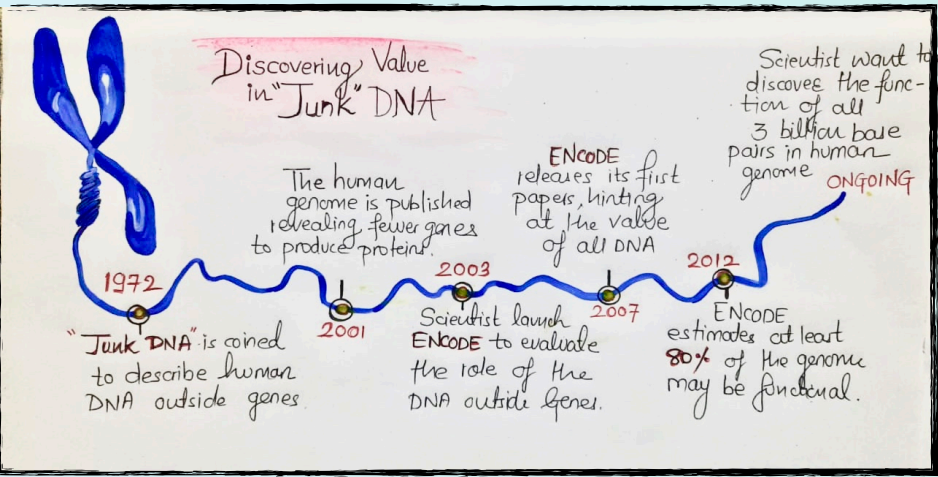


Illustration 4 : Benchmarks in discovery of Junk DNA



Illustrator : Aqsareha Mujawar
S. Y. Bsc Biotechnology

responsible for cancer growth; eRNAs (enhancer RNAs; regulatory elements) produced by junk DNA have direct role in activation of genes that are important for tumour development by interacting with BRD4 (protein known as cancer disseminator).They also have been known to influence the development of breast and prostate cancer.

Autism and Junk DNA

Non-coding genome is thought to be linked with various other mental disorders like schizophrenia, depression, chronic anxiety and autism. Autism spectrum disorder (ASD) is a cluster of neurodevelopmental diseases, which make it challenging for the patient to deal with complex social and interpersonal interactions. These individuals also show repetitive behaviour, speech and non- verbal communication.

It isn't surprising that most of the existing genetic disorders are a result of mutations. Autism is another product of mutations; a third of them being de-novo mutations (hereditary or somatic mutations, occurred in either of the parents' reproductive cells), the remaining are confirmed to be in the non-coding genome. One astonishing finding of current research is that non-coding DNA contributes to this disease by mutations that result in alteration in the regulation of transcription of the coding segments. Another interesting study suggests; mutations in non-coding DNA that confirms risk of Autism are inherited from the father whereas, mutations in coding DNA that increase the risk of Autism are thought to be of maternal origin. Weaker nature of changes in non- coding variants may lead to their better toleration than the stronger effects due to coding variants.

The more scientists explore the so called 'junk DNA', the less the label seems to fit.



By Sanskruti Deshmukh
S. Y. BSc. Biotechnology



And Aqsareha Mujawar
S. Y. BSc. Biotechnology

Powerhouse of the cell carries it's own blueprint
The Mitochondrial Genome

We get half our DNA from our mother and the other half from our father, right? Well, when a sperm and an egg come together, the sperm donates it's DNA but not much else. This means that the main volume of the cell comes from the egg and this volume includes all of its organelle.

In our cells, there are several thousand copies of an organelle that maintains its own genome. The genome of mitochondria is very much similar to prokaryotes as is evident from the Endosymbiotic Theory which states that mitochondria in a eukaryotic cell arose due to a process called symbiosis between aerobic prokaryotes and host anaerobic eukaryotes. The mitochondria possess its own DNA and protein synthesising machinery.

In humans, mitochondrial DNA (mtDNA) makes up 1% of the total cellular DNA. It contains 2-10 copies of a small circular dsDNA molecule (approximately 16 Kbps). The mitochondrial genome is built up of 16,569 DNA base pairs. It encodes 37 structural genes which in turn encodes 2 rRNAs, 22 mitochondrial tRNAs, large 16S rRNA and 12S rRNA. It also contains 13 protein subunits of respiratory chain (Q), out of which 7 are subunits of NADH dehydrogenase (complex I), cytochrome b of complex III, 3 are subunits of cytochrome oxidase (complex IV) and 2 subunits of ATP synthase. These 13 mitochondrial gene-encoded proteins instruct cells to produce enzyme complexes of oxidative phosphorylation system, thus enabling mitochondria to act as powerhouse of cells.

