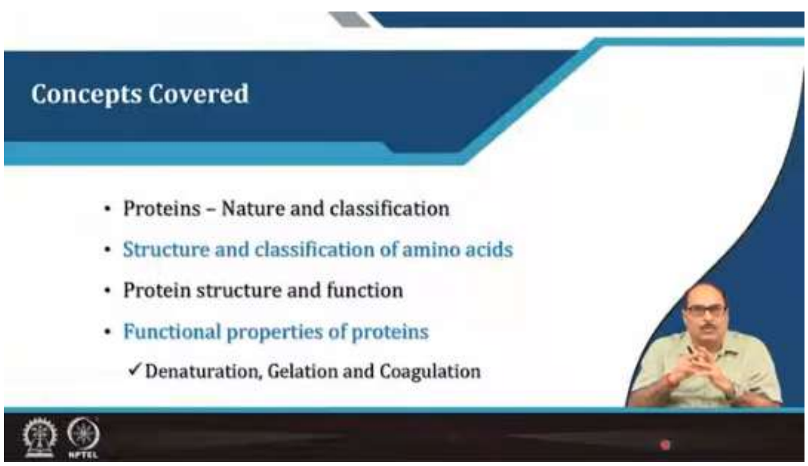
FOOD SCIENCE AND TECHNOLOGY

Lecture24

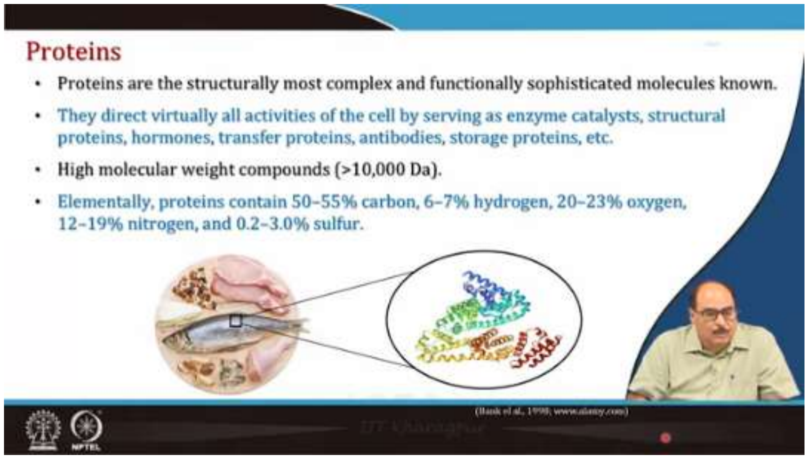
Lecture 24: Proteins and Polypeptides

Hello friends, Namaskar.

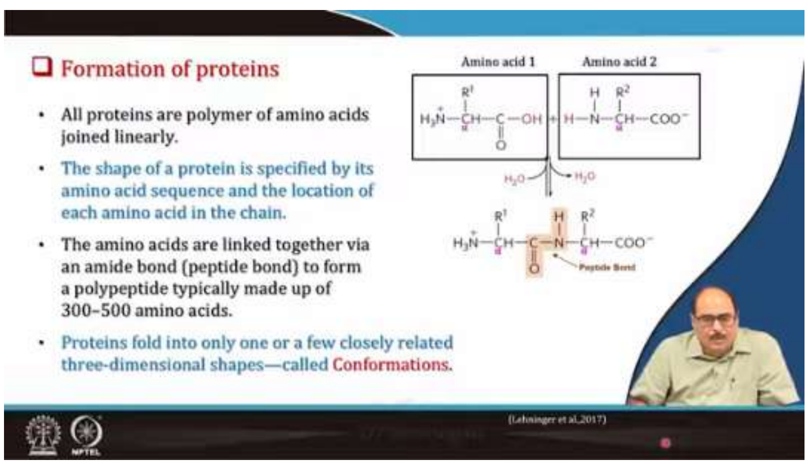
So now, in this lecture 24, we will talk about proteins and polypeptides. We are in module 5, where we are discussing food macronutrients, their structures, and functions. So, in today's lecture, the concepts that will be covered are what proteins are, their nature, and their classification.



Then we will talk about the structure and classification of amino acids, protein structure, and function. Functional properties of proteins like denaturation, gelation, and coagulation.

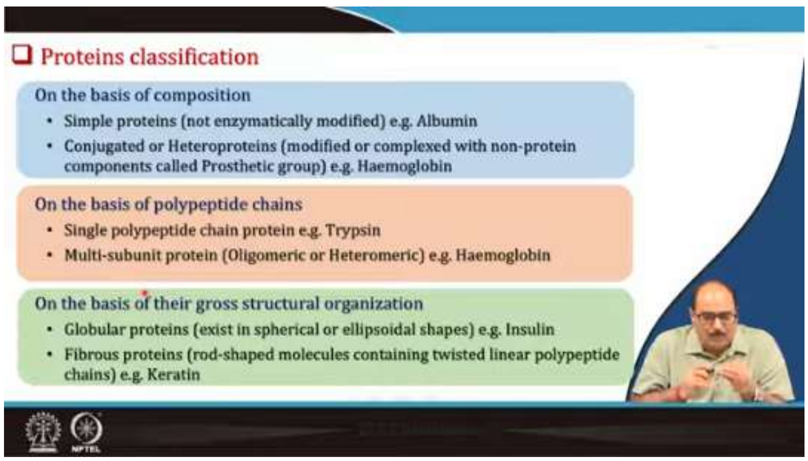


So, what are proteins? They are the most structurally complex and functionally sophisticated molecules ever known. They drive virtually all cell activities by serving as enzyme catalysts. They are structural proteins, acting as hormones and playing roles in the transfer of proteins, antibodies, storage proteins, and many other functions. Almost all cellular functions are carried out by proteins. They are the building blocks of any cell in our body. Proteins are high molecular weight compounds, typically exceeding 10,000 Daltons. Elementally, they consist of approximately 50 to 55% carbon, 6 to 7% hydrogen, 20 to 23% oxygen, 12 to 19% nitrogen, and 0.2 to 0.3% sulfur. This represents the general composition of proteins. Proteins, like polysaccharides, are the building blocks of life, where the building blocks of polysaccharides are monosaccharides. Similarly, amino acids serve as the building blocks for proteins.

