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Effect of various irreligious things on individual's genetic makeup which erect some changes in their codons and ultimately fails to balance the emotions/behaviour

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Abstract:

In the era of science and technology we can't believe in many of the things which are associated with irreligious aspects. We have seen that sometimes a few people behave in a totally different personality than their own. They are not aware of what they are exactly doing and sometimes, may be they are not in controlled senses. Things like this are observed by a number of people but they are not generally believed by all. In order to heal such type of problems people choose to move to ***tantriks*** because they think that the affected person is under the control of an invisible evil power and can cause various harm to the person as well as the surroundings. Till now science has also not given suitable answers for such types of queries. The governing part for all the information is our DNA. The DNA codes are responsible for the genetic characters. If any one of the code is missing or change due to various conditions then automatically total information will interrupt/misbehave. These interruptions may lead to change in human personality. Complete process is governed by biotechnology not particular religion. Now how all this process will proceed we are going to discuss in this scientific paper in the terms of biotechnology.

Keywords: Chromosomes, Genes, DNA, Genetic codes

Introduction

In this paper we are going to explain some unwinded question like-

1. What is upri hwa (foul air)?
2. Entering of any soul in person and observing that the person starts behaving like any other person and loses his/her own identity or originality.

Till now nobody give the answers of these types of questions. Always there is a

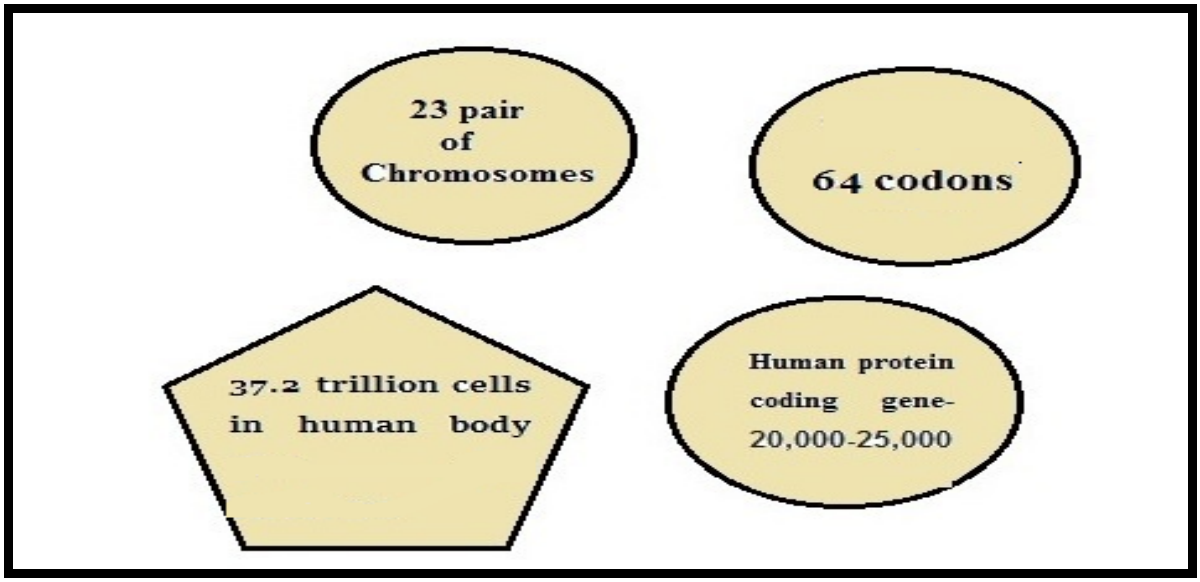

Fig 1. This figure depicts the organization of cellular level in organism.

fraction in between science and religious beliefs. Some religion follows this type of beliefs and other was not. According to us religion gives birth to science then science is able to give all the answers of religious beliefs. Today science is too advanced and able to give all types of explanation especially these types.

Bhoot, Upri hwa and other irreligious things is nothing but it is change in DNA nucleotide sequence. Our external environment is somehow capable to change the nucleotide sequences. When nucleotide sequence change the persons behaviour is totally different. Because every codon is associated with any of the character in human beings. Second thing which govern our body is endocrine system many hormones are also responsible for this type of activities. In this paper we only take modifications in which occur in DNA. The figure 1 depicts how the complete organism is manufactured by the chromosomes and each chromosome is made up of DNA.

Chromosomes

In the nucleus of each cell, the DNA molecule is packaged into thread-like structures called chromosomes. Each chromosome is made up of DNA tightly coiled many times around proteins called histones that support its structure see Figure 2.