Mitochondrial DNA differs from nuclear DNA in many ways. Intriguingly, it has a unique genetic code. Some mitochondrial coding sequences do not follow universal codon rules when translated to proteins.

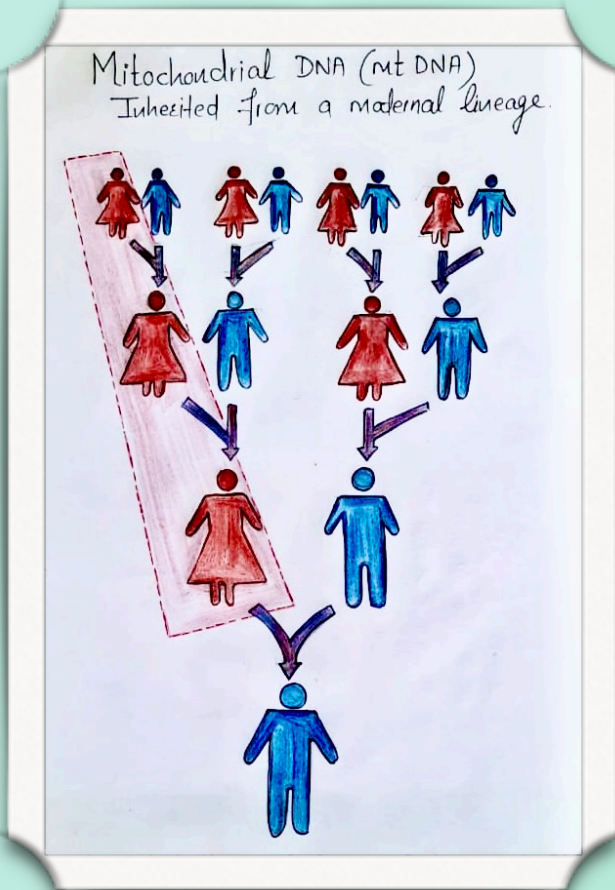


Illustration 5 : mtDNA inheritance



Illustrator : Aqsareha Mujawar
S. Y. BSc. Biotechnology

For example, for the codon AUA, the nuclear DNA code is isoleucine but mitochondrial DNA code is methionine! Other than this, mutation rate of mtDNA is very high because only 3% of mitochondrial genome is made up of introns or non-coding DNA, no protective histones (mtDNA is not enveloped, neither packed into chromatin) and no effective repair enzymes or proofreading mechanisms.

The mitochondrial mode of inheritance is strictly maternal. This means that a person shares mitochondrial DNA sequence with all of his or her maternal relatives. The mitochondrial DNA is hence used to establish maternal family ties and can be a very powerful tool for tracking genetic lineages. It is considered a really accurate way to test for biological siblings. This testing technique can also be used by the military to identify skeletons found in war zones by accurately linking them back to living relatives. Mitochondrial DNA is also used in studying molecular evolution, genomics and in analysing genetic disorders.

An important observation made regarding the mtDNA is that since it strictly follows maternal pattern of inheritance, genetic disorders caused by mitochondria-associated mutations are also always inherited maternally. Some examples of maternally inherited mitochondrial disorders are MELAS syndrome (Mitochondrial Encephalopathy, Lactic Acidosis and Stroke-like-episodes), MNGIE (Myoneurogenic gastrointestinal Encephalopathy) LHON (Leber's Hereditary Optic Neuropathy) and many others.

Over the years, scientists have discovered that mitochondrial dysfunctions due to mutations in mtDNA has implicated a wide range of age-related disorders and neurodegenerative diseases. Mutation in mtDNA has also been correlated with aging and cancer.

Hence, this small amount of mitochondrial DNA present inside the mitochondria in the cell is considered a special structure as it bequeaths certain unique features to the cell; it helps the mitochondria divide independently from the cell, all its genes are responsible for its normal functioning and it is inherited exclusively from the mother. All these properties make its study a great interest for the scientists.