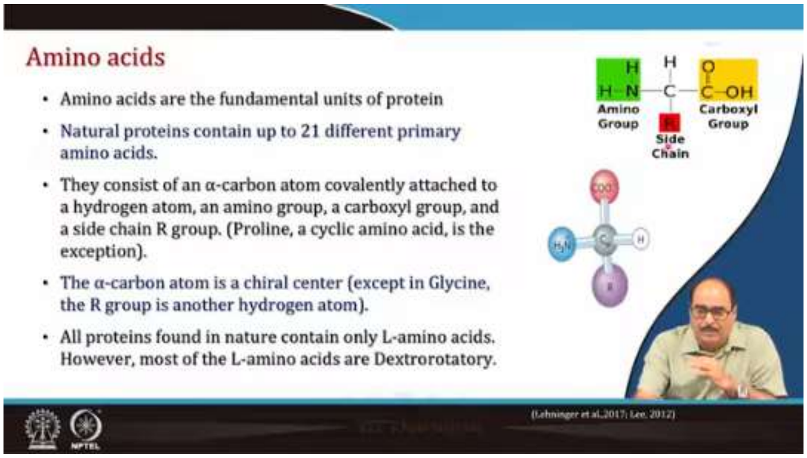


All proteins are polymers of amino acids. These amino acids contain a CONH group, an NH_3 group, and a COOH group. When two amino acids combine, the COOH group of one amino acid reacts with the NH_3 group of another. In this process, the OH from the COOH group and the H from the NH_2 group combine to release a water molecule, forming a

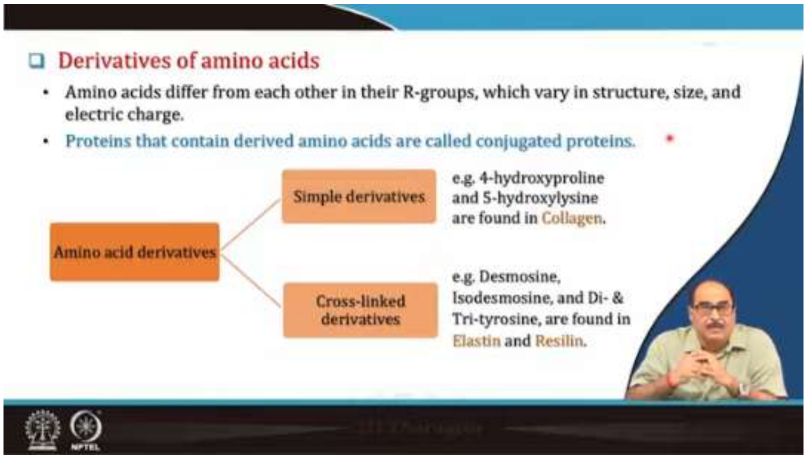
CONH linkage. This bond is known as a peptide linkage. When two amino acids join, they form a dipeptide. Similarly, three amino acids form a tripeptide, and four form a tetrapeptide. When an n number of amino acids are joined together, it becomes a polypeptide, which is generally referred to as a peptide linkage. Essentially, all proteins are peptides. The shape of a protein is determined by the nature and sequence of its amino acids, as well as the location and positioning of each amino acid in the peptide chain. Amino acids are linked together by an amide bond, forming a peptide. A polypeptide typically consists of 300 to 500 amino acid residues, which may be present in one peptide chain. These proteins then fold into one or a few types of highly organized three-dimensional structures known as their three-dimensional conformational structures.



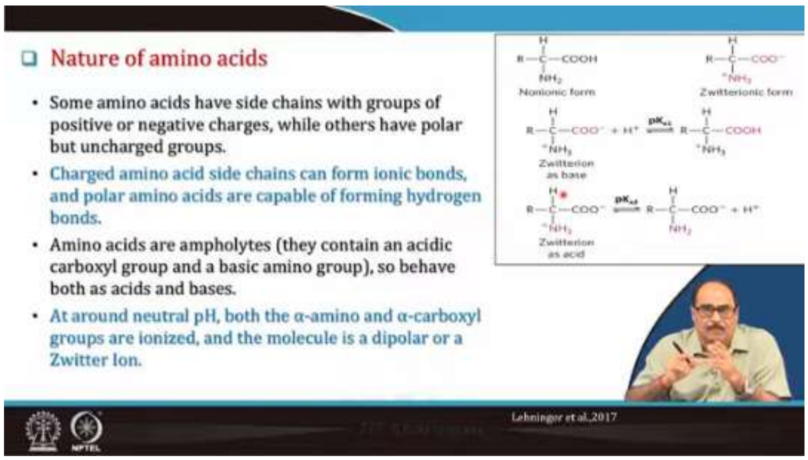
So, proteins can be classified in different ways, one of which is based on their composition. Simple proteins, such as non-enzymatically modified albumin, exist, or they may be conjugated proteins, also called heteroproteins. These proteins may be modified or complexed with non-protein elements known as prosthetic groups. For example, in haemoglobin, the heme is the prosthetic group, and globin is the protein. Proteins can also be classified based on their peptide chains. Some proteins have a single polypeptide chain, like trypsin, while others consist of multiple subunits, such as four or five polypeptides, which are referred to as individual subunits. These subunits may join to form oligomeric or heteromeric proteins, as seen in haemoglobin. Proteins can also be categorized based on their structural organization. For instance, globular proteins have spherical or ellipsoidal shapes, like insulin, while fibrous proteins consist of rod-shaped molecules with twisted linear polypeptides, as in keratin, which is found in hair. Another classification of proteins is based on their nutritional value. Proteins may be categorized as complete, partially complete, or incomplete depending on their essential amino acid content. A complete protein contains all the essential amino acids required for the proper functioning of the body in adequate amounts.