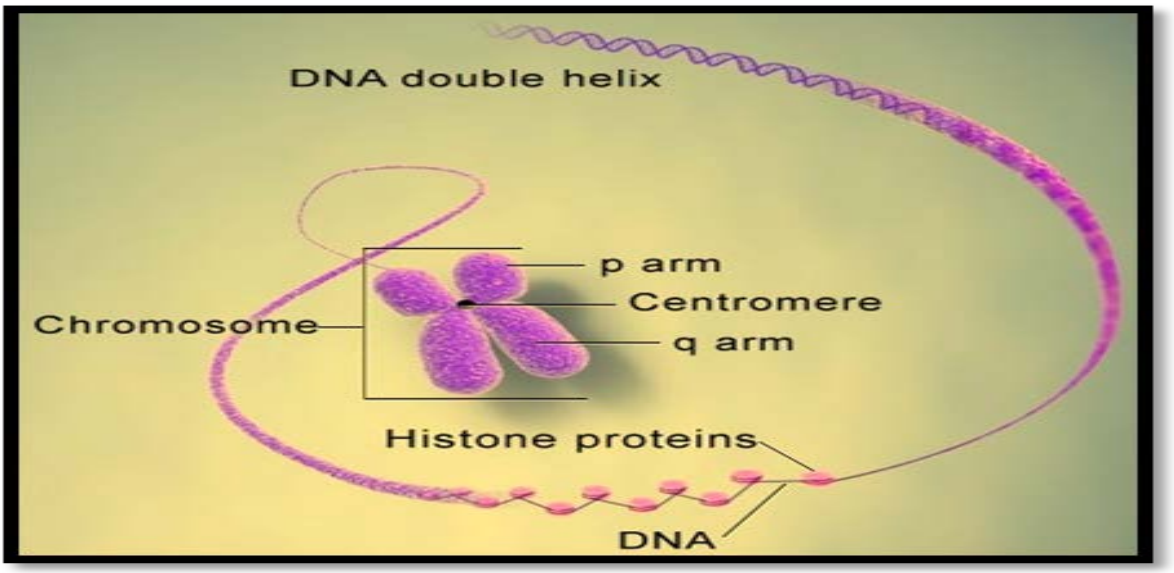

Fig 2:- Arrangement of DNA in chromosomes [Figure adopted from https://ghr.nlm.nih.gov/handbook/basics/chromosome and done some modifications]

Chromosomes are not visible in the cell's nucleus—not even under a microscope—when the cell is not dividing. However, the DNA that makes up chromosomes becomes more tightly packed during cell division and is then visible under a microscope. Most of what researchers know about chromosomes was learned by observing chromosomes during cell division.

Each chromosome has a constriction point called the centromere, which divides the chromosome into two sections, or "arms." The short arm of the chromosome is labelled the "p arm." The long arm of the chromosome is labelled the "q arm." The location of the centromere on each chromosome gives the chromosome its characteristic shape, and can be used to help describe the location of specific genes. [1]**.**

Genes and Deoxyribonucleic Acid (DNA)

A gene is the basic physical and functional unit of heredity. Genes, which are made up of DNA, act as instructions to make molecules called proteins. DNA gives instruction to RNA to make suitable and appropriate proteins. This protein gives complete structure to body. In humans, genes vary in size from a few hundred DNA bases to more than 2 million bases. The Human Genome Project has estimated that humans have between 20,000 and 25,000 genes.

Fig 3: Artistic approach of DNA and Earth [figure adopted from http://beforeitsnews.com/strange/2013/04/et-genetic-code-may-be-found-in-human-dna-according-to-kazakhstan-scientists-biological-seti-theory-2448242.html]

DNA (refer **figure 3**) consist of four nucleotide bases (refer figure 4) i.e. Adenine (A), Thymine (T) , Guanine (G) and Cytosine (C) that are paired to each other. A is paired with T and G is with C. The basic unit of the DNA molecule is the nucleotide. Nucleotides are found in the cell either as components of nucleic acids or as individual molecules. Nucleotides have several different roles and are not just used to make DNA. For example, some nucleotides are important in the cell as carriers of energy used to power enzymatic reactions. The nucleotide is itself quite a complex molecule, being made up of three distinct components. These are a sugar, a nitrogenous base, and a phosphate group.