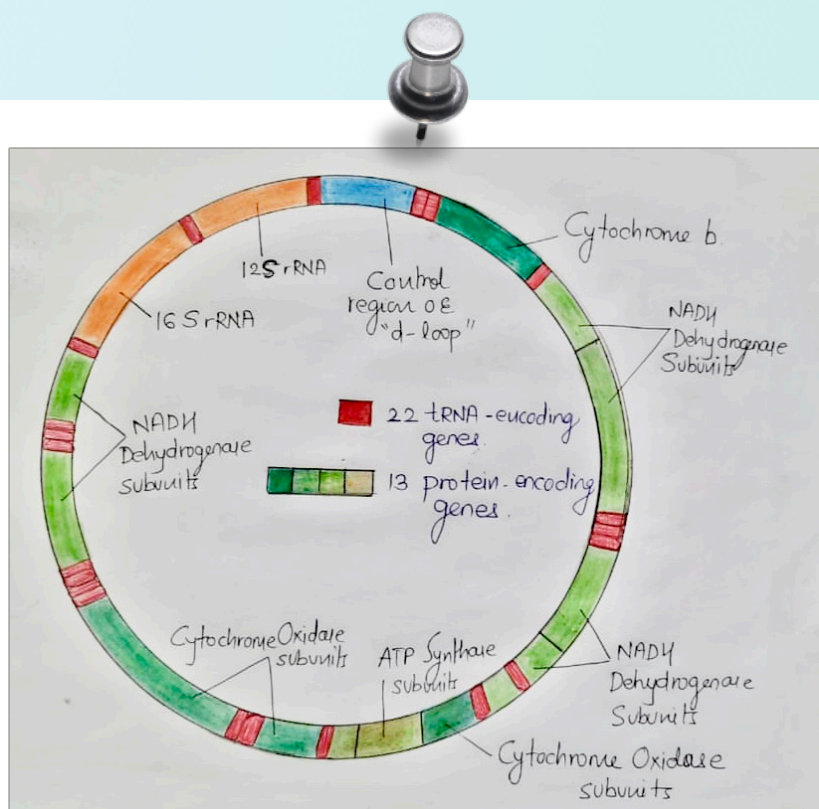


Illustration 6 : Mitochondrial Genome



Illustrator : Aqsareha Mujawar
S. Y. BSc. Biotechnology



By Sifa Lalani
S. Y. BSc. Biotechnology



And Pragyananda Choudhury
S. Y. BSc. Biotechnology

So we know the Human Genome, what use is it?

Gene Editing, Solution for WAGR Syndrome

Gene editing is a group of technologies that give scientists the ability to change an organism's DNA. These technologies allow genetic material to be added, removed, or altered at particular locations in the genome. Several approaches to genome editing have been developed.

A recent one is known as Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) and is now being used to fix a genetic brain disorder, WAGR syndrome. WAGR syndrome is a type of brain disorder in which many body functions get affected. It gets its name from its main features: Wilms Tumour, aniridia, genitourinary anomalies and intellectual disability.

A study published in the journal "Nature Communication" noted, that by using gene editing technology, researchers have successfully reversed one gene mutation in mice that leads to WAGR (caused by mutation on chromosome 11 in the 11p13 region). It was also found that a gene 'C11orf46' acts as a regulator during brain development and it helps guide the long fibres growing out of the newly formed nerve cells. These long fibres form the bundle which connects the two hemispheres of brain called, corpus callosum. According to the study, researchers revealed that the WAGR syndrome also known as chromosome 11p13 deletion syndrome can result due to the deletion of some necessary genes on C11orf46 including the PAX6 ocular developmental gene and Wilms tumour gene (WT1) and this might lead to the conditions such as intellectual disability, autism or many other brain developmental disorders.

The researchers carried out gene editing technology in which they used a genetic tool called 'Short Hairpin RNA', to cause less of the C11orf46 protein to be made in the brain of mice. Experimental results showed that less amount of C11orf46 protein in the

brain of mice resulted in improper development of the corpus callosum as was seen in WAGR syndrome in humans.