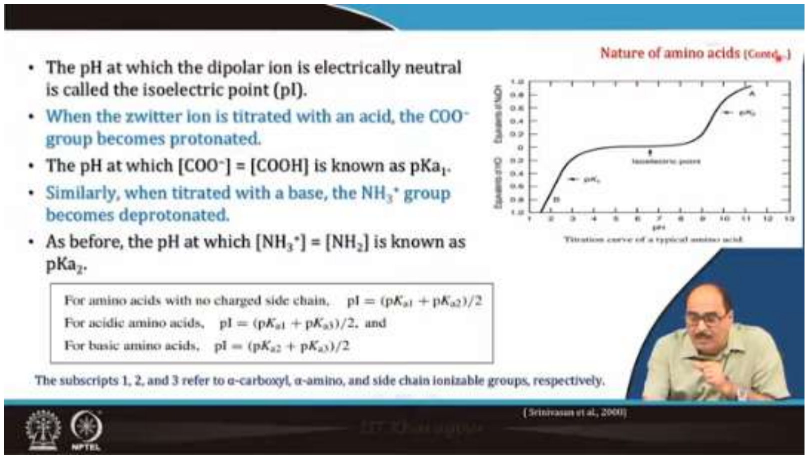
Now, in an amino acid, the carbon has four vacancies - one occupied by a hydrogen atom, another by an amino group, a third by a carboxyl group, and the fourth by an alkyl or side chain. This combination constitutes an amino acid. These are the fundamental units of proteins, the building blocks of proteins. There are about 21 dietary primary amino acids, each consisting of an alpha carbon. This alpha carbon is bonded to an alpha carboxyl group, an amino group, a hydrogen atom, and an R-side chain. The alpha carbon atom serves as a chiral center, except in glycine. In glycine, the R group is another hydrogen atom. All proteins found in nature contain only L-amino acids. However, most L-amino acids are also dextrorotatory.



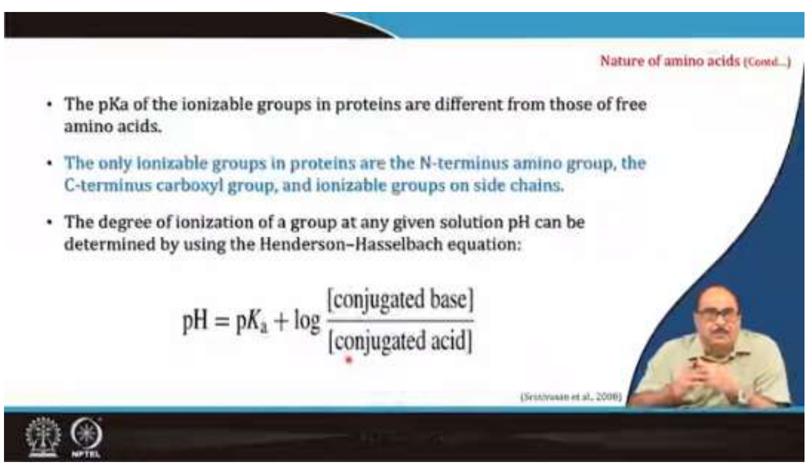
So, the proteins that are derivatives of amino acids may differ. There are different types of amino acids, and mainly, as seen in the earlier figure, all three components—Carboxyl, H, and NH_2 group will be common. It is only the R group, the side chain, that varies, making one protein different from another. Depending upon the number and type of side chains, protein amino acids vary in their structure, size, shape, and electrical charge. Proteins that contain derived amino acids are called conjugated proteins, which may include simple derivatives or cross-linked derivatives. Simple derivatives, such as 4-hydroxyproline and 5-hydroxylysine, are found in collagen, while cross-linked derivatives like desmosine or di- and tri-tyrosine are found in elastin and resilin, etc.



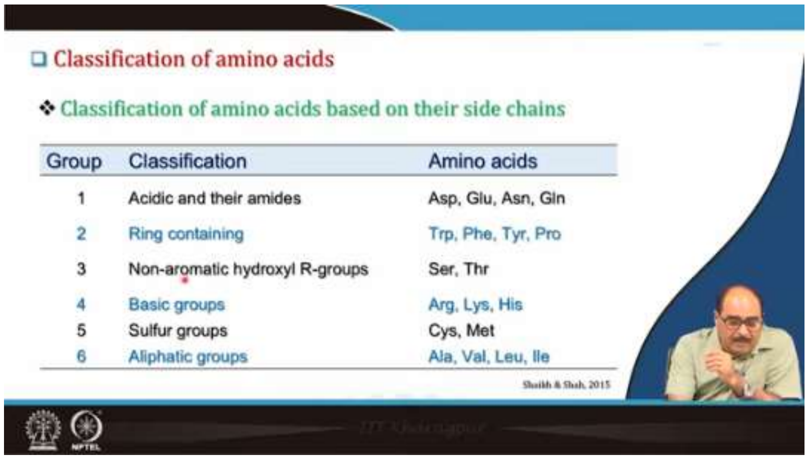
As far as the nature of amino acids is concerned, they can be classified as acidic amino acids or basic amino acids, depending on their specific properties. Particularly, the overall charge on the amino acid depends on the R group present, which determines whether the charge is positive or negative. Amino acids have a side chain, as mentioned earlier, with groups that may carry positive or negative charges, while others are polar, and some are uncharged. Depending on the R group, an amino acid can be classified as neutral, acidic, or alkaline. The charged amino acid side chains can form ionic bonds with polar amino acids and are capable of forming hydrogen bonds. Amino acids are ampholytes, meaning they contain an acidic carboxyl group and a basic amino group, enabling them to behave as both acids and bases. At neutral pH, both the alpha-amino and alpha carboxyl groups are ionized, resulting in the molecule forming a zwitterion. In this form, the COOH group loses a proton and becomes a COO minus ion, while the NH_2 group accepts a proton and becomes NH_3 plus. This dual charge, both positive and negative, is characteristic of a zwitterion.