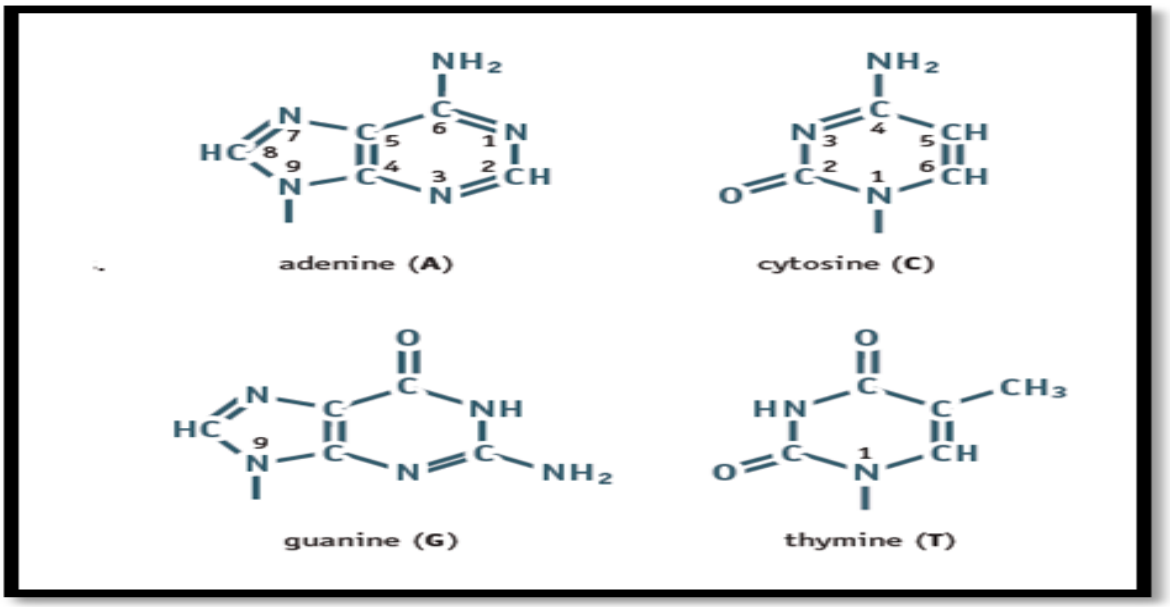

Fig 4:- The structure of 4 bases occurs in DNA which further makes the genetic codes.

Genetic Codes

Every genetic code has some information which is specific to the person if that information has been lost then how will he work. For example if we save anything in computer's hard disk when we require we just open that particular folder in hard disk only . If we delete that folder than how the computer search that particular folder . Same will be happened in case of human.

The genetic language consists of only four letters contained in the word "GACU". These four letters can be combined to form 64 genetic words, each consisting of 3 letters. Each triplet word (codon) has a specific meaning which the cell understands. It codes for a particular amino acid. The genetic code, as at present known, is shown in **Fig. 5.**

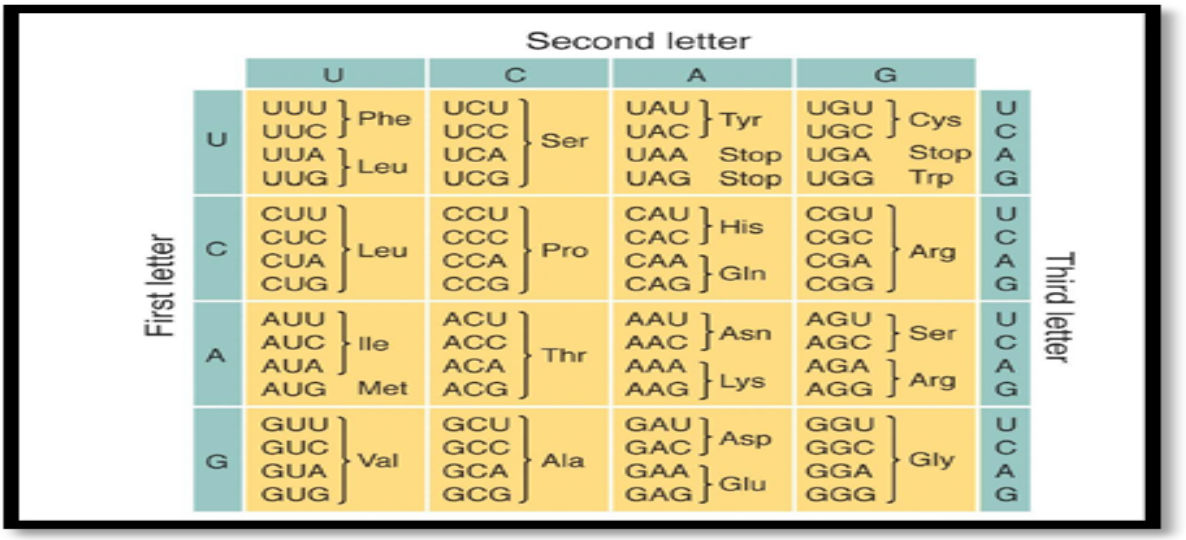

Fig 5: Genetic Codes

It shows the base sequences of the various codons (triplets) and against each codon is given the amino acid that it codes. Just as different combinations of different words make different sentences, each having a specific meaning, similarly different sequences of codons on mRNA specify different proteins, each with a specific sequence of amino acids. Although the genetic information resides in DNA, the terms genetic code and codon are used with reference to mRNA because mRNA is the nucleic acid which directly determines the sequence of amino acids in a protein. This expression of genetic information in the amino acid sequence of proteins by mRNA is called **translation.** *The DNA-RNA-Protein code may be* expressed as under :

	Amino Acid	Abbreviation	mRNA Codons		Total no. of codon(s)
			Common bases	Complete codon(s)	
1.	Alanine	Ala	GC–	GCU, GCC, GCA, GCG	4
2.	Arginine	Arg	CG– AG–	CGU, CGC, CGA, CGG AGA, AGG	6
3.	Asparagine	Asn	AA–	AAU, AAC	2
4.	Aspartic acid	Asp	GA–	GAU, GAC	2
5.	Cysteine	Cys	UG–	UGU, UGC	2
6.	Glutamic acid	Glu	GA–	GAA, GAG	2
7.	Glutamine	Gln	CA–	CAA, CAG	2
8.	Glycine	Gly	GG–	GGU, GGC, GGA, GGG	4
9.	Histidine	His	CA–	CAU, CAC	2
10.	Isoleucine	Ile	AU–	AUU, AUC, AUA	3
11.	Leucine	Leu	UU– CU–	UUA, UUG CUU, CUC, CUA, CUG	6
12.	Lysine	Lys	AA–	AAA, AAG	2
13.	Methionine	Met	AU–	AUG	1
14.	Phenylalanine	Phe	UU–	UUU, UUC	2
15.	Proline	Pro	CC–	CCU, CCC, CCA, CCG	4
16.	Serine	Ser	UC– AG–	UCU, UCC, UCA, UCG AGU, AGC	6
17.	Threonine	Thr	AC–	ACU, ACC, ACA, ACG	4
18.	Tryptophan	Trp	UG–	UGG	1
19.	Tyrosine	Tyr	UA–	UAU, UAC	2
20.	Valine	Val	GU–	GUU, GUC, GUA, GUG	4
Terminator triplets		Trm	UA– UG–	UAA, UAG UGA	3
				Total	64