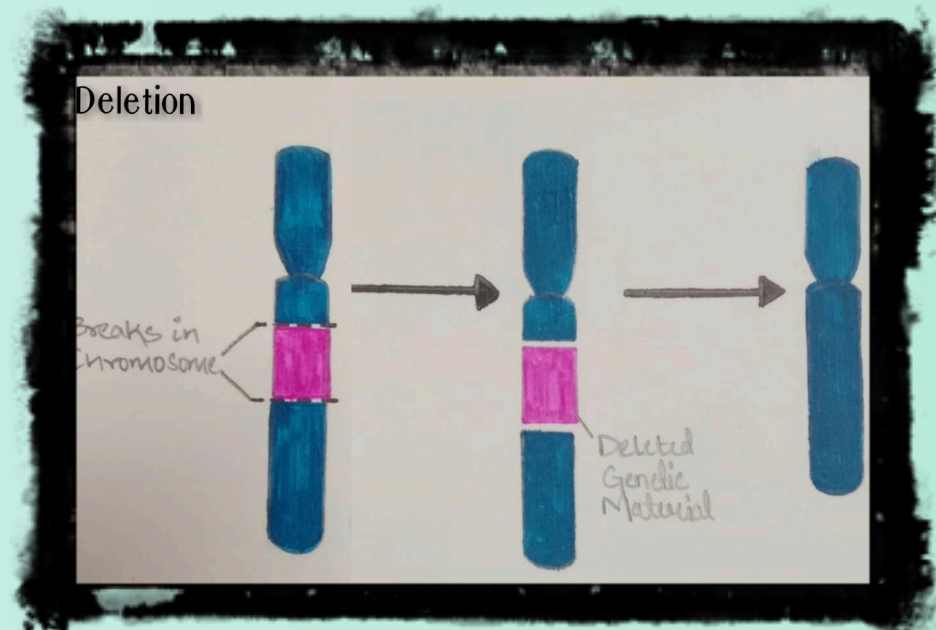


Illustration 7 : Deletion in Chromosome 11



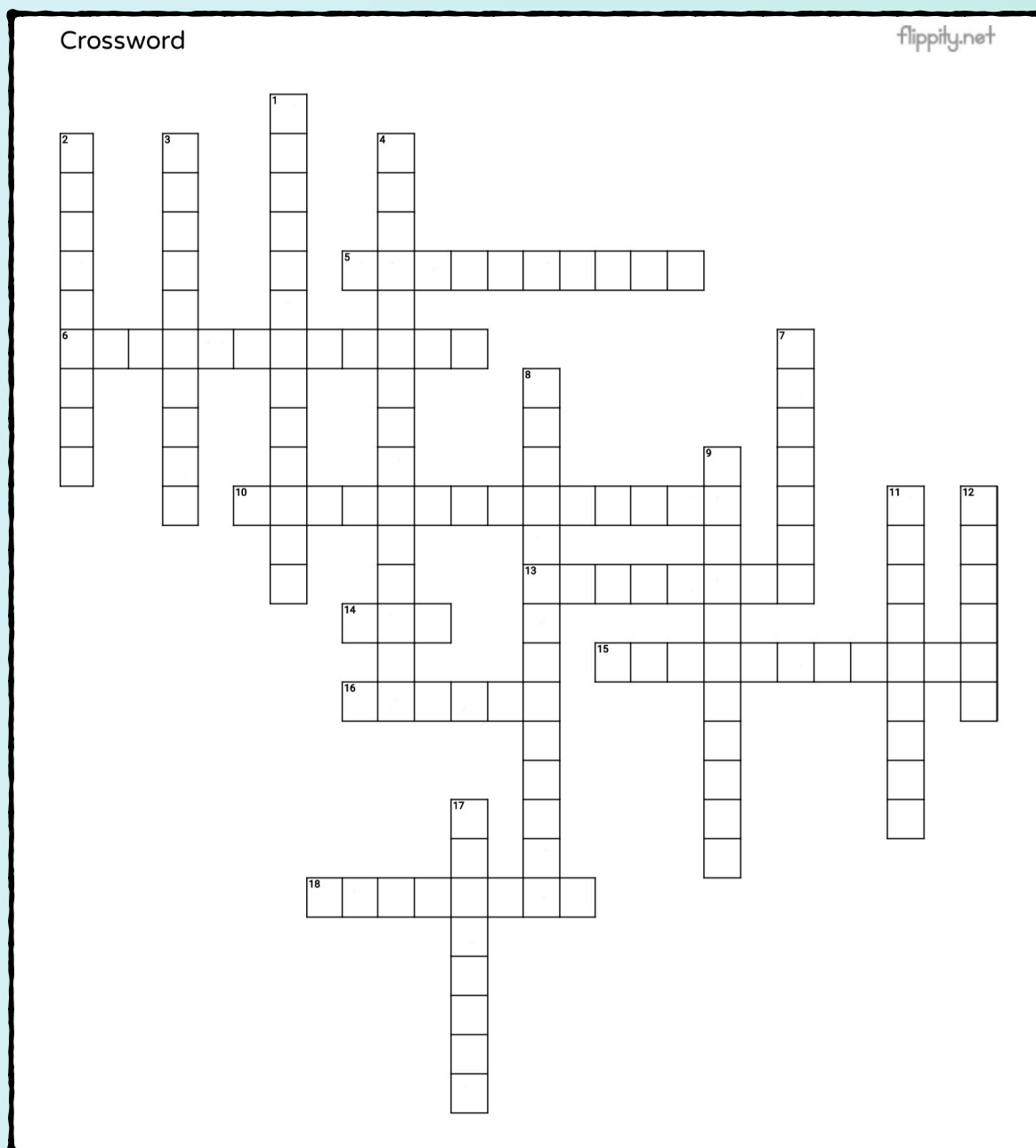
Illustrator : Divyashi Motwani
S. Y. BSc. Biotechnology

Following this, researchers performed the CRISPR technique and removed a portion of gene which regulates the production of Semaphorin 6a protein. According to the study, scientists found out that the removal of this gene allows the C11orf46 protein to function normally as it does in the brain of normal healthy mice.



By Ayush G Punwatkar
T. Y. BSc. Biotechnology

Can you solve this?



i. A type of a VNTR that consists of tandem repeats of up to 25 bps in length found mostly in the telomeric regions of the chromosome.

2. Is needed for compressing and packaging DNA into the nucleus

3. sequence of nucleotides that resembles a genuine gene but does not specify a functional RNA or protein

4. Transcriptionally inactive ,compacted DNA

7. A complex family of DNA repetitive sequences composed of 170 bp repeat segments ,placed in tandem order

8. A region of chromatin which is cleaved easily by DNaseI and various other nucleases.

9. A chromosome in which the centromere is placed at the edge of chromosome

II. A diagram depicting the whole set of chromosomes of a species

12. DNA in between two nucleosomes.

17. The study of all genes and their interactions to identify their combined influence on the growth and development of the organism.

5. The process of determining the genetic differences between individuals by using a set of markers

6. The structure which is made up of the nucleosome and H1 histone

10. A type shorter tandem repeats that is used for PCR typing

13. A model proposed for the 30 nm fibre..

14. DNA sequence generally between 100 to 500 bp in length that is easily recognisable and occurs only once in the chromosome or genome.

15. A disc shaped structure made of DNA and protein attached to centromere during cell division

16. A type of a mutation caused by insertions and deletions of nucleotides in genomic DNA

18. A regulatory DNA sequence that increase the gene expression



By Sandalu Romeshika Perera
MSc II Biotechnology

The Merry Game-te Corner

1. Code Decode

Fill in the blanks and unjumble the highlighted letters to decode the word of this issue.

- i. The father of genetics: - M _ _ _ _ _
- ii. Alternation in the nucleotide sequence: _ _ _ _ _ G
- iii. The complete set of heritable genes: G _ _ _ _ _ G
- iv. The variant form of gene: _ _ _ M _ _
- v. A sequence of three bases in DNA or RNA: _ _ _ _ G

Word Of The Issue: _ _ _ _ _

2. Heredity Hunt

Find the words listed in the word search below:

M J P H E N O T Y P E G H L O R F N I B
S Y W D N F D E R B E R U P Z T U F O E
U I Z H L W I G I D T G E N E T I C S E
O Y T I L I B A B O R P G J H G Y A O R
G L R K D O M I N A N T E O M G D U W G
Y G E N E T I C E N G I N E E R I N G I
Z J A G D I L N J A W P O Y T E Q V F D
O E W L E V Y P U N N E T T S Q U A R E
M K K Y L I E O E O Y N Y E P O Y B N P
O Q E K G E N M N V D S P Q F L O R D F
H U N W O A L V T E O B E D M E N W M H
E C N A T I R E H N I C I N E G Y L O P

Find Us:

PHENOTYPE
HOMOZYGOUS
DOMINANT
ALLELE
GENOTYPE
PUNNETT SQUARE
POLYGENIC INHERITANCE
PUREBRED
PEDIGREE
GENETIC ENGINEERING
PROBABILITY
GENETICS

Interesting tid-bits for the take-away

- ✦ There are between 20000 to 25000 genes in the human genome
- ✦ Hundreds of genes appear to have come from bacteria - one of which has been associated with depression.
- ✦ Your DNA can stretch from the earth to the sun and back approximately 61 times.
- ✦ The haploid human genome is about 3 billion base pairs long. Since every pair can be coded to 2 bits, this is about 750 megabytes of data.
- ✦ The Y chromosome has about 57 million base pairs, whereas X has about 156 million. Hence, women have more base pairs compared to men.



3. Gags by Gregor

What do you call a genetically engineered cow? - A Mootant

Did you have a tough time solving it? Check the next issue for the answers...



By Divya Bhardwaj
S. Y. BSc. Biotechnology

How did you find it? Any feedback? Suggestions?

We would like to know what you thought of this issue of Genophilic, any suggestions are welcome.

Our next issue will be on the topic ‘Methods in Genetics’, and we would appreciate any contributions on said topic.

Contact us on : editor.genophilic@gmail.com

References:

The Human Genome Project

- <https://ghr.nlm.nih.gov/primer/hgp/elsi>
- <https://web.archive.org/web/20150722060952/http://www.genoscope.cns.fr/spip/The-Human-Genome-Project.html?artsuite=1#FAQ2>
- <https://www.ncbi.nlm.nih.gov/books/NBK21134/>
- <https://plato.stanford.edu/entries/human-genome/#EthImpHumGenPro>
- <https://www.genome.gov/human-genome-project/What>
- <https://www.genome.gov/human-genome-project/results>
- India and it's first Human Genome database
- Genome sequencing: A solution to India's problem of rare genetic diseases - The Economic Times. (n.d.). Retrieved August 11, 2020, from <https://economictimes.indiatimes.com/news/science/genome-sequencing-a-solution-to-indias-problem-of-rare-genetic-diseases/articleshow/71870805.cms>
- Genomics for Public Health. (n.d.). Retrieved August 11, 2020, from <https://indigen.igib.in/home>
- Human Genetics & Genome Analysis | Department of Biotechnology. (n.d.). Retrieved August 11, 2020, from <http://dbtindia.gov.in/schemes-programmes/research-development/medical-biotechnology/human-genetics-genome-analysis>

The Non-Genome

- <https://theconversation.com/discovering-how-genetic-dark-matter-plays-a-role-in-mental-illness-is-just-the-tip-of-the-iceberg-for-human-health-142326>
- <https://www.discovermagazine.com/health/our-cells-are-filled-with-junk-dna-heres-why-we-need-it>
- <https://theconversation.com/how-much-junk-is-in-our-dna-53929>
- <https://www.news-medical.net/health/Autism-and-Junk-DNA.aspx>
- <https://www.darkdaily.com/researchers-discover-links-between-non-coding-dna-and-cancer-growth-that-could-lead-to-new-clinical-laboratory-biomarkers-for-cancer-and-other-chronic-diseases/>
- <https://www.advancedsciencenews.com/that-junk-dna-is-full-of-information/>
- <https://www.news-medical.net/life-sciences/What-is-Junk-DNA.aspx>
- <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3352212/>

The Mitochondrial Genome

- <https://www.nature.com/scitable/topicpage/mtdna-and-mitochondrial-diseases-903/>
- <https://www.khanacademy.org/science/biology/classical-genetics/sex-linkage-non-nuclear-chromosomal-mutations/a/mitochondrial-and-chloroplast-dna-inheritance>
- <https://www.nature.com/articles/s41580-020-0213-4>

Gene Editing, Solution for WAGR Syndrome

- <https://dx.doi.org/10.1038/s41467-019-12013-y>
- <https://www.theweek.in/home.html/404.html>
- <https://www.cancer-genetics.org/WAGR.html>
- https://www.researchgate.net/publication/294110493_Rare_Syndromes_and_Common_Variants_of_the_Brain-Derived_Neurotrophic_Factor_Gene_in_Human_Obesity

Illustration 3 adapted from : <https://sandwalk.blogspot.com/2018/03/whats-in-your-genome-pie-chart.html?m=1>

Illustration 4 adapted from : <https://www.quora.com/Would-removing-useless-junk-DNA-change-humans-significantly>

Illustration 5 adapted from : <https://www.khanacademy.org/science/biology/classical-genetics/sex-linkage-non-nuclear-chromosomal-mutations/a/mitochondrial-and-chloroplast-dna-inheritance>

Illustration 6 adapted from : <https://www.nature.com/scitable/topicpage/mtdna-and-mitochondrial-diseases-903/>

Illustration 7 adapted from : <https://images.app.goo.gl/qsofiSWBaNvfQ6Ez9>