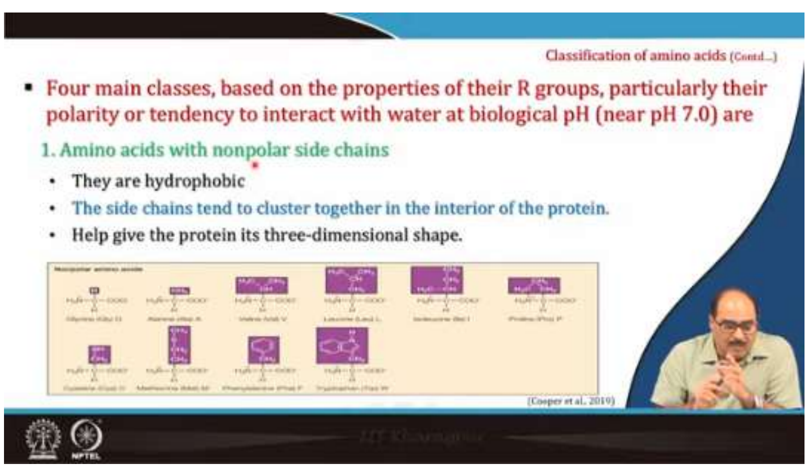
So, the pH at which the dipolar ion is electrically neutral is called its isoelectric pH, as you can see here, is called pI. When the zwitterion is titrated with an acid, the COO minus group becomes protonated. The pH at which the concentration of COO minus groups protonates to form COOH is referred to as pKa_1. Conversely, when titrated with a base like NH_3, the NH_3 plus group becomes deprotonated. The pH at which the NH_3 plus concentration equals the combined concentration of its dissociated forms marks the dissociation point, known as pKa_2. For an amino acid without a charged side chain, its isoelectric point (pI) is calculated as the average of pKa_1 and pKa_2: pI is equal to pKa_1 plus pKa_2 by 2. For acidic amino acids, the pI is determined as the average of pKa_1 and the side chain pKa_3 i.e. pI is equal to pKa_1 plus pKa_3 by 2. For basic amino acids, the pI is derived from the average of pKa_2, and the side chain pKa_3 i.e. pI is equal to pKa_2 plus pKa_3 by 2. Here, pKa_1, pKa_2, and pKa_3 correspond to the dissociation constants of the alpha-carboxyl, alpha-amino, and side chain ionizable groups, respectively.



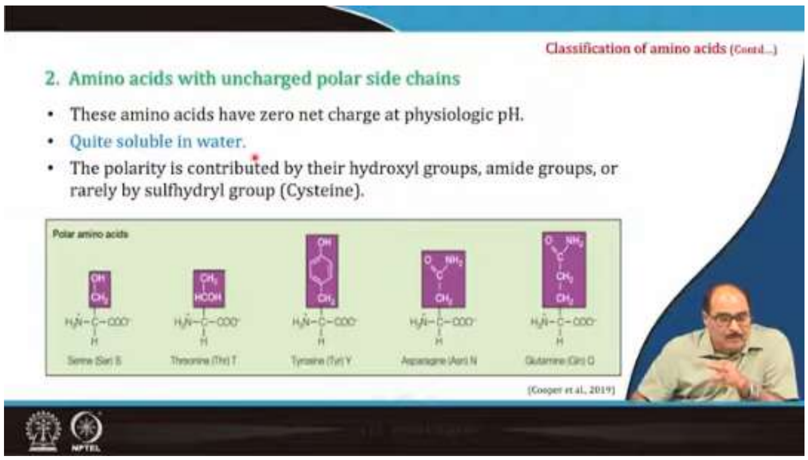
The isoelectric point of the pH is an important characteristic and is utilized in the precipitation, fractionation, etc., of proteins. Additionally, the pKa of the ionizable group of the protein differs from that of the free amino group. The only ionizable groups of the protein are the N-terminus amino group, the C-terminus carboxyl group, and the ionizable groups of the side chain. So, pH is equal to pKa plus the log of the conjugate base divided by the conjugate acid.



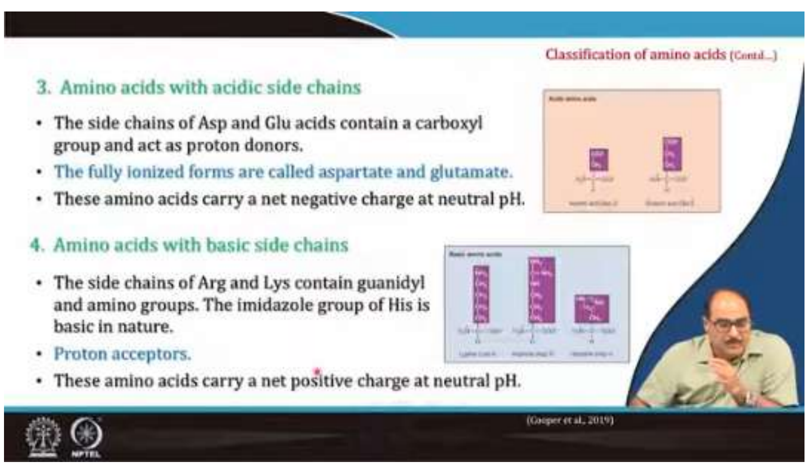
So, these amino acids can be classified based on their side chains, like acidic and their amides, such as asparagine, glutamine, aspartic acid, and glutamic acid, then ring-containing amino acids like tryptophan, phenylalanine, tyrosine, proline, etc. which contain an aromatic ring. Non-aromatic hydroxyl groups like serine and threonine, basic groups like arginine, lysine, and histidine, sulfur-containing groups like cysteine and methionine, aliphatic groups like alanine, valine, leucine, and isoleucine. So, these are the names of the amino acids and their classification based on the side chain R, which is the alkyl side chain they have. It may be acidic, non-acidic, basic, sulfur-containing, and so on. It may be a ring, an aromatic ring, or other structures.



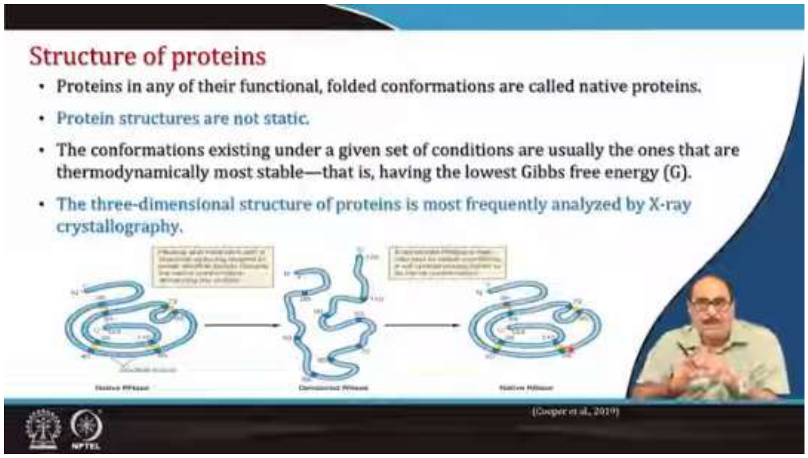
So, there are four main classes based on the properties of their R group. Particularly their polarity or tendency to interact with water at biological pH. Those four groups are number one, that is, amino acids with non-polar side chains, as they are hydrophobic. The side chains tend to cluster together in the interior of the protein, and they help give the protein its three-dimensional shape. They are glycine, alanine, valine, isoleucine, proline, cysteine, methionine, tryptophan, phenylalanine, and so on. These are the non-polar, that is, amino acids with the non-polar side chains.



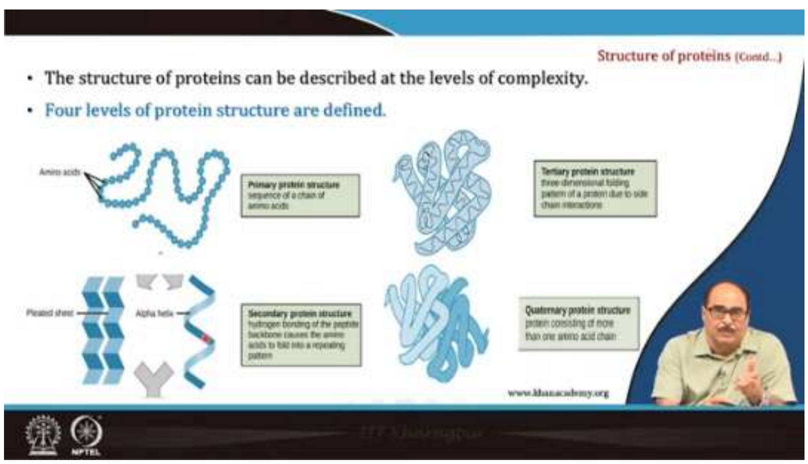
Then amino acids with uncharged polar side chains like serine, threonine, tyrosine, asparagine, etc. These amino acids have zero net charge at physiological pH. They are quite stable and soluble in water and the polarity is contributed by their hydroxyl group, amide groups, or rarely by sulfhydryl groups.



Then the third category is the amino acids with acidic side chains like those found in aspartic acid and glutamic acid. So, these side chains of aspartic acid and glutamic acid also contain a carboxylic group and act as proton donors. The fully ionized forms are called aspartate or glutamate. These amino acids carry a net negative charge at neutral pH. The fourth category is amino acids with basic side chains like those in lysine, arginine, and histidine. The side chains of arginine and lysine contain guanidyl and amino groups, and the imidazole group of histidine is basic in nature. They are proton acceptors, and these amino acids carry a net positive charge at neutral pH.

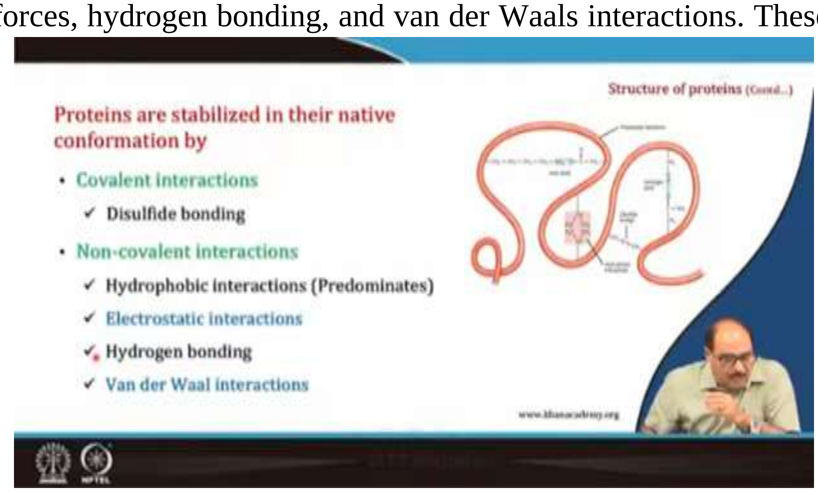


Now, let us talk about the structure of protein. This is how the three-dimensional conformation of the structure is. These proteins have very ordered structures. The structures of proteins are not very stable, although each protein has a definite three-dimensional ordered configuration. It changes depending upon various conditions, etcetera.



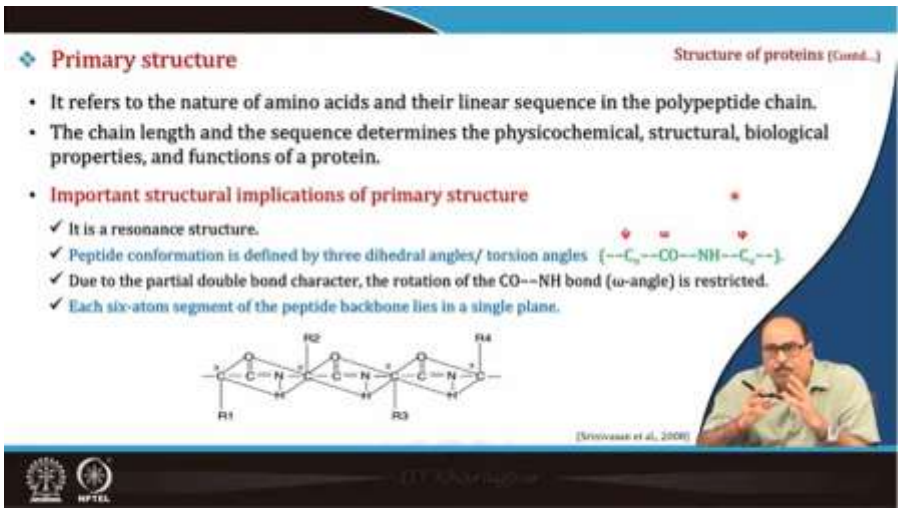
So, now this three-dimensional structure of protein is most frequently analyzed by X-ray crystallography. This is a structure when you talk about their folded functional conformation, etcetera, of the native protein, and it is understood in four levels. The first is the primary structure, which refers to the linear sequence of amino acids. For instance, in a peptide chain with 50 amino acids, identifying the amino acids at positions 35 or 49 is part of the primary structure. This is crucial because even a single change in the position of an amino acid can significantly influence the protein's final characteristics. Next is the secondary structure, where proteins are stabilized in their native conformation through hydrogen bonding in the peptide backbone. This bonding causes the amino acids to fold into repeating patterns, such as pleated sheets or alpha helices. The tertiary structure refers to the protein's three-dimensional conformational folding pattern, which results from side-chain interactions. This is key to the overall functionality of protein. Thus, for a single chain, the primary structure is its linear sequence, while the secondary structure involves the coiling of the amino acids into alpha helices or beta-pleated sheets. This explanation highlights the various levels of protein structure while maintaining their relationship to one another. The tertiary structure involves the folding of the protein, creating its three-dimensional conformational pattern. Following this, the quaternary structure is characterized by the interaction of multiple subunits within an individual peptide chain. For instance, if there are three or four subunits, their interaction determines the overall characteristics of the protein, forming a three-dimensional regular pattern of polypeptide structures. These organized three-dimensional structures, however, are not very stable and may change under varying conditions. This change in the organized structure, while preserving the peptide bonds, is referred to as denaturation of the protein. We will address this concept in more detail later.

Proteins are typically stabilized by their native conformation, which depends on the type of amino acids present. For example, in the coiling, the CONH group interacts with positively charged groups that come into bonding distance with negatively charged groups from other amino acids. There may be amide linkages, hydrostatic interactions, hydrogen bonding, or van der Waals forces. Proteins are held together by both covalent interactions, such as disulfide bonds, and non-covalent interactions, such as hydrophobic interactions, electrostatic forces, hydrogen bonding, and van der Waals interactions. These bonds play



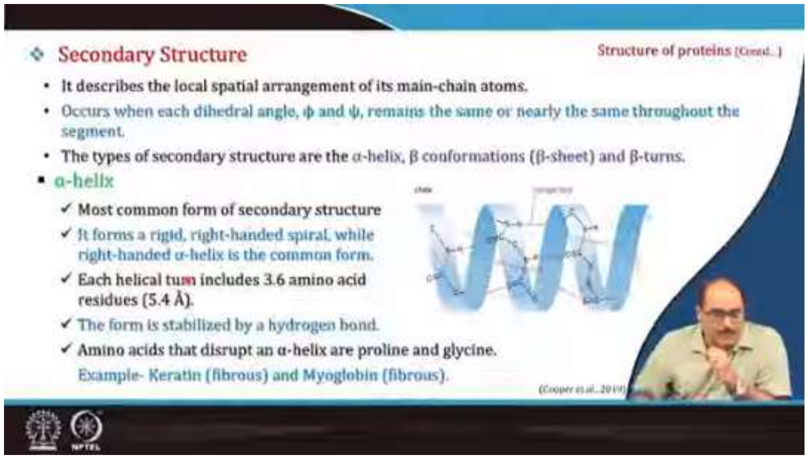
a vital role in maintaining the protein's primary, secondary, tertiary, and quaternary structures. During denaturation, while the peptide bonds remain intact, these structural interactions may be disrupted. During denaturation, the three-dimensional conformation of the protein is altered, but the peptide bond—and thus the primary structure—remains unchanged. Any alteration to the primary structure would result in proteolysis, not denaturation. In denaturation, the integrity of the primary structure is preserved.

Now, let us explore the details of these structures step by step. Starting with the primary structure, as mentioned, it pertains to the nature of the amino acids and their linear sequence



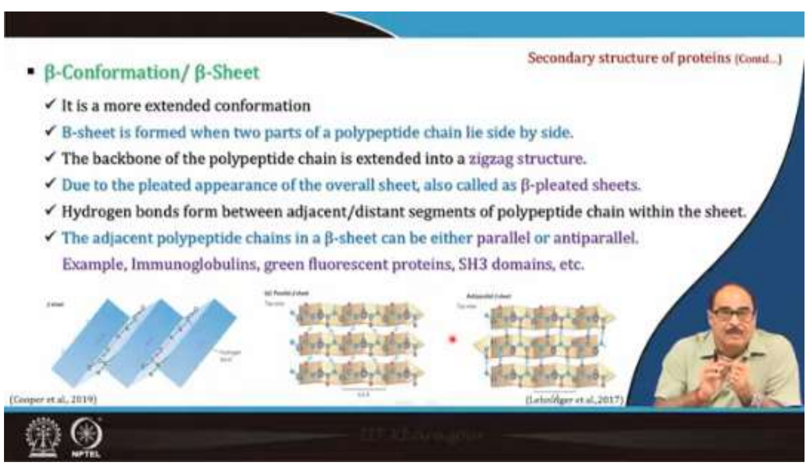
within the polypeptide chain. This sequence is fundamental, as it dictates the protein's overall structure and function. The chain length and sequence of amino acids determine the physical, chemical, structural, biological, and functional properties of the protein. As mentioned, even the precise position of each amino acid in a polypeptide chain—whether it contains 50, 60, or 70 amino acids—is crucial for defining the protein's biological and functional characteristics. The primary structure plays a significant role in structural applications, and its resonance structure is particularly noteworthy. The peptide conformation is characterized by three-dimensional dihedral angles or torsion angles. Due to the partial double-bond character of the CONH bond, the rotation, particularly around the omega angle, is restricted. Moreover, each six-atom segment within the peptide backbone lies in a single plane, contributing to the rigidity and defined geometry of the structure.

Now, the secondary structure describes the local spatial arrangement of its main chain atoms. It occurs when the dihedral angle remains the same or nearly the same throughout the segment. The types of secondary structures are the alpha helix, beta conformations or beta sheets, and sometimes also beta turns.

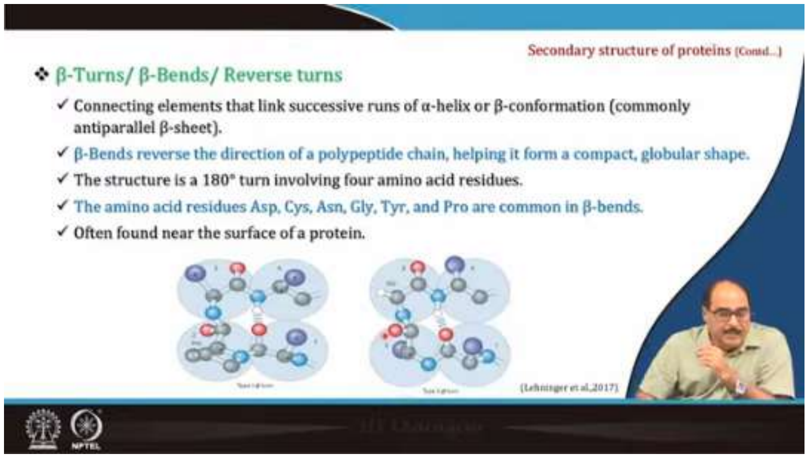


So, the alpha helix is the most common form of secondary structure, it forms a rigid right-handed spatial arrangement, while the right-handed alpha helix is the common form. Each helical turn, that is here, you see that this comes, and this is called one turn. So, each turn may include 3.6 amino acid residues, and this form is stabilized by hydrogen bonds. There are intensive hydrogen bonds, you can see here, which keep this secondary structure in place. The amino acids that disrupt the alpha helix are proline and glycine, like in the case of creatine and myoglobin. Myoglobin is fibrous, and Keratin is also a fibrous structure.

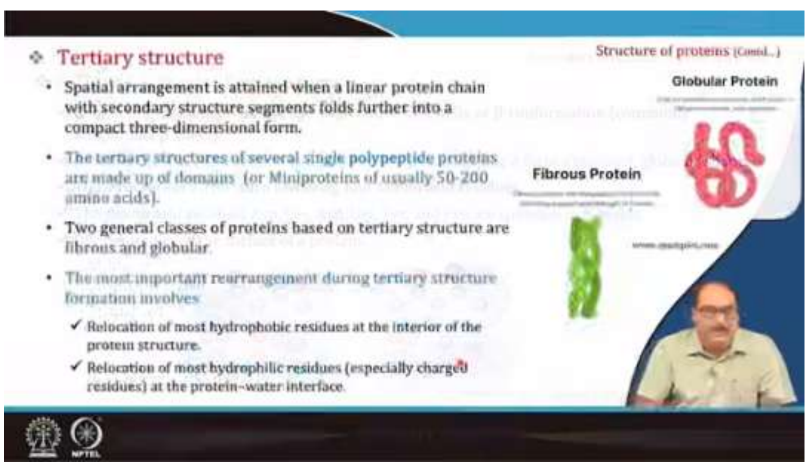
Then, the beta conformation or beta sheet, you can see here in the figure, is a more extended conformation. The beta sheet is formed when two parts of a polypeptide chain lie side by side.



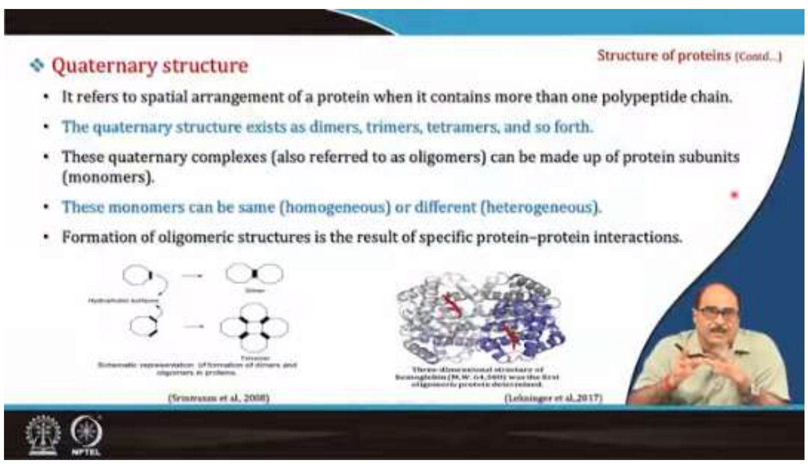
The backbone of the polypeptide chain is extended into a zigzag structure. And due to the pleated appearance of the overall sheet, they are also called the beta-pleated sheet. The hydrogen bonds form between adjacent or distant segments of the polypeptide chain within the sheet and the adjacent polypeptide chains in a beta sheet. They can be either parallel or anti-parallel, as in the case of immunoglobulins, green fluorescent proteins, SH3 domains, and so on.



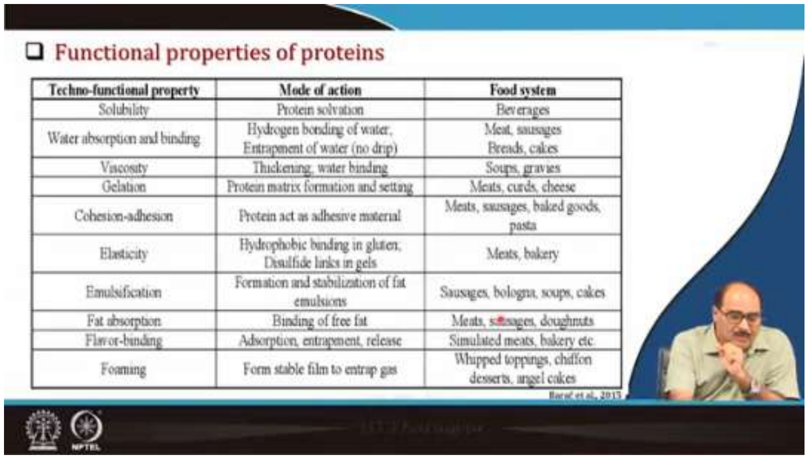
Then beta turns, beta bends, reverse turns, etc. You can see here in these figures: it is the type 1 beta turn, type 2 beta turn. And these connecting elements that link successive runs of alpha helix or beta conformation are commonly anti-parallel beta sheets. So, beta bends reverse the direction of a polypeptide chain, helping it form a compact globular shape. The structure is a 180-degree turn involving four amino acid residues. The amino acid residues are aspartate, cysteine, asparagine, glycine, threonine, and proline. These are common in beta bends. Others, which are found near the surface of the proteins, are also there.



Then, after this, the tertiary structure. Tertiary structure means the folding of the coiled chain. The spatial arrangement is attained when the linear protein chain with secondary structure segments folds further into a compact 3-dimensional conformation as you can see whether it is getting a fibrous structure or a globular structure. In the globular structure, there are interior wide spaces. So, the water can easily penetrate into it. Sometimes, they are water-soluble; these fibrous structures are very compact. There is no interior space, so the water cannot penetrate into them; they are mostly water-insoluble proteins. Though the tertiary structure of several single polypeptide proteins is made up of domains There are mini proteins of usually 50 to 200 amino acids. Two general classes of proteins based on tertiary structure are the discussed fibrous and globular proteins. The most important rearrangement during tertiary structure formation involves the relocation of the most hydrophobic residues at the interior of the protein structure and the relocation of the most hydrophilic residues that is, especially charged residues at the protein-water interface. So, that is the part and also the part organization of the R group, that is, the polar R groups, that is, the formation of the 3-dimensional structure. If all the polar R groups of the amino acids are extended towards the exterior of the protein molecule, then it will be a water-soluble protein. If these R groups, polar R groups, are extended towards the interior, then it may be a water-insoluble protein and all those things. So, even the protein's characteristics, functionality, and other properties are all regulated by the manner in which the three-dimensional conformation is decided.



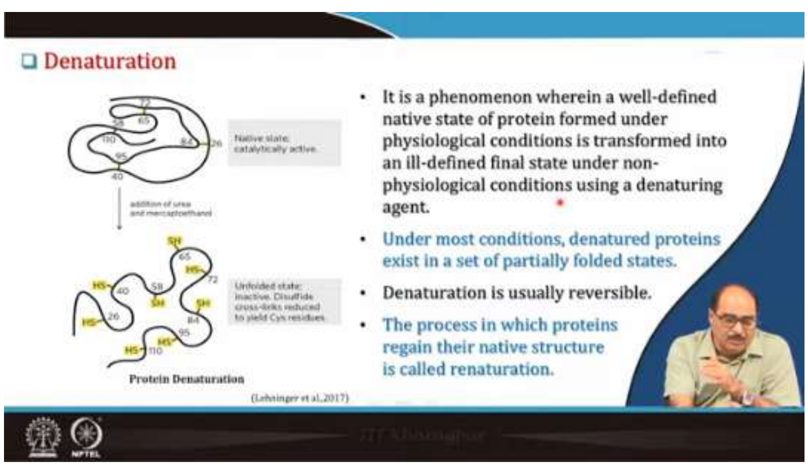
Then comes the quaternary structure. It refers to a spatial arrangement of a protein when it contains more than one polypeptide chain. The quaternary structure can exist as dimers, trimers, tetramers, and so forth. These quaternary complexes, also referred to as oligomers, can be made up of protein subunits that are monomers, like different ones. And these monomers can be the same, like homogeneous, or different, heterogeneous. The formation of oligomer structures is the result of specific protein-protein interactions, and different interactions are there. So, you get a three-dimensional protein conformation, which is the quaternary structure.



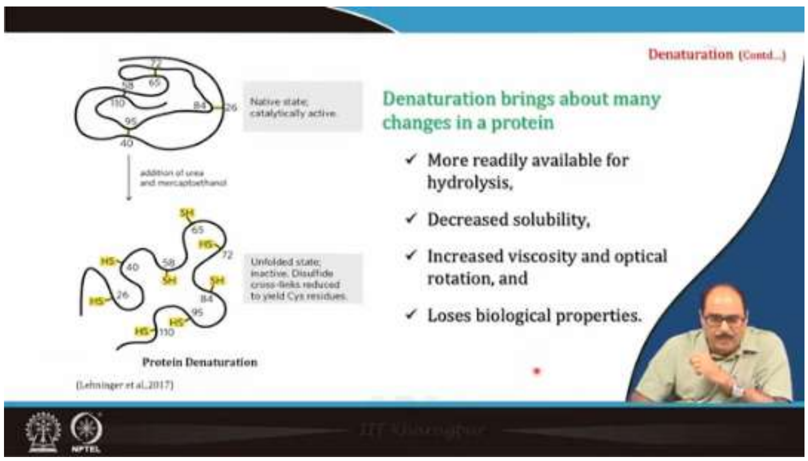
Functional properties of proteins

Techno-functional property	Mode of action	Food system
Solubility	Protein solvation	Beverages
Water absorption and binding	Hydrogen bonding of water, Entrapment of water (no drip)	Meat, sausages Breads, cakes
Viscosity	Thickening, water binding	Soups, gravies
Gelation	Protein matrix formation and setting	Meats, curds, cheese
Cohesion-adhesion	Protein act as adhesive material	Meats, sausages, baked goods, pasta
Elasticity	Hydrophobic binding in gluten, Disulfide links in gels	Meats, bakery
Emulsification	Formation and stabilization of fat emulsions	Sausages, bologna, soups, cakes
Fat absorption	Binding of free fat	Meats, sausages, doughnuts
Flavor-binding	Adsorption, entrapment, release	Simulated meats, bakery etc.
Foaming	Form stable film to entrap gas	Whipped toppings, chiffon desserts, angel cakes

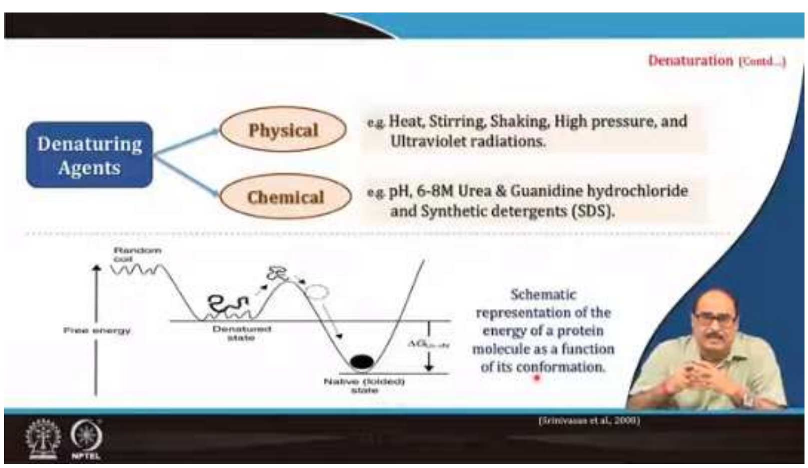
So, all these structures, are actually very important as far as the functionality of the protein is concerned. Functional properties of the protein, like solubility, where protein solvation is the major mechanism, are very important in foods like beverages, etc. