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# Central Dogma of Molecular Biology: The way of diverting the instruction from DNA to protein synthesis and this change ultimately make the conversion of organism into another organism

**Priyank Bharati*[1], Garima Tyagi[2]**

*1 Assistant Professor, School of Biological Engineering, Shobhit University, Adarsh Instutuional Area, Babu Vijendra Marg, *Gangoh*, Distt. Saharanpur - 247341. U.P., India

2 Natural Sciences Trust, Meerut, U.P., India

## Abstract

"*MayaviShaktiya*", "*Chamatkar*" these things are beyond any religious belief but which used to happen and will continue to happen even in future if a person will have deep knowledge as well as better understanding of scientific concept behind it. This is again an example of the developed Vedic Sciences which is still unreachable by current people. It is also clear that there was not any laboratory apparatus as used these days and people used to synthesize natural chemicals in place of artificial chemicals that time for their work even if we talk of the *Birth of Kauravas in Mahabharat*a or *to commute the physical morphology in Ramayana*. Our daily life also has science in it, that depends on our observation and perception that how we co-relate both. In this research paper we are explaining about the methodology to commute the physical morphology which is a scientific process controlled by central dogma of molecular biology which shows that DNA forms the RNA which finally forms proteins and these proteins determines the structural and functional properties of a body.

**Keywords: - Central Dogma, Proteins, Amino Acids**

## Introduction

All of us have heard somewhere or even seen in the television that a person changes his the entire body and takes up the morphology of some different species like "*Ichadhari naag and nagin*". Some evidences like this are also mentioned in Ramayana, that at the time of Sita *haran*, a person took the morphology of golden deer which shows that this technique was also known by people at that time**. In Mahabharata** also Shri Krishna was expert in this technique and at the time of Kurukshetra War, he showed his enlarged body size (***vikraal roop***) which explains that his bones were flexibility (due **to contractile protein**). We generally study and link all these things to religion **(*dhrama*)** and give them a name of

"***chamatkar or Mayavi shaktiya*".** Even Science has always denied such things which are conceptually a part on science only. In this 21st century, researches are going on in various fields, in various parts of the World to know that which techniques were used at that time. If we are talking of such powers then we must first study the process responsible for all this. This paper will explain the scientific concept behind these type of processes.

**Proteins: Structural and Functional Unit**

Proteins are the most abundant molecule within the living cells. Proteins are basic and functional unit of life.. Scientific literatures show that proteins constitute about 50% of the cellular dry weight. The term protein is derived from a Greek word **proteios** meaning holding the first place. Berzelius (Swedish chemist) suggested the name proteins to the group of organic compounds that are utmost important to life. Mulder (Dutch chemist) in 1838 used the term proteins for the high molecular weight nitrogen- rich and most abundant substances present in animals and plants. Protein contains 50-55% of Carbon, 6-7% Hydrogen, 19-24% Oxygen. 15-18% Nitrogen and 0-4% Sulphur.. They are widely distributed in living matter. All enzymes are proteins. Around 300 amino acids occur in nature but 20 of them are found in proteins. These amino acids are known as "Standard or Principle amino acids" .In proteins the amino acids are linked up by polypeptide bonds to form long chain called polypeptides. Proteins are like long necklaces with differently shaped beads. Each "bead" is a small molecule called an amino acid. There are 20 standard amino acids, each with its own shape, size, and properties. Proteins typically contain from 50 to 2,000 amino acids hooked end to end in many combinations. Each protein has its own sequence of amino acids **[1].** Proteins are primarily responsible for structure and strength of body. Muscles contraction in higher organism and flagella movement in micro-organism takes place by contractile assemblies. These contractile assemblies are made up of Proteins e.g. actin and myosin proteins play important role in muscles contraction. Till 1940s, it was generally assumed that genes were made of protein, since proteins were the only biochemical entities that, at the time, seemed complex enough to serve as agents of inheritance.

Proteins are worker molecules that are necessary for virtually every activity in your body **[1].** Proteins carry out a diverse

array of functions, including catalysis, defense, transport of substances, motion and regulation of cell and body functions. The proteins within living organisms are immensely diverse in structure and function They perform following functions **[2]**

- **Enzyme catalysis.** One class of proteins, enzymes, which are biological catalysts that facilitate specific chemical reactions. Because of this property, the appearance of enzymes was one of the most important events in the evolution of life. Enzymes are globular proteins, with a three dimensional shape that fits snugly around the chemicals they work on, facilitating chemical reactions by stressing particular chemical bonds.
- **Defense.** Other globular proteins use their shapes to "recognize" foreign microbes and cancer cells. These cell surface receptors form the core of the body's hormone and immune systems.
- **Transport.** A variety of globular proteins transport specific small molecules and ions. The transport protein hemoglobin, for example, transports oxygen in the blood, and myoglobin, a similar protein, transports oxygen in muscle. Iron is transported in blood by the protein transferrin.
- **Support.** Fibrous, or threadlike, proteins play structural roles; these structural proteins include keratin in hair, fibrin in blood clots, and collagen, which forms the matrix of skin, ligaments, tendons, and bones and is the most abundant protein in a vertebrate body.
- **Motion.** Muscles contract through the sliding motion of two kinds of protein filament: actin and myosin. Contractile proteins also play key roles in the cell's cytoskeleton and in moving materials within cells. By the use of this protein Shri Krishna moulded his body in the war of Mahabharata and made them flexible. Similar types of properties were observed in the body of "Karan" and "Draupadi". **[3]**
- **Regulation.** Small proteins called hormones serve as intercellular messengers in animals. Proteins also play many regulatory roles within the cell, turning on and shutting off genes during development, for example. In addition, proteins also receive

information, acting as cell surface receptors.

| Function | Class of Protein | Examples | Use |
|---|---|---|---|
| Metabolism (Catalysis) | Enzymes | Hydrolytic enzymes | Cleave polysaccharides |
| | | Proteases | Break down proteins |
| | | Polymerases | Produce nucleic acids |
| | | Kinases | Phosphorylate sugars and proteins |
| Defense | Immunoglobulins | Antibodies | Mark foreign proteins for elimination |
| Cell recognition | Toxins | Snake venom | Block nerve function |
| Transport throughout body | Cell surface antigens | MHC proteins | "Self" recognition |
| | Globins | Hemoglobin | Carries $O_2$ and $CO_2$ in blood |
| | | Myoglobin | Carries $O_2$ and $CO_2$ in muscle |
| | | Cytochromes | Electron transport |
| Membrane transport | Transporters | Sodium-potassium pump | Excitable membranes |
| | | Proton pump | Chemiosmosis |
| | | Anion channels | Transport $Cl^-$ ions |
| Structure/Support | Fibers | Collagen | Cartilage |
| | | Keratin | Hair, nails |
| | | Fibrin | Blood clot |
| Motion | Muscle | Actin | Contraction of muscle fibers |
| | | Myosin | Contraction of muscle fibers |
| Osmotic regulation | Albumin | Serum albumin | Maintains osmotic concentration of blood |
| Regulation of gene action | Repressors | lac repressor | Regulates transcription |
| Regulation of body functions | Hormones | Insulin | Controls blood glucose levels |
| | | Vasopressin | Increases water retention by kidneys |
| | | Oxytocin | Regulates uterine contractions and milk production |
| Storage | Ion binding | Ferritin | Stores iron, especially in spleen |
| | | Casein | Stores ions in milk |
| | | Calmodulin | Binds calcium ions |

**Table 1: Function of Proteins [2]**

## Structure of Proteins [2]

The structure of proteins is discussed in terms of four levels of structure, as primary, secondary, tertiary, and quaternary

**Primary Structure**-The specific amino acid sequence of a protein is its primary structure. This sequence is determined by the nucleotide sequence of the gene that encodes the protein. Because the R groups that distinguish the various amino acids play no role in the peptide backbone of proteins, a protein can consist of any sequence of amino acids. Thus, a protein containing 100 amino acids could form any of $20^{100}$ different amino acid sequences (that's the same as $10^{130}$, or 1 followed by 130 zeros—more than the number of atoms known in the universe).

This is an important property of proteins because it permits such great diversity.

**Secondary Structure-**The amino acid side groups are not the only portions of proteins that form hydrogen bonds. The —COOH and —$NH_2$ groups of the main chain also form quite good hydrogen bonds—so good that their interactions with water might be expected to offset the tendency of non-polar side groups to be forced into the protein interior. Inspection of the protein structures determined by X-ray diffraction reveals why they don't —the polar groups of the main chain form hydrogen bonds with each other. Two patterns of H bonding occur. In one, hydrogen bonds form along a single chain, linking one amino acid to another farther down the chain. This tends to pull the chain into a coil called an alpha (α) helix. In the other pattern, hydrogen bonds occur across two chains, linking the amino acids in one chain to those in the other. Often, many parallel chains are linked, forming a pleated, sheet like structure called a β-pleated sheet. The folding of the amino acid chain by hydrogen bonding into these characteristic coils and pleats is called a protein's secondary structure.