Fig 6: Proteinogenic Amino acids and their mRNA codons[4]

The synthesis of cellular proteins takes place in the joining together of several amino acids to form a linear polypeptide chain of variable length. There are 20 different amino acids which are commonly found in protenis (hence called protein amino acids) and which take part in their synthesis. The mRNA codons for these 20 protein amino acids, as can be deduced.

The alphabet by which you can encode the information needed to build a protein. The code has many properties **[2],** namely:

1. There are 64 codons, each of which is a triplet of nucleotide bases.
2. Only 20 amino acids are used. These are called the standard amino acids
3. There appear to be some rules, together with some exceptions:
   - ❖ –XYU and XYC always code the same amino acid.
   - ❖ XYA and XYG often code the same amino acid.
   - ❖ In 8 out of the 16 possible cases, XY· encodes a single amino acid, where · represents any of the four bases.
4. The code is nearly universal. That is, it seems that the vast majority of living organisms on Earth use this code. This particular code is known as the Canonical Genetic Code.

5. Besides simple grouping, it seems that the code is not just a random association of codons and amino acids. There seems to be an intriguing underlying order. For instance, all codons with U in the second place code for hydrophobic amino acids [3].

Properties of Genetic Codes [4]

1. **Triplet nature**

As earlier outlined, singlet and doublet codes are not adequate to code for 20 amino acids; Therefore, it was pointed out that triplet code is the minimum required. But it could be a quadruplet code or of a higher order. As pointed out above, in a triplet code of 64 codons, there is an excess of (64 – 20) = 44 codons and, therefore, more than one codons are present for the same amino acid. This excess will be still greater if more than three-letter words are used. In a *quadruplet code* there will be 44 (4 × 4 × 4 × 4) = 256 possible codons. An account of the 20 amino acids along with their corresponding codons.

2. Degeneracy

The code is degenerate which means that the same amino acid is coded by more than one base triplet. Degeneracy, as used here, does not imply lack of specificity in protein synthesis. It merely means that a particular amino acid can be directed to its place in the peptide chain by more than one base triplets. For example, the three amino acids arginine, alanine and leucine each have six synonymous codons. A non-degenerate code would be one where there is one to one relationship between amino acids and the codons, so that from the 64 codons, 44 will be useless or nonsense codons. It has been definitely shown that there are no nonsense codons. The codons which were initially called nonsense codons were later shown to mean stop signals. The code degeneracy is basically of 2 types: partial and complete. In *partial degeneracy*, the first two nucleotides are identical but the third (*i.e.,* 3′ base) nucleotide of the degenerate codon differs; for example, CUU and CUC code for leucine. *Complete degeneracy* occurs when any of the 4 bases can take third position and still code for the same amino acid; for example, UCU, UCC, UCA and UCG all code for serine. Degeneracy of genetic code has certain biological advantages. For example, it permits essentially the same complement of enzymes and other proteins to be specified by the microorganisms varying widely in their DNA base composition. Degeneracy also provides a mechanism of minimizing mutational lethality. Degeneracies occur frequently in the third letter of the codon. Exceptions are, however, arginine (Arg), leucine (Leu) and serine (Ser) which have 2 groups of codons or triplets, which differ in either the first base only (Arg, Leu) or in both the first and second bases (Ser).

3. Non overlapping

The genetic code is non overlapping, *i.e.*, the adjacent codons do not overlap. A non overlapping code means that the same letter is not used for two different codons. In other words, no single base can take part in the formation of more than one codon. Fig. 30–4 shows that an overlapping code can mean coding for four amino acids from six bases. In actual practice, six bases code for not more than two amino acids. As an illustration, an end-to-end sequence of 5′ UUUCCC 3′ on mRNA will code only 2 amino acids, *i.e.,* phenylalanine (UUU) and proline (CCC).

4. Commaless

There is no signal to indicate the end of one codon and the beginning of the next. The genetic code is commaless (or comma-free). A commaless code means that no codon is reserved for punctuations or the code is without spacers or space words. There are no intermediary nucleotides (or commas) between the codons. In other words, we can say that after one amino acid is coded, the second amino acid will be automatically coded by the next three letters and that no letters are wasted for telling that one amino acid has been coded and that second should now be coded.

5. Non-ambiguity

By non-ambiguous code, we mean that there is no ambiguity about a particular codon. A particular codon will always code for the same amino acid. In an ambiguous code, the same codon could code for two or more than two different amino acids. Such is not the case. While the same amino acid can be coded by more than one codon (the code is degenerate), the same codon shall not code for two or more different amino acids (non-ambiguous). But sometimes the genetic code is ambiguous, that is, same codon may specify more than one amino acid. For example, UUU codon usually codes for phenylalanine but in the presence of streptomycin, may also code for isoleucine, leucine or serine.