Motifs- The elements of secondary structure can combine in proteins in characteristic ways called motifs, or sometimes "super secondary structure." One very common motifis the β α β motif, which creates a fold or crease; the so called "Rossmann fold" at the core of nucleotide binding sites in a wide variety of proteins is a β α β α β motif. A second motif that occurs in many proteins is the β barrel, a β sheet folded around to form a tube. A third type of motif, the α turn α motif, is important because many proteins use it to bind the DNA double helix.

**Tertiary Structure-** The final folded shape of a globular protein, which positions the various motifs and folds non polar side groups into the interior, is called a protein's tertiary structure. A protein is driven into its tertiary structure by hydrophobic interactions with water. The final folding of a protein is determined by its primary structure—by the chemical nature of its side groups. Many proteins can be fully unfolded ("denatured") and will spontaneously refold back into their characteristic shape .The stability of a protein, once it has folded into its 3-D shape, is strongly influenced by how well its interior fits together. When two non polar chains in the interior are in very close proximity, they experience a form of molecular attraction called Van der Waal's forces. Individually quite weak, these forces can add up to a strong attraction

when many of them come into play, like the combined strength of hundreds of hooks and loops on a strip of Velcro. They are effective forces only over short distances, however; there are no “holes” or cavities in the interior of proteins. That is why there are so many different non polar amino acids (alanine, valine, leucine, isoleucine). Each has a different sized R group, allowing very precise fitting of non polar chains within the protein interior. Now you can understand why a mutation that converts one non polar amino acid within the protein interior (alanine) into another (leucine) very often disrupts the protein’s stability; leucine is a lot bigger than alanine and disrupts the precise way the chains fit together within the protein interior. A change in even a single amino acid can have profound effects on protein shape and can result in loss or altered function of the protein.

Domains-Many proteins in our body are encoded within our genes in functional sections called exons. Each exon-encoded section of a protein, typically 100 to 200 amino acids long, folds into a structurally independent functional unit called a **domain.** As the polypeptide chain folds, the domains fold into their proper shape, each more-or-less independent of the others. This can be demonstrated experimentally by artificially producing the fragment of polypeptide that forms the domain in the intact protein, and showing that the fragment folds to form the same structure as it does in the intact protein. A single polypeptide chain connects the domains of a protein, like a rope tied into several adjacent knots. Often the domains of a protein have quite separate functions—one domain of an enzyme might bind a cofactor, for example, and another the enzyme’s substrate.

**Quaternary Structure-** When two or more polypeptide chains associate to form a functional protein, the individual chains are referred to as subunits of the protein. The subunits need not be the same. Hemoglobin, for example, is a protein composed of two α-chain subunits and two β-chain subunits. A protein’s subunit arrangement is called its quaternary structure. In proteins composed of subunits, the interfaces where the subunits contact one another are often non polar, and play a key role in transmitting information between the subunits about individual subunit activities. **A change in the identity of one of these amino acids can have profound effects**. Sickle cell hemoglobin is a mutation that alters the identity of a single amino acid at the corner of the β subunit from polar

glutamate to non polar valine putting a non polar amino acid on the surface creates a“ sticky patch” that causes one hemoglobin molecule to stick to another, forming long non functional chains and leading to the cell sickling characteristic of this hereditary disorder.

**Central Dogma of Molecular Biology: Scientific process which hold “*Mayavi Shaktiya*”**

The biochemical activity of a cell depends on production of a large number of proteins, each with a specific sequence. The ability to produce the correct proteins is passed between generations of organisms, even though the protein molecules themselves are not [2].Nucleic acids are the information storage devices of cells, just as disks or tapes store the information that computers use, blueprints store the information that builders use, and road maps store the information that tourists use. There are two varieties of nucleic acids: *Deoxyribonucleic Acid* (**DNA**) and *Ribonucleic Acid* (**RNA**). The way in which DNA encodes the information used to assemble proteins is similar to the way in which the letters on a page encode information. Unique among macromolecules, nucleic acids are able to serve as templates to produce precise copies of themselves, so that the information that specifies what an organism is can be copied and passed down to its descendants. For this reason, DNA is often referred to as the hereditary material. Cells use the alternative form of nucleic acid, RNA, to read the cell’s DNA-encoded information and direct the synthesis of proteins. RNA is similar to DNA in structure and is made as a transcripted copy of portions of the DNA. This transcript passes out into the rest of the cell, where it serves as a blueprint specifying a protein’s amino acid sequence.

The central dogma states that once information has passed into proteins it cannot get out again in more detail, the transfer of information from nucleic acid to protein may be possible, but transfer from protein to protein, or from protein to nucleic acid is impossible. Here information means the precise determination of sequence, either of bases in the nucleic acid or of amino acid residues in protein **[5]**. The quotation above is from a seminal paper, ‘On Protein Synthesis,’ presented by Francis Crick at the 1957 annual meeting of the Society of Experimental Biology and published in 1958. In this paper, Crick listed the standard set of 20 amino acid residues for the first time; argued that ‘the specificity

of a piece of nucleic acid is expressed solely by the sequence of its bases, and that this sequence is a (simple) code for the amino acid sequence of a particular protein'; argued that the 3-D conformation of a protein must be determined by its amino acid sequence; pointed out that protein synthesis must be sequential; and presented his hypothesis of 'adaptor' molecules mediating protein formation at the ribosome. Most importantly, Crick formulated what he called the 'Central Dogma' When the structure of DNA was figured out in 1953, there was a strong belief among the pioneers of the new science of molecular biology that they had uncovered the physic chemical basis of heredity and fundamental life processes **[4]**. Following discoveries about the process of protein synthesis, the consensus view was most cogently summarized a half-century again 1958**[5]** (and then again in 1970**[6]**) by Crick's declaration of "the central dogma of molecular biology." The concept was that information basically flows from **DNA to RNA to protein**, which determines the cellular and organismal phenotype. While it was considered a theoretical possibility that RNA could transfer information into DNA, information transfer from proteins to DNA, RNA, or other proteins was considered outside the dogma and "would shake the whole intellectual basis of molecular biology."**[6]** This DNA/nucleic acid-centred view is still dominant in virtually all public discussions of biological questions, ranging from the role of heredity in disease to arguments about the process of evolutionary change. Even in the technical literature, there is a widespread assumption that **DNA, as the genetic material, determines cell action** and that observed deviations from strict genetic determinism must be the result of stochastic processes [7].

**Protein Synthesis [8]**

The sequence of amino acids has a bearing on the properties of a protein, and is characteristic for a particular protein. The basic mechanism of protein synthesis is that DNA makes RNA, which in turn makes protein. The central dogma of protein synthesis is expressed as follows:

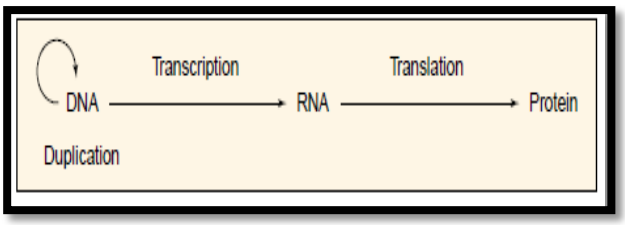


**Fig 1 :- Process of Central Dogma**

Proteins are widely used in cells to serve diverse functions. Some proteins provide the structural support for cells while others act as enzymes to catalyze certain

reactions. We have already seen the roles that different enzymes play in building the cell's structure and in catalyzing metabolic reactions, but where do proteins come from?

Since the **beginning of evolution**, cells have developed the ability to synthesize proteins. They can produce new proteins either for reproduction or to simply replace a degraded one. To manufacture proteins, cells follow a very systematic procedure that first transcribes DNA into mRNA (messenger RNA) and then translates the mRNA into chains of amino acids. The amino acid chain then folds into specific proteins.

Protein synthesis mainly done in two steps: *transcription* and *translation*.

***Transcription-***

Protein synthesis begins in the cell's nucleus when the gene encoding a protein is copied into RNA (Fig 2). Genes, in the form of DNA, are embedded in in the cell's chromosomes. The process of transferring the gene's DNA into RNA is called transcription. Transcription helps to magnify the amount of DNA by creating many copies of RNA that can act as the template for protein synthesis. The RNA copy of the gene is called the mRNA. DNA and RNA are both constructed by a chain of nucleotides. However, RNA differs from DNA by the substitution of uracil (U) for thymine (T). Also, because only one strand of mRNA is needed when synthesizing proteins, mRNA naturally exists in single-stranded forms.

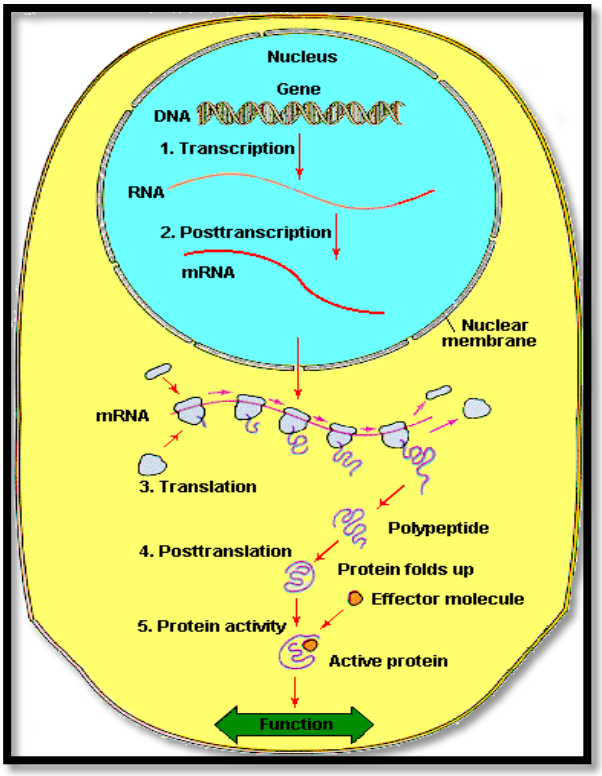


**Fig 2: Eukaryotic cell show the place where translation and transcription takes place [9]**

After transcription, the mRNA is transported out of the cell's nucleus through nuclear pores to go to the site of translation, the rough endoplasmic reticulum (Rough endoplasmic reticulum is named for its rough appearance, which is due to the ribosomes attached to its outer (cytoplasmic) surface. Rough Endoplasmic Reticulum lies immediately adjacent to the cell nucleus, and its

membrane is continuous with the outer membrane of the nuclear envelope. The ribosomes on rough Endoplasmic Reticulum specialize in the synthesis of proteins that possess a signal sequence that directs them specifically to the Endoplasmic Reticulum for processing. (A number of other proteins in a cell, including those destined for the nucleus and mitochondria, are targeted for synthesis on free ribosomes, or those not attached to the Endoplasmic Reticulum membrane). Proteins synthesized by the rough Endoplasmic Reticulum have specific final destinations. Some proteins, for example, remain within the Endoplasmic Reticulum, whereas others are sent to the Golgi apparatus, which lies next to the Endoplasmic Reticulum. Proteins secreted from the Golgi apparatus are directed to lysosomes or to the cell membrane; still others are destined for secretion to the cell exterior. Proteins targeted for transport to the Golgi apparatus are transferred from ribosomes on rough Endoplasmic Reticulum into the rough Endoplasmic Reticulum lumen, which serves as the site of protein folding, modification, and assembly)**[10]**.

Transcription is a process of making an RNA strand from a DNA template, and the RNA molecule that is made is called transcript. In the synthesis of proteins, there are actually three types of RNA that participate and play different roles:

**a. mRNA(messenger RNA)** carries the genetic information from DNA and is used as a template for protein synthesis.

**b. rRNA(Ribosomal RNA)**which is a major constituent of the cellular particles called ribosomes on which protein synthesis actually takes place.

**c. tRNA (transfer RNA)** molecules, each of which incorporates a particular amino acid subunit into the growing protein when it recognizes a specific group of three adjacent bases in the mRNA.

DNA maintains genetic information in the nucleus. RNA takes that information into the cytoplasm, where the cell uses it to construct specific proteins, RNA synthesis is transcription; protein synthesis is translation. RNA differs from DNA in that it is single stranded, contains Uracil instead of Thymine and ribose instead of deoxyribose, and has different functions. The central dogma depicts RNA as a messenger between gene and protein, but does not adequately describe RNA's other function.

Transcription is highly controlled and complex. In Prokaryotes, genes are expressed as required, and in multicellular organisms, specialized cell types express

subsets of gene. Transcription factors recognize sequences near a gene and bind sequentially, creating a binding transcription. Transcription proceeds as RNAP inserts complementary RNA bases opposite the coding strand of DNA. Antisense RNA blocks gene expression.

Messenger RNA transmits information in a gene to cellular structures that build proteins. Each three mRNA bases in a row forms a codon that specifies a particular amino acid. Ribosomal RNA and proteins form ribosomes, which physically support the other participants in protein synthesis and help catalyze formation of bonds betweens amino acids.

In eukaryotes, RNA is often altered before it is active. Messenger RNA gains a cap of modified nucleotides and a poly A tail. Introns are transcribed and cut out, and exons are reattached by ribozymes. RNA editing introduced bases changes that alter the protein product in different cell types.

The genetic code is triplet, non-overlapping, continuous, universal, and degenerate. As translation begins, mRNA, tRNA with bound amino acids, ribosomes, energy molecules and protein factors assemble. The mRNA leader sequence binds to rRNA in the small subunit of a ribosome, and the first codon attracts a tRNA bearing methionine. Next, as the chain elongates, the large ribosomal subunit attaches and the appropriate anticodon parts of tRNA molecules form peptide bonds, a polypeptide grows. At a stop codon, protein synthesis ceases. Protein folding begins as translation proceeds, with enzymes and chaperone proteins assisting the amino acid chain in assuming its final functional form. Translation is efficient and economical, as RNA, ribosomes, enzymes, and key proteins are recycled.

**RNA transcription requires the following components**

The enzyme RNA polymerase

- A DNA template
- All four types of ribonucleoside triphosphates (ATP, GTP and UTP)
- Divalent metal ions $Mg^{++}$ or $Mn^{++}$ as a co-factor
- No primer is needed for RNA synthesis
- RNA transcription is a process that involves the following steps:
  - Binding of RNA polymerase to DNA Double Helix

The histone coat protecting the DNA double helix of the gene to be transcribed is removed, on a signal from the cytoplasm, exposing the polynucleotide sequences in this region of DNA. The RNA polymerase enzyme binds to a

specific site, called promoter, in the DNA double helix. This site is located on the 5 side of the gene to be transcribed. It signals the beginning of RNA synthesis. The promoter also determines the DNA strand that is to be transcribed.

- Exposure of RNA Bases

The histone coat protecting the DNA double helix of the gene to be transcribed is removed, on a signal from the cytoplasm, exposing the polynucleotide sequences in this region of DNA. The RNA polymerase enzyme binds to a specific site, called promoter, in the DNA double helix. This site is located on the 5 side of the gene to be transcribed. It signals the beginning of RNA synthesis. The promoter also determines the DNA strand that is to be transcription is not known.

- Base pairing

The ribonucleoside triphosphates, namely, adenosine triphosphate (ATP), guanosine triphosphate (GTP), cytidine triphosphate (CTP) and uridine triphosphate (UTP), floating free in the nucleus, serve as the raw material for RNA synthesis. They are formed by activation (phosphorylation) of ribonucleoside monophosphates, viz., adenosine monophosphate (AMP), guanosine monophosphate (GMP), cytidine monophosphate (CMP) and uridine monophosphate (UMP) as a result of their combining with ATP. The enzyme phosphorylase catalyses this activation process. The ribonucleotide triphosphates are joined to the bases of the DNA template chain one by one by hydrogen bonding according to the base pairing rule i.e., A U, U A, C G, G C. This base pairing is brought about by the RNA polymerase

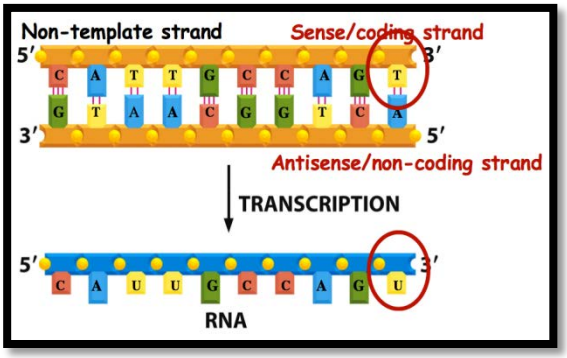


**Fig 3:- Synthesis of mRNA from DNA [11]**

- Conversion to Ribonucleoside Monophosphates

The various ribonucleoside triphosphates on linking to the DNA template chain break off their high-energy bonds. This changes them to ribonucleoside monophosphates which represent the normal components of RNA, and sets free pyrophosphate groups (P~P). Pyrophosphate contains a high-energy bond (~). It undergoes hydrolysis by the enzyme pyrophosphotase, releases energy and sets free inorganic phosphate Pi. The first ribonucleotide phosphate retains all

the three phosphates and is, thus, chemically distinct from the other nucleotides added after it.

- Formation of RNA Chain

Each ribonucleoside monophosphate attached to the DNA template chain then combines with the ribonucleotide arrived earlier, making the RNA chain become longer. The process is catalysed by the enzyme RNA polymerase and requires a divalent ion Mg++ or Mn ++. The RNA chain, thus formed, contains nitrogenous bases that are complementary to those of the template **DNA** chain.

- Separation of RNA Chain

As transcription proceeds, the hybrid DNA-RNA molecule dissociates, partly releasing the RNA molecule under synthesis. When polymerase reaches a terminator signal on the DNA, it leaves the DNA. The fully formed RNA chain is now totally released by this process; one gene forms several molecules of RNA, which get released from the DNA template one after the other. In some cases, such as in E. coli, a specific chain terminating protein, called rho factor (P), stops the synthesis of RNA chain. In most cases, the enzyme RNA polymerase on its own can stop transcription.

- Return of DNA Segment to Original Form

As the RNA chain grows, the transcribed region of the DNA molecule gets hydrogen bonded to the opposite strand and the two become spirally coiled to assume the original double helical form. When the last ribonucleotide is added, the RNA polymerase and RNA chain are completely released from the DNA, and now the DNA completes its winding into a double helix. The protective protein coat is added again to the DNA duplex.

The sequence of nitrogen bases from the promoter to the terminator sites form a transcription unit. It may include one or more genes. An entire transcription unit gets transcribed into a single RNA chain.

**Processing of RNAs**

The forms of RNAs originally transcribed from DNA are called primary transcripts. These undergo extensive changes, termed processing or post-transcriptional modification of RNAs, before they can become functional in both prokaryotes and eukaryotes.

1. Larger RNA precursors are cut into smaller RNAs by a ribonuclease-P cleaving enzyme
2. Unwanted nucleotides are removed by enzymes called nucleases (splicing)
3. Useful regions are rejoined by ligase enzyme

4. Certain nucleotides are added at the terminal ends enzymatically (terminal addition)
5. The RNA molecule may fold on itself to assume proper shape (folding)
6. Some nucleotides may be modified (nucleotide modification)

**Types of RNA**

The three different types of RNA, namely, messenger RNA (mRNA), ribosomal RNA (rRNA) and transfer RNA (tRNA) are transcribed from different regions of the DNA molecule. Three different RNA polymerases: I, II and III catalyses the transcription of rRNA, mRNA and tRNA respectively in eukaryotes. In prokaryotes, a single RNA polymerase composed of different subunits does this work. Transcription of RNA also occurs in the 5-3 direction like the replication of DNA.

***Translation*–**

After the mRNA has been transported to the rough endoplasmic reticulum, it is fed into the ribosomal translation machineries. Ribosomes begins to read the mRNA sequence from the 5` end to the 3` end. To convert the mRNA into protein, tRNA is used to read the mRNA sequence, 3 nucleotides at a time. Fig 5 depicts the complete process of Translation.

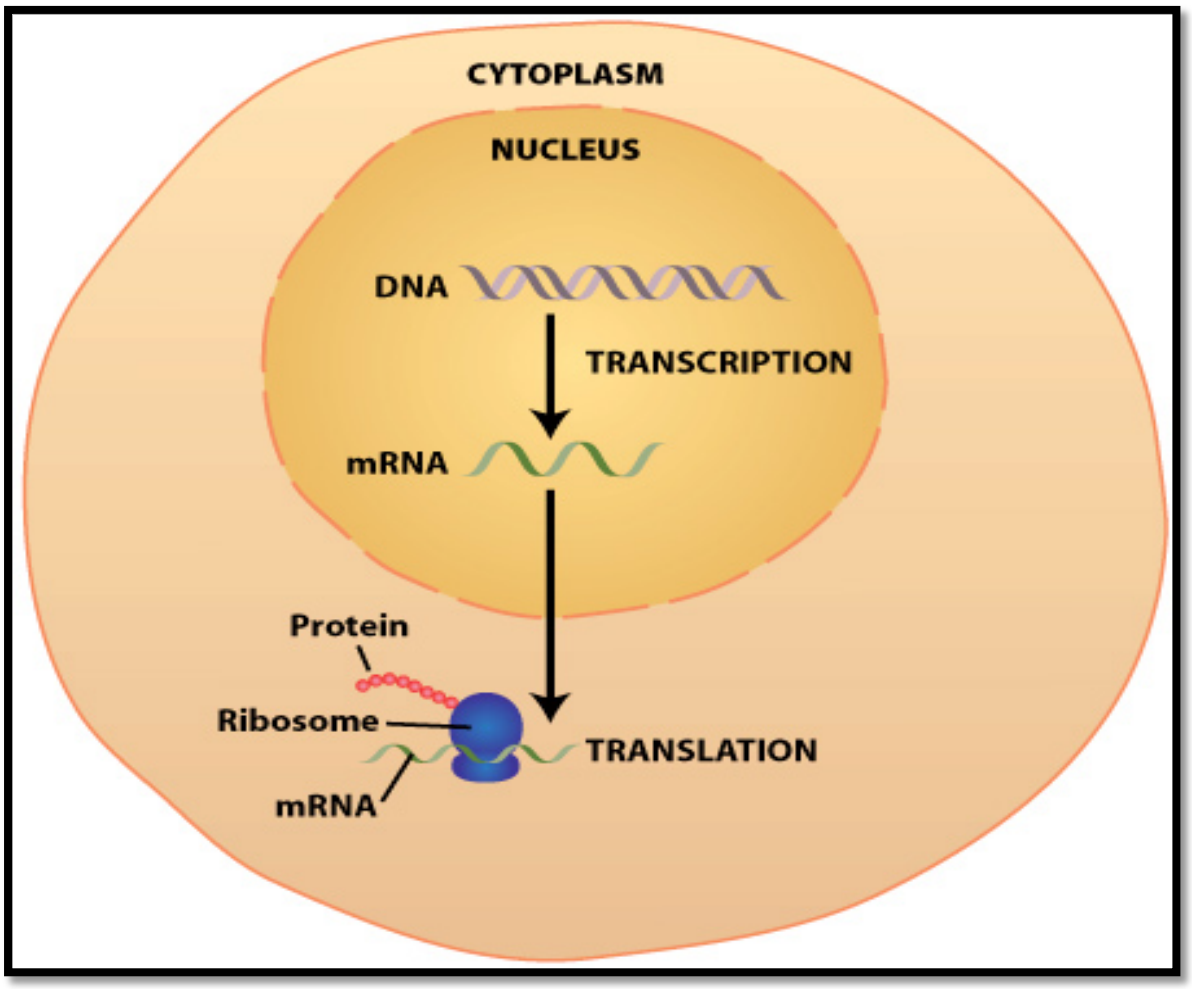


**Fig 4: The mRNA carries the message out of the nucleus to the ribosome in the cytoplasm where the tRNA helps translate the message to make a protein in cytoplasm** (.https://sites.duke.edu/apep/module-2-the-abcs-of-intoxication/biology-and-chemistry-connections/dna-transcription-translation-synthesis-of-proteins)

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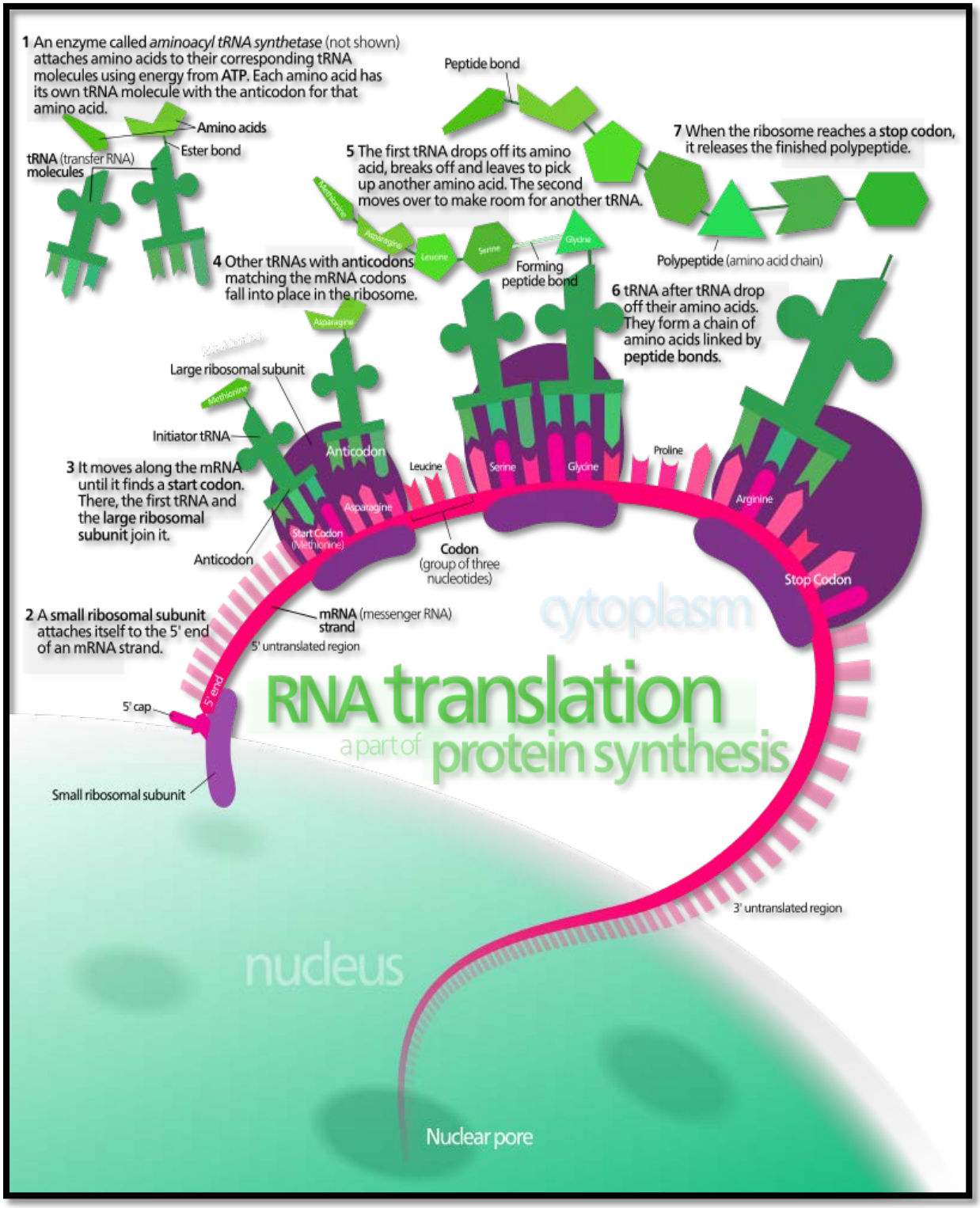



**Fig 5: RNA translation a part of protein synthesis**

[https://en.wikipedia.org/wiki/Translation_(biology)#/media/File:Protein_synthesis.svg]

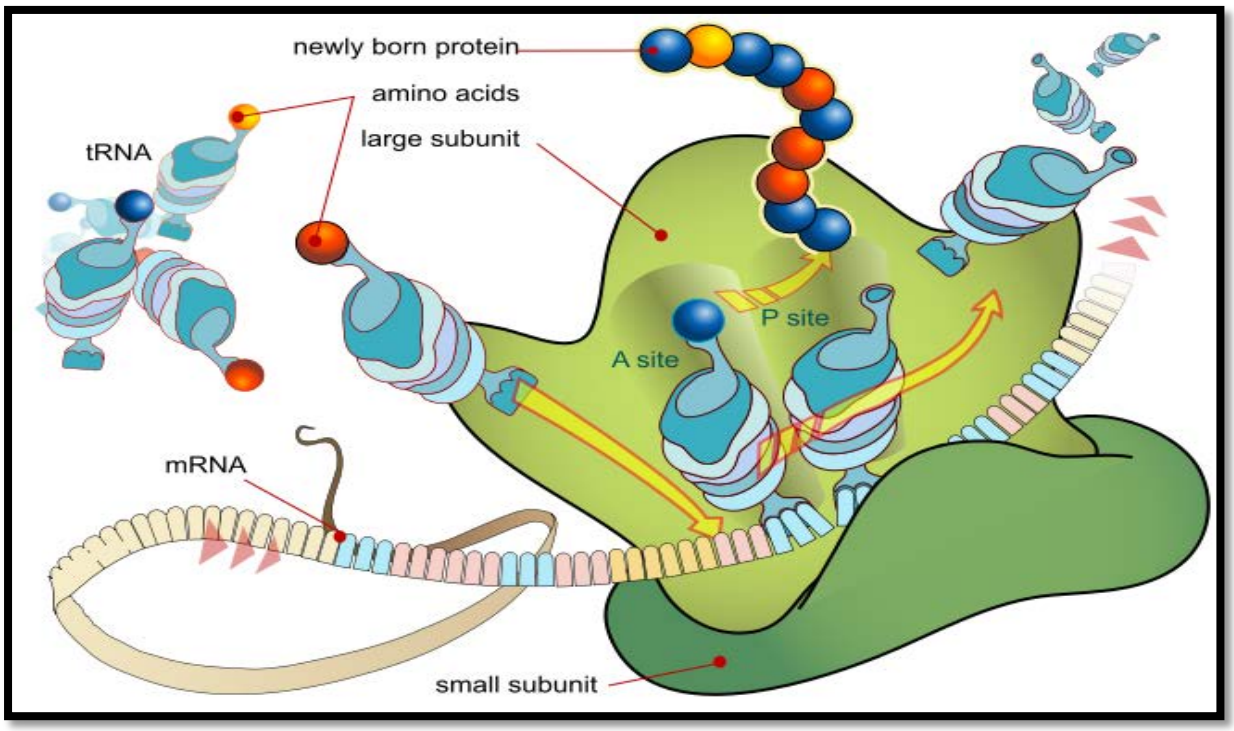



**Fig 6 -Translation of mRNA and the synthesis of proteins by a ribosome** (https://en.wikipedia.org/wiki/Translation_(biology)#/media/File:Ribosome_mRNA_translation_en.svg)

Ribosome orchestrates the translation of mRNA to synthesize polypeptides, it is helpful to assimilate the following points [12]-

1. ***Polypeptide synthesis proceeds from the N-terminus to the C-terminus****;* that is, a peptidyl transferase activity appends an incoming amino acid to a growing polypeptide's C-terminus. This was shown to be the case in 1961 by Howard Dintz is, who exposed reticulocytes (immature red blood cells) that were actively synthesizing hemoglob into $^{3}$H-labeled leucine for less time than it takes to synthesize an entire polypeptide. The extent to which the tryptic peptides from the soluble (completed) hemoglobin molecules were labelled increased with their proximity to the C-terminus, thereby indicating that incoming amino acids are appended to the growing polypeptide's C-terminus.
2. ***Chain elongation occurs by linking the growing polypeptide to the incoming tRNA's amino acid residue****:* If the growing polypeptide is released from the ribosome by treatment with high salt concentrations, its C-terminal residue is esterified to a tRNA molecule as a peptidyl–tRNA. The nascent (growing) polypeptide must therefore

grow by being transferred from the peptidyl–tRNA in the P site to the incoming aa–tRNA in the A site to form a peptidyl–tRNA with one more residue. After the peptide bond has formed, the new peptidyl–tRNA, which now occupies the A site, is translocated to the P site so that a new aa–tRNA can enter the A site. The uncharged tRNA in the P site moves to the E site before it dissociates from the ribosome.

3. ***Ribosomes read mRNA in the 5'to 3'direction:*** This was shown through the use of a cell-free protein-synthesizing system in which the mRNA was poly(A) with a 3'-terminal C: **5' A-A-A-‴-A-A-A-C 3'**

   Such a system synthesizes a poly (Lys) that has a C-terminal Asn: Together with the knowledge that AAA and AAC code for Lys and Asn and the polarity of peptide synthesis, this established that the mRNA is read in the 5' to 3' direction. Because mRNA is also synthesized in the 5' to 3' direction; prokaryotic ribosomes can commence translation as soon as a nascent mRNA emerges from RNA polymerase. This, however, is not possible in eukaryotes because the nuclear membrane separates the site of transcription (the nucleus) from the site of translation (the cytosol).

4. ***Active translation occurs on polysomes***. In both prokaryotes and eukaryotes, multiple ribosomes can bind to a single mRNA transcript, giving rise to a beads-on-a-string structure called a polyribosome (polysome) Individual ribosomes are separated by gaps of 50 to 150 Å so that they have a maximum density on the mRNA of ~1 ribosome per 80 nt. Polysomes arise because once an active ribosome has cleared its initiation site on mRNA, a second ribosome can initiate translation at that site.

**Ribosomes- Protein Factory**

In the early 1950s, Paul Zamecnik *et al* conducted an experiment to find out the site of protein synthesis. They injected radioactive amino acids into rats and then after different time intervals, the liver was removed, homogenized and fractionated by centrifugation. The sub cellular fractions were then examined for the presence of radioactive protein. After few hours or days of the labelled amino acids injected, all the sub cellular fractions contained labelled proteins. However, when the liver was removed and fractionated only minutes after injection of the labelled amino acids, labelled protein

was found only in a fraction containing ribonucleoprotein particles,which were later named ribosomes.

The ribosome is a complex molecular machine found within all living cells, that serves as the site of biological protein synthesis (translation). Ribosomes link amino acids together in the order specified by messenger RNA molecules. Ribosomes consist of two major components: the small ribosomal subunit, which reads the RNA, and the large subunit, which joins amino acids to form a polypeptide chain. Each subunit is composed of one or more ribosomal RNA (rRNA) molecule and a variety of proteins. The ribosomes and associated molecules are also known as the translational apparatus.

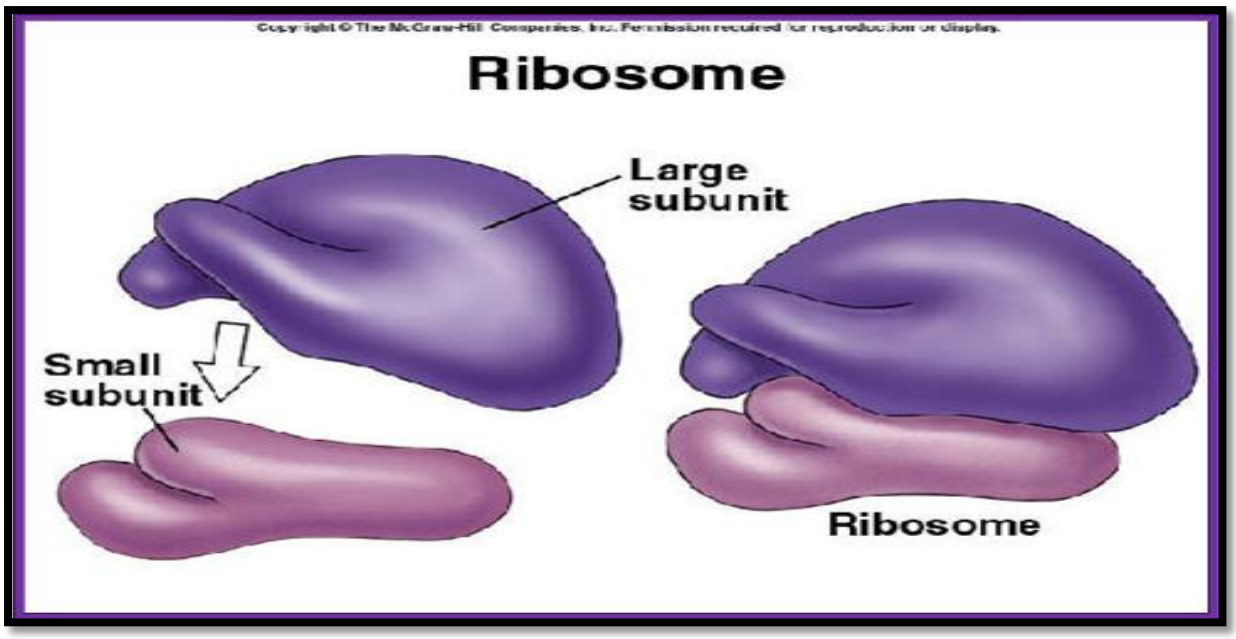



**Fig 7 : Ribosomes** [http://mol-biol4masters.masters.grkraj.org/html/Protein_Synthesis5-Ribosome_as_Translation_Machine.htm]

The sequence of DNA, which encodes the sequence of the amino acids in a protein, is copied into a messenger RNA chain. It may be copied many times into RNA chains. Ribosomes can bind to a messenger RNA chain and use its sequence for determining the correct sequence of amino acids. Amino acids are selected, collected, and carried to the ribosome by transfer RNA molecules, which enter one part of the ribosome and bind to the messenger RNA chain. It is during this binding that the correct translation of nucleic acid sequence to

amino acid sequence occurs. For each coding triplet in the messenger RNA there is a distinct transfer RNA that matches and which carries the correct amino acid for that coding triplet. The attached amino acids are then linked together by another part of the ribosome. Once the protein is produced, it can then fold to produce a specific functional 3-Dstructure although during synthesis some proteins start folding into their correct form.

A ribosome is made from complexes of RNAs and proteins and is therefore a ribonucleo protein. Each ribosome is divided into two subunits:

1. a smaller subunit which binds to a larger subunit and the mRNA pattern,
2. a larger subunit which binds to the tRNA, the amino acids, and the smaller subunit.

When a ribosome finishes reading an mRNA molecule, these two subunits split apart. Ribosomes are ribozymes, because the catalytic peptidyl transferase activity that links amino acids together is performed by the ribosomal RNA. Ribosomes are often embedded in the intracellular membranes that make up the rough endoplasmic reticulum.

Ribosomesfrom bacteria, archaea and euka ryotes (the three domains of life on Earth) resemble each other to a remarkable degree, evidence of a common origin. They differ in their size, sequence, structure, and the ratio of protein to RNA. The differences in structure allow some antibiotics to kill bacteria by inhibiting their ribosomes, while leaving human ribosomes unaffected. In bacteria and archaea, more than one ribosome may move along a single mRNA chain at one time, each "reading" its sequence and producing a corresponding protein molecule.

The ribosomes in the mitochondria of eukaryotic cells (mitoribosomes), are produced from mitochondrial genes, and functionally resemble many features of those in bacteria, reflecting the likely evolutionary origin of mitochondria. The ribosome is responsible for the synthesis of proteins in cells and is found in all cellular organisms. It serves to convert the instructions found in messenger RNA (mRNA, which itself is made from instructions in DNA) into the chains of amino-acids that make up proteins. The ribosome is a cellular machine which is highly complex. It is made up of dozens of distinct proteins (the exact number varies slightly between species) as well as a few specialized RNA molecules known as ribosomal RNA (rRNA). These rRNAs

do not carry instructions to make specific proteins like mRNAs. The ribosomal proteins and rRNAs are arranged into two distinct ribosomal pieces of different size, known generally as the large and small subunit of the ribosome. Ribosomes consist of two subunits that fit together and work as one to translate the mRNA into a polypeptide chain during protein synthesis. Because they are formed from two subunits of non-equal size, they are slightly longer in the axis than in diameter. Prokaryotic ribosomes are around 20 nm (200 Å) in diameter and are composed of 65% rRNA and 35% ribosomal proteins. Bacterial ribosomes are composed of one or two rRNA strands. Eukaryotic ribosomes contain one or three very large rRNA molecules and multiple smaller protein molecules. Crystallographic work has shown that there are no ribosomal proteins close to the reaction site for polypeptide synthesis. This proves that the protein components of ribosomes do not directly participate in peptide bond formation catalysis, but rather suggests that these proteins act as a scaffold that may enhance the ability of rRNA to synthesize protein .

The ribosomal subunits of prokaryotes and eukaryotes are somehow similar. [13].

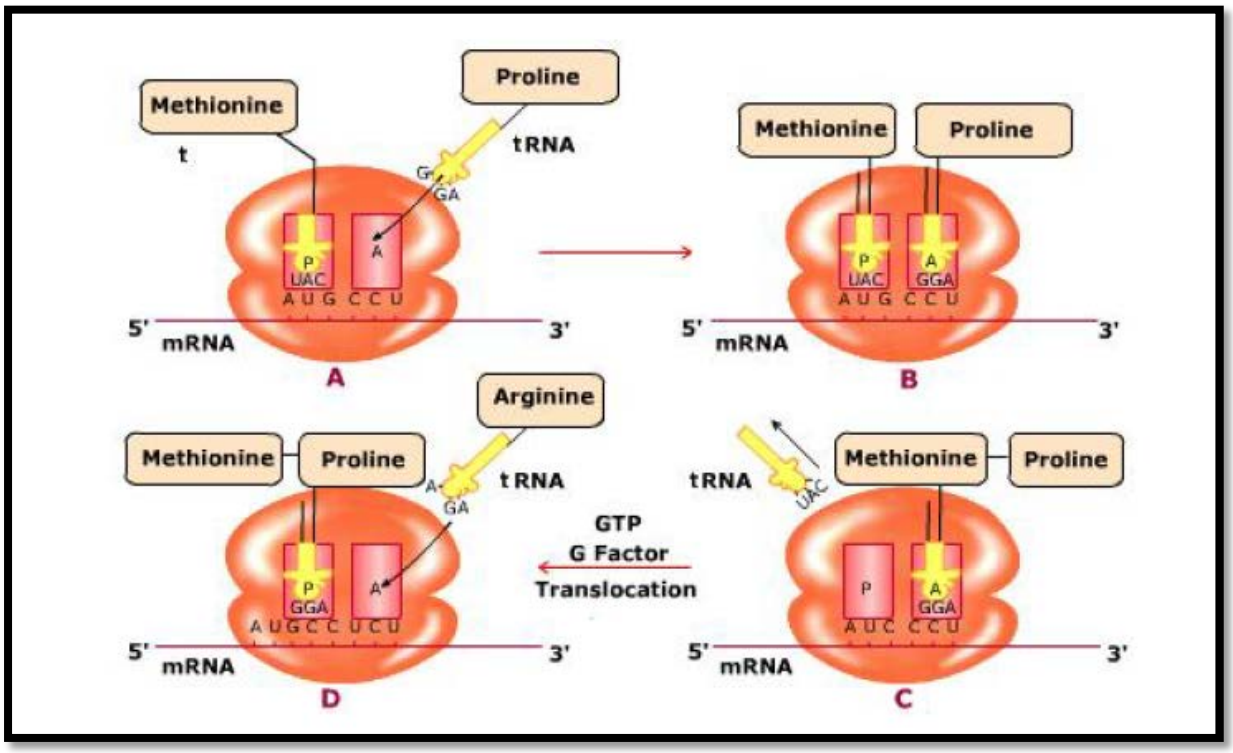
**Mechanism of Protein Synthesis** [8][14]

***Stage 1: Activation of Amino Acids*** For the synthesis of a polypeptide with a defined sequence, two fundamental chemical requirements must be met: (1) the carboxyl group of each amino acid must be activated to facilitate formation of a peptide bond, and (2) a link must be established between each new amino acid and the information in the mRNA that encodes it. Both these requirements are met by attaching the amino acid to at RNA in the first stage of protein synthesis. Attaching the right amino acid to the right tRNA is critical. This reaction takes place in the cytosol, not on the ribosome. Each of the 20 amino acids is covalently attached to a specific tRNA at the expense of ATP energy, using $Mg^{2+}$dependent activating enzymes known as amino acyl-tRNA synthetases. When attached to their amino acid (amino acylated) the tRNAs are said to be “charged.”

***Stage 2: Initiation*** The mRNA bearing the code for the polypeptide to be made binds to the smaller of two ribosomal subunits and to the initiating amino acyl-tRNA. The large ribosomal subunit then binds to form an initiation complex. The initiating amino acyl- tRNA base pairs with the mRNA codon AUG that signals the beginning of the polypeptide. This

process, which requires GTP, is promoted by cytosolic proteins called initiation factors.

***Stage 3: Elongation*** The nascent polypeptide is lengthened by covalent attachment of successive amino acid units, each carried to the ribosome and correctly positioned by its tRNA, which base-pairs to its corresponding codon in the mRNA. Elongation requires cytosolic proteins known as elongation factors. The binding of each incoming amino acyl-tRNA and the movement of the ribosome along the mRNA are facilitated by the hydrolysis of GTP as each residue is added to the growing polypeptide.




The above figure shows,

- ❖ charged tRNA arriving at the A site, reading its codon on the mRNA
- ❖ Amino acid of tRNA at P site is ready to be transferred to the amino acid of tRNA at A site
- ❖ Amino acids are joined by peptide bond and tRNA is discharged from P site
- ❖ D. Peptide chain-carrying tRNA is translocated to P site, making A site free to receive another charged tRNA

Three elongation factors (EF Tu, EF Ts and EF G) assist in the elongation of the polypeptide chain. A charged tRNA

molecule along with its amino acid, proline, for example, enters the ribosome at the A site. Its anticodon GGA locates and binds with the complementary codon CCU of mRNA chain by hydrogen bonds. The amino acid methionine is transferred from its tRNA onto the newly arrived proline tRNA complex where the two amino acids join by a peptide bond. The process is catalyzed by the enzyme peptidyl transferase located on the ribosome. In this process, the linkage between the first amino acid and its tRNA is broken, and the -COOH group now forms a peptide bond with the free -NH2 group of the second amino acid. Thus, the second tRNA carries a dipeptide, formylmethionineproline.The energy required for the formation of a peptide bond comes from the free energy released by separation of amino acid (formylmethionine or methionine) from its tRNA.

The first tRNA, now uncharged, separates from mRNA chain at the P site of the ribosome and returns to the mixed pool of tRNAs in the cytoplasm. Here, it is now available to transport another molecule of its specific amino acid.

Now the ribosome moves one codon along the mRNA in the 3 direction. With this, tRNA dipeptide complex at the A site is pulled to the P site. This process is called translocation. It requires GTP and a translocase protein called EF-G factor. The GTP is hydrolysed to GDP and inorganic phosphate (iP) to release energy for the process. At this stage, a third tRNA molecule with its own specific amino acid, arginine, for example arrives at the A site of the ribosome and binds with the help of anticodon AGA to the complementary codon UCU of the mRNA chain. The dipeptide formylmethionineproline is shifted from the preceding tRNA on the third tRNA where it joins the amino acid arginine again with the help of peptidyl transferase enzyme. The dipeptide, thus, becomes a tripeptide, formyl-methionine-proline-arginine. The second tRNA being now uncharged, leaves the mRNA chain, vacating the P site. The tRNA tripeptide complex is translocated from A site to P site. The entire process involving arrival of tRNA-amino acid complex, peptide bond formation and translocation is repeated. As the ribosome moves over the mRNA, all the codons of mRNA arrive at the A site one after another, and the peptide chain grows. Thus, the amino acids are linked up into a polypeptide in a sequence communicated by the DNA through the mRNA. A polypeptide chain which is in the process of synthesis is often called a

nascent polypeptide. The growing polypeptide chain always remains attached to its original ribosome, and is not transferred from one ribosome to another. Only one polypeptide chain can be synthesized at a time on a given ribosome

***Stage 4: Termination and Release***

Completion of the polypeptide chain is signalled by a termination codon in the mRNA. The new polypeptide is released from the ribosome, aided by proteins called release factors.

At the terminal end of mRNA chain there is a stop, or terminator codon (UAA, UAG or UGA). It is not joined by the anticodon of any tRNA amino acid complex. Hence, there can be no further addition of amino acids to the polypeptide chain. The linkage between the last tRNA and the polypeptide chain is broken by three release factors. (RF 1, RF 2 and RF 3) and GTP. The release is catalyzed by the peptidyl transferase enzyme, the same enzyme that forms the peptide bonds. The ribosome jumps off the mRNA chain at the stop codon and dissociates into its two subunits. The completed polypeptide (amino acid chain) becomes free in the cytoplasm. The ribosomes and the tRNAs on release from the mRNA can function again in the same manner and result in the formation of another polypeptide of the same protein.

***Stage 5: Posttranslational Modifications :***

In order to achieve its biologically active form, the new polypeptide must fold into its proper three-dimensional conformation. Before or after folding, the new polypeptide may undergo enzymatic processing, including removal of one or more amino acids (usually from the amino terminus); addition of acetyl, phosphoryl, methyl, carboxyl, or other groups to certain amino acid residues; proteolytic cleavage; and/or attachment of oligosaccharides or prosthetic groups.

The just released polypeptide is a straight, linear exhibiting a primary molecule, structure. It may lose some amino acids from the end with the help of a peptidase enzyme, and then coil and fold on itself to acquire secondary and tertiary structure. It may even combine with other polypeptides, to have quaternary structure. The proteins synthesized on free polysomes are released into the cytoplasm and function as structural and enzymatic proteins. The proteins formed on the polysomes attached to ER pass into the ER channels and are exported as cell secretions by exocytosis after packaging in the Golgi apparatus.

When the ribosome has moved sufficiently down the mRNA chain towards 3 end, another ribosome takes up position at the

initiator codon of mRNA, and starts synthesis of a second molecule of the same polypeptide chain. At any given time, the mRNA chain will, therefore, carry many ribosomes over which are similar polypeptide chains of varying length, shortest near the initiator codon and longest near the terminator codon. A row of ribosomes joined to the mRNA molecule, is called a polyribosome, or a polysome. Synthesis of many molecules of the same polypeptide simultaneously from one mRNA molecule by a polysome is called translational amplification.

**Genes instruct when protein would be Synthesis**

In experiments with the mold *Neurospora crassa* in the 1940s, George Beadle and Edward Tatum found that *there is a specific connection between genes and enzymes, the one gene–one enzyme theory*. Beadle and Tatum showed that mutant varieties of *Neurospora* that were generated by irradiation with X-rays required additional nutrients in order to grow. Presumably, the offspring of the radiation-damaged cells lacked the specific enzymes necessary to synthesize those nutrients.

The link between DNA and enzymes (nearly all of which are proteins) is RNA. The DNA of a gene is transcribed to produce an RNA molecule that is complementary to the DNA. The RNA sequence is then translated into the corresponding sequence of amino acids to form a protein. These transfers of biological information are summarized in the so-called central dogma of molecular biology formulated by Crick in 1958.Just as the daughter strands of DNA are synthesized from free deoxynucleoside triphosphates that pair with bases in the parent DNA strand, RNA strands are synthesized from free ribonucleoside triphosphates that pair with the complementary bases in one DNA strand of a gene. The RNA that corresponds to a protein-coding gene (called messenger RNA, or mRNA) makes its way to a ribosome, an organelle that is itself composed largely of RNA (ribosomal RNA, or rRNA). At the ribosome, each set of three nucleotides inthe mRNA pairs with three complementary nucleotides in a small RNA molecule called a transfer RNA, or tRNA. Attached to each tRNA molecule is its corresponding amino acid. The ribosome catalyzes the joining of amino acids, which are the monomeric units of proteins. Amino acids are added to the growing protein chain according to the order in which the tRNA molecules bind to the mRNA. Since the nucleotide sequence

of the mRNA in turn reflects the sequences of nucleotides in the gene, DNA directs the synthesis of proteins. It follows that alterations to the genetic material of an organism (mutations) may manifest themselves as proteins with altered structures and functions. Researchers can compile a catalog of all the information encoded in an organism's DNA. The study of the genome's size, organization, and gene content is known as genomics. By analogy, transcriptomics refers to the study of gene expression, which focuses on the set of mRNA molecules, or transcriptome, that is transcribed from DNA under any particular set of circumstances. Finally, proteomics is the study of the proteins (the proteome) produced as a result of transcription and translation. Although an organism's genome remains essentially unchanged throughout its lifetime, its transcriptome and proteome may vary significantly among different types of tissues, developmental stages, and environmental conditions [12].

**Emotions also change the path of Genetic information** [15]

Scientific research shows that as if genes changing expression in response to environmental factors such as nutrients wasn't enough, other researchers have demonstrated that this "environment" that your genes respond to also includes your conscious thoughts, emotions, and unconscious beliefs.

Science has indeed taken us far beyond Newtonian physics, which says you live in a mechanical universe. According to this belief, your body is just a biological machine, so by modifying the parts of the machine, we can modify our health. Also, as a biological machine, our body is thought to respond to physical "things" like the active chemicals in drugs, and by adjusting the drugs that modify our machinery, doctors can modify and control health. However, with the advent of quantum physics, scientists have realized the flaws in Newtonian physics, as quantum physics shows us that the invisible, immaterial realm is actually far more important than the material realm. In fact, our thoughts may shape our environment far more than physical matter. According to Cellular biologist Bruce Lipton the true secret to life does not lie within our DNA, but rather within the mechanisms of your cell membrane. Each cell membrane has receptors that pick up various environmental signals, and this mechanism controls the "reading" of the genes inside your cells. Our cells can choose to read or not read the genetic blueprint depending on the signals being

received from the environment. So having a "cancer program" in your DNA does not automatically mean you're destined to get cancer. This genetic information does not ever have to be expressed. What this all means is that we are not controlled by your genetic makeup. Instead, our genetic readout (which genes are turned "on" and which are turned "off") is primarily determined by your thoughts, attitudes, and perceptions.

**Editing the central dogma**

According to the ***Nature*** [16], research the central dogma says that there is faithful transcription of DNA into RNA. This challenges that idea on a much larger scale than was known. The work suggests that RNA editing is providing a previously unappreciated source of human genetic diversity that could affect, for instance, how vulnerable different people are to disease. Research article published in ***Science*** [17] shows that not know whether there are heritable changes, passed down from parent to child, that affect how much RNA editing occurs in different people. But scientists already know of a handful of RNA editing proteins that play a role in human health, such as the APOBEC enzymes, some of which have antiviral activity. Researchers investigating the connection between genetics and disease have been stymied by their inability to find strong connections between genetic variation and risk for most common diseases, leading researchers to wonder where the 'missing heritability' is hiding. The new study at least provides one place to look.

**Conclusion and Discussion**

Literature shows that in Vedic time or in ancient India (*Aryavrat, Bharat ancient names of India* ) “Sadhus”, “Mahatmas” and even Gods have power to change in complete organism into another organism. When we review scientific literatures and researches we studied that by yoga, meditation and chanting of Vedic mantras written in Samveda, Yujurveda, Atherveda and Rigveda we modify our genetic codes, DNA sequence and the process of central dogma also. By modifying genetic codes and DNA we connect to supreme powers or attain divine powers which we have seen in every era or Yuga whether it is Satya Yuga, Treta Yuga , Dvapara Yuga and also in Kali Yuga**.** One among in thousands attain such type of powers this was mentioned in Shrimad Bhagwad Gita in Chapter 7 verse 3.


These types of "*Sidhiya*" or "*Shaktiya*" are not situated outside our body but outside environment influence the cell metabolism. These all are happen due to the cell signalling process of particular cell. According to Francis Crick, the co-discoverer of the structure of DNA, prepared a genetic principle which he entitled, "The Central Dogma". The transfer of information from nucleic acid to nucleic acid or from nucleic acid to protein may be possible. But vice versa is not possible. All this process of changing the structure of organism into another is governed by Central Dogma. The central dogma is an important scientific process. The complex coding within the DNA in the cell nucleus decides the trait for the organism. Species cannot change from one into another species. All the members in a species can only be the outcome of the wide range of "gene pool" data in the DNA, but no member of that species can, because of the environment or what has happened to that individual, **changes into another species**. Only change in the DNA coding can produce such changes [18]; nothing else can do it. Central Dogma has proved a fruitful principle, ever since James Watson and Crick discovered the double helix structure of DNA in the 1950s. DNA is the blueprint, it gives instructions to the RNA and to protein it about how to arrange themselves. The whole changing process starts from here when we modify the instructions path from DNA the whole body get converted into another. Our body is nothing but a well-mannered organization of proteins which are formed by the codes of DNA and carried by RNA to form these proteins. Every living being on the earth whether plants or animal species; are made up proteins only that depends on DNA. If it is possible to change the codes of DNA through yoga or meditation then the RNA will carry the coded information for the formation of corresponding protein and if the proteins would be changed then the entire morphology would change. Not only yoga and meditation but the external environment is also responsible for such type of changes. According to *Nature* and one scientific article it is mentioned that outside environment [15] can also edit [16] the process of Central dogma to produce new protein. It means that science accepts the fact that the process of central dogma can be edited to form new proteins. But

science doesn't tells that what type of proteins would be formed finally, this concept is cleared by religious texts that if a specified amount of DNA codes are changed then the entire physical morphology of an organism can change from one species to the other.

10 heads of Ravana, *Panchmukhi* of Lord Hanuman, enlarged body (*viraat roop*) form of Lord Krishna and similar type of texts show that everything in a living body is determined by the proteins only. All these things are the higher level of science mentioned in religious scriptures, which we call "*Chamatkaar*". In actual state, this is not any "*Chamatkaar*" but a scientific process called "central dogma of molecular biology" in which the code from the DNA is the controller of the entire protein synthesis. In previous time when people used to do such things, there was not any name given to any process but currently along with the scientific researches different process were given specified scientific names. During various researches, the role of proteins was also determined that they help in the formation of a living being and may be this is the reason proteins are known as the "**building blocks**".

At last on the behalf of scientific literature shown in this paper and other researches we conclude that by changing the DNA codes and diverting the information path of Central Dogma we can change the organism structure as we know that majority of the body constitutes different types of protein.

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