6. Universality

The genetic code applies to all modern organisms with only very minor exceptions. Although the code is based on work conducted on the bacterium *Escherichia coli* but it is valid for other organisms. This important characteristic of the genetic code is called its **universality.** It means that the same sequences of 3 bases encode the same amino acids in all life forms from simple microorganisms to complex, multi celled organisms such as human beings. Consider any codon. It codes for the same amino acid from the smallest organism to the largest, plant or animal. Thus, UUU codes for phenylalanine and GUC for valine in all living things, from

amoeba to ape, bacteria to the banyan tree, and from cabbage to kings. The genetic code which was first developed in the bacteria about 3 billion (300 crore) years ago has not undergone any change and has been preserved in its almost original form in the course of evolution. In other words, *the code is a conservative one, i.e.*, the code was fixed early in the course of evolution and has been maintained to the present day.

7. Polarity

The genetic code has polarity, that is, the code is always read in a fixed direction, *i.e.*, in the 5′ → 3′ direction. It is apparent that if the code is read in opposite direction (*i.e.*, 3′ → 5′), it would specify 2 different proteins, since the codon would have reversed base sequence:

Codon:	UUG	AUC	GUC	UCG	CCA	ACA	AGG
Polypeptide :	→ Leu	Ile	Val	Ser	Pro	Thr	Arg
	Val	Leu	Leu	Ala	Thr	Thr	Gly ←

8. Chain Initiation Codons

The triplets AUG and GUG play double roles in *E. coli*. When they occur in between the two ends of a cistron (intermediate position), they code for the amino acids methionine and valine, respectively in an intermediate position in the protein molecule. But when they occur immediately after a terminator codon, they act as “chain initiation” (C.I.) signals or “starter codons” for the synthesis of a polypeptide chain. It has also been shown that the initiating methionine molecule should be found in the formylated state. This makes a distinction between the initiating methionine and the methionine at internal position. The methionine when required at internal position should not be formylated. Also while formyl methionine is carried by $tRNA^{fMet}$, there is a separate species of tRNA for internal methionine and it is designated as $tRNA^{mMet.}$

9. Chain Termination Codons

The 3 triplets UAA, UAG, UGA do not code for any amino acid. They were originally described as **non-sense codons,** as against the remaining 61 codons, which are termed as **sense codons.** The so-called non-sense codons have now been found to be of “special sense”. When any one of them occurs immediately before the triplet AUG or GUG, it causes the release of the polypeptide chain from the ribosome. Hence, the use of the term ‘non-sense’ is unfortunate. These special-sense codons perform the function of punctuating genetic message like a full stop at the end of a sentence. They are also called chain termination codons because these codons are used by the cell to signal the natural end of translation of a particular peptidyl chain. However, their inclusion in any mRNA results in the abrupt

termination of the message at the point of their location even though the polypeptide chain has not been completed. The codons UAA and UAG were discovered in bacteria and were respectively associated with the *ochre* and *amber* mutations. Hence, UAA is also called **ochre** and UAG is also known as **amber** (because an investigator who studied the properties of this codon belonged to the Bernstein family, and Bernstein means amber in German). UGA is also called **opal.** They resulted in the formation of incomplete polypeptide chains. UGA is the usual terminator codon in all cases.

Central Dogma: Journey of DNA to Protein

During the process of transcription, the information stored in a gene's DNA is transferred to a similar molecule called RNA (ribonucleic acid) in the cell nucleus. Both RNA and DNA are made up of a chain of nucleotide bases, but they have slightly different chemical properties. The type of RNA that contains the information for making a protein is called messenger RNA (mRNA) because it carries the information, or message, from the DNA out of the nucleus into the cytoplasm. Translation, the second step in getting from a gene to a protein, takes place in the cytoplasm. The mRNA interacts with a specialized complex called a ribosome, which "reads" the sequence of mRNA bases. Each sequence of three bases, called a codon, usually codes for one particular amino acid. (Amino acids are the building blocks of proteins.) A type of RNA called transfer RNA (tRNA) assembles the protein, one amino acid at a time. Protein assembly continues until the ribosome encounters a "stop" codon (a sequence of three bases that does not code for an amino acid). The flow of information from DNA to RNA to proteins (**refer figure 6**) is one of the fundamental principles of molecular biology. It is so important that it is sometimes called the "**central dogma**."[5]

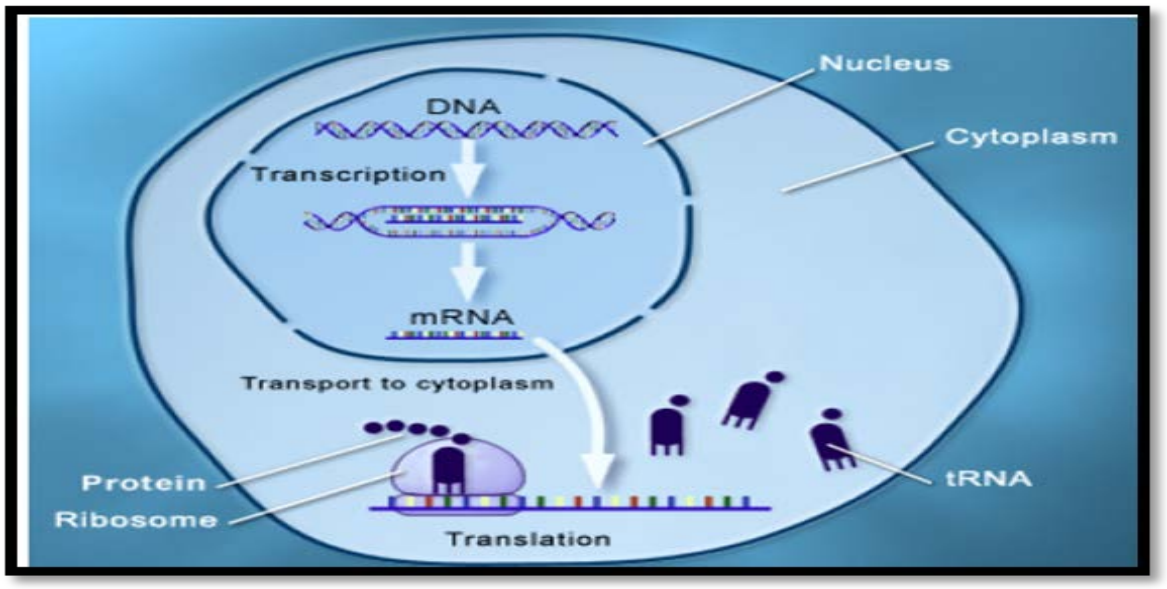

Fig 6: Central Dogma [Figure adopted from Handbook Help Me Understand Genetics https://ghr.nlm.nih.gov/handbook.pdf **]**

Mutation and type of mutation

Mutation is a permanent change in the DNA sequence that makes up a gene. Mutations range in size from one DNA base to a whole chromosome change. Gene mutations occur in two ways**:** they can be inherited from a parent (hereditary mutations or germline mutations) or acquired during a person's lifetime and occur in the DNA of individual cells (acquired or sporadic mutations). These changes can be caused by **environmental factors** [6] such as ultraviolet radiation from the sun, or can occur if a mistake is made as DNA copies itself during cell division. Acquired mutations in somatic cells cannot be passed on to the next generation, but the germline mutations can do [6]. The triplet nature of the genetic code means that base changes within coding sequence can have several different outcomes.

Types of Mutation [7]

1. **Missense mutation**: changes an amino acid to another amino acid. This may or may not affect protein function, depending on whether the change is "conservative" or "non conservative," and what the amino acid actually does.
2. **Nonsense mutation**: changes an amino acid to a STOP codon, resulting in premature termination of translation.
3. **"Silent" mutation**: does not change an amino acid, but in some cases can still have a phenotypic effect, *e.g.*, by speeding up or slowing down protein synthesis, or by affecting splicing.
4. **Frameshift mutation**: Deletion or insertion of a number of bases that is *not* a multiple of 3. Usually introduces premature STOP codons in addition to lots of amino acid changes.

All Mutations Are Random.

The bulk of the scientific data regarding mutagenesis is that mutations, whether the result of polymerase errors, spontaneous modification, or chemical damage to DNA, occur at random. This paradigm was challenged by John Cairns, who demonstrated that bacteria unable to

digest lactose preferentially acquired the mutations they needed in order to use lactose when it was the only nutrient available. This observation, which suggests that bacteria can "direct" mutations that benefit them, more likely reflects a nonspecific adaptive response in which the overall rate of mutation—useful as well as nonuseful—increases when the cells are under metabolic stress. *The hypermutable state appears to reflect the activation of error-prone DNA repair and recombination systems that are relatively inactive in normally growing cells* **[8].**

Chemical and Biological components which alter DNA [9]

A large number of chemicals may interact directly with DNA. However, many such as PAHs, aromatic amines, benzene are not necessarily mutagenic by themselves, but through metabolic processes in cells they produce mutagenic compounds.

1. **Reactive oxygen species (ROS)** – These may be superoxide, hydroxyl radicals and hydrogen peroxide, and large number of these highly reactive species are generated by normal cellular processes, for example as a by-products of mitochondrial electron transport, or lipid peroxidation. As an example of the latter, 15-hydroperoxyicosatetraenocic acid, a natural product of cellular cyclooxygenases and lipoxygenases, breaks down to form 4-hydroxy-2(*E*)-nonenal, 4-hydroperoxy-2(*E*)-nonenal, 4-oxo-2(*E*)-nonenal, and *cis*-4,5-epoxy-2(*E*)-decanal; these bifunctional electophils are mutagenic in mammalian cells and may contribute to the development and/or progression of human cancers (see 15-Hydroxyicosatetraenoic acid).[26] A number of mutagens may also generate these ROS. These ROS may result in the production of many base adducts, as well as DNA strand breaks and crosslinks.
2. **Deaminating agents,** for example nitrous acid which can cause transition mutations by converting cytosine to uracil.
3. **Polycyclic aromatic hydrocarbon (PAH),** when activated to diol-epoxides can bind to DNA and form adducts.
4. **Alkylating agents** such as ethylnitrosourea. The compounds transfer methyl or ethyl group to bases or the backbone phosphate groups. Guanine when alkylated may be mispaired with thymine. Some may cause DNA crosslinking and breakages. Nitrosamines are an important group of mutagens found in tobacco, and may also be formed in smoked meats and fish via the interaction of amines in food

with nitrites added as preservatives. Other alkylating agents include mustard gas and vinyl chloride.

5. **Aromatic amines and amides** have been associated with carcinogenesis since 1895 when German physician Ludwig Rehn observed high incidence of bladder cancer among workers in German synthetic aromatic amine dye industry. 2-Acetylaminofluorene, originally used as a pesticide but may also be found in cooked meat, may cause cancer of the bladder, liver, ear, intestine, thyroid and breast.
6. **Alkaloid** from plants, such as those from Vinca species , may be converted by metabolic processes into the active mutagen or carcinogen.
7. **Bromine** and some compounds that contain bromine in their chemical structure.
8. **Sodium azide, an azide salt** that is a common reagent in organic synthesis and a component in many car airbag systems
9. **Psoralen combined with ultraviolet radiation** causes DNA cross-linking and hence chromosome breakage.
10. **Benzene,** an industrial solvent and precursor in the production of drugs, plastics, synthetic rubber and dyes.
11. **Intercalating agents,** such as ethidium bromide and proflavine, are molecules that may insert between bases in DNA, causing frameshift mutation during replication. Some such as daunorubicin may block transcription and replication, making them highly toxic to proliferating cells.
12. **Heavy Metals:-** Many metals, such as arsenic, cadmium, chromium, nickel and their compounds may be mutagenic, but they may act, however, via a number of different mechanisms. Arsenic, chromium, iron, and nickel may be associated with the production of ROS, and some of these may also alter the fidelity of DNA replication. Nickel may also be linked to DNA hypermethylation and histone deacetylation, while some metals such as cobalt, arsenic, nickel and cadmium may also affect DNA repair processes such as DNA mismatch repair, and base and nucleotide excision repair.

Biological agents

Transposon, a section of DNA that undergoes autonomous fragment relocation/multiplication. Its insertion into chromosomal DNA disrupts functional elements of the genes. **Virus**, DNA may be inserted into the genome and disrupts genetic function. Infectious agents have been suggested to cause cancer as early as 1908 by Vilhelm Ellermann

and Oluf Bang, and 1911 by Peyton Rous who discovered the Rous sarcoma virus. Some bacteria such as *Helicobacter pylori* cause inflammation during which oxidative species are produced, causing DNA damage and reducing efficiency of DNA repair systems, thereby increasing mutation.

Role of Social Environment on Gene Expression and genetic codes

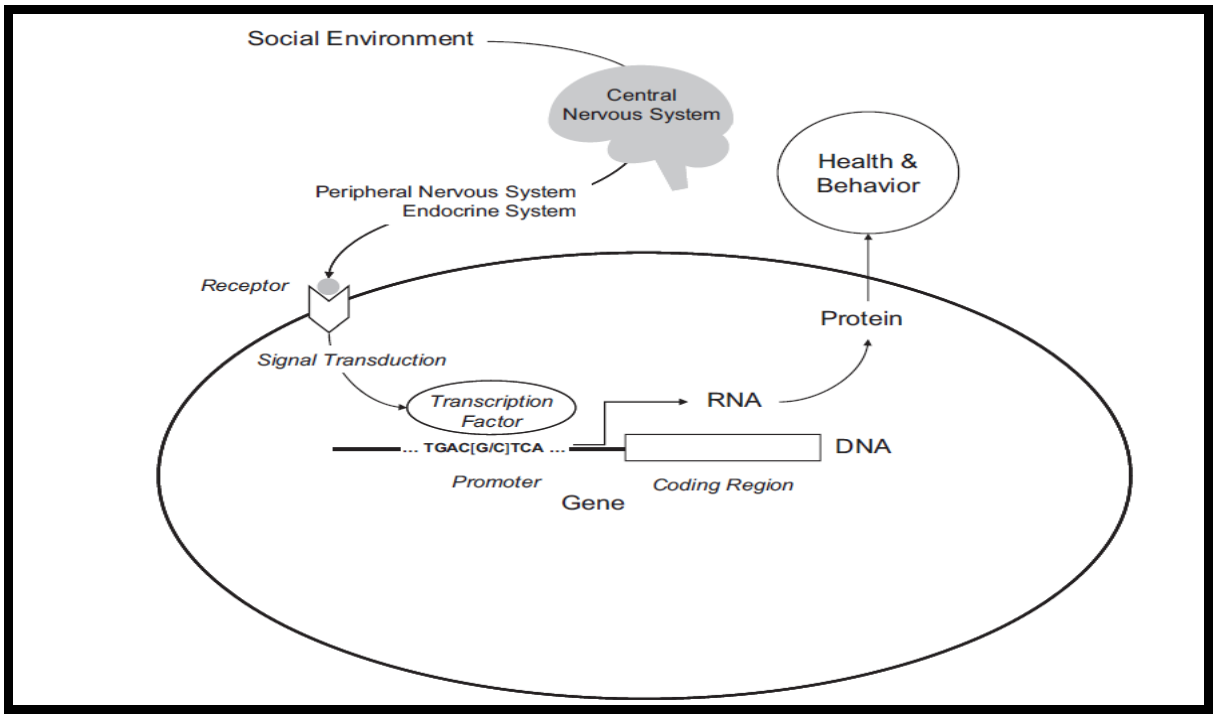

Fig 7: Social Signal Transduction Socio-environmental processes regulate human gene expression by activating central nervous system processes that subsequently influence hormone and neurotransmitter activity in the periphery of the body. Peripheral signaling molecules interact with cellular receptors to activate transcription factors, which bind to characteristic DNA motifs in gene promoters to initiate (or repress) gene expression. Only genes that are transcribed into RNA actually influence health and behavioral phenotypes. Individual differences in promoter DNA sequences (e.g., the [G/C] polymorphism shown here) can affect the binding of transcription factors and thereby influence the sensitivity of genomic response to socio environmental conditions.[Figure adopted from Steve W. Cole Social Regulation of Human Gene Expression, CURRENT DIRECTIONS IN PSYCHOLOGICAL SCIENCE, Vol 18 no 3, 132-137]

Beside environment some studies shows that social environment factors also responsible for changing in gene expression figure 7 depicts the same. Several studies have shown that social influences can penetrate remarkably deeply into our bodies. The nervous system plays a key role in perceiving and responding to social stimuli, and social conditions have been found to regulate the expression of neural genes such as the nerve growth factor (NGF) gene [10] and the glucocorticoid receptor gene [11]. More surprising is the discovery that key immune

system genes are also sensitive to social conditions [10]. Immune cells exert selective pressure on the evolution of viral genomes, and many viruses also appear to have developed a genomic sensitivity to our social conditions

Conclusion

In daily life we have seen the many cases of *Bhoot, Upri hawa*, etc. To free the body from all such type of effects, people waste their money and time. But actually they don't know that this is just a change in the genetic makeup. We use the word "genetic makeup" after review of many scientific literatures and reach on the conclusion that there is no fault of *jadu- tona-totka.* Due to heavy load of environmental pollution (environmental agents) such as ultraviolet light, extreme use of medical technique (ionizing radiations such as X rays) certain chemical agents can physically damage DNA. For example, UV radiation (200–300 nm) promotes the formation of a cyclobutyl ring between adjacent thymine residues on the same DNA strand to form an intrastrand **thymine dimer**. Similar cytosine and thymine–cytosine dimmers also form but less frequently. Such **pyrimidine dimers** locally distort DNA's base-paired structure, interfering with transcription and replication. Ionizing radiation also damages DNA either through its direct action on the DNA molecule or indirectly by inducing the formation of free radicals, particularly the hydroxyl radical ($HO^{\cdot}$), in the surrounding aqueous medium. This can lead to strand breakage. Mutagens cause changes to the DNA that can affect the transcription and replication of the DNA, which in severe cases can lead to cell death. The mutagen produces mutations in the DNA, and deleterious mutation can result in aberrant, impaired or loss of function for a particular gene, and accumulation of mutations may lead to cancer. However, some mutagens exert their mutagenic effect through their metabolites, and therefore whether such mutagens actually become carcinogenic may be dependent on the metabolic processes of organisms, and a compound shown to be mutagenic in one organism may not necessarily be carcinogenic in another. Different mutagens act on the DNA differently. Powerful mutagens may result in chromosomal instability, causing chromosomal breakages and rearrangement of the chromosomes such as translocation, deletion, and inversion. Such mutagens are called clastogens. Mutagens may also modify the DNA sequence; the changes in nucleic acid sequences by mutations include substitution of nucleotide base-pairs and insertions and deletions of one or more nucleotides in DNA sequences. Although some of these mutations are lethal or cause serious disease, many have minor effects as they do not result in residue changes that have significant effect on the structure and function of the proteins. Many mutations are silent mutations, causing no

visible effects at all, either because they occur in non-coding or non-functional sequences, or they do not change the amino-acid sequence due to the redundancy of codons.

The Royal Swedish Academy of Sciences has decided to award Tomas Lindahl, Paul Modrich and Aziz Sancar the Nobel Prize in Chemistry 2015 for their "Mechanistic studies of DNA repair" [12]. They quote in their scientific literature that the human genome encodes the information needed to create a complete human being. During every cell division, more than three billion DNA base pairs are replicated and copies of the genome are transferred to the daughter cells. Although very efficient, the DNA replication machinery responsible for this task still makes occasional mistakes. Given the size of the human genome and the large number of cells in a human body (about 3.7×10^{13}) mistakes will inevitably accumulate during the lifetime of an individual. Most of these errors will remain silent, but they can also cause serious diseases.

In our (Priyank and Garima) research we found that DNA is formed by chromosomes and genetic codes. These genetic codes govern the particular tasks in our body. If mutation occurs due to any of the reason then it confirms that any particular code responsible for a task is not working properly. It is the situation when a person behaves like someone else, losing his/her own identity. At last we conclude that *upri hwa and bhoot preat* is not anything but they are only the result of genetic disorders for which environmental conditions/environmental pollution are responsible.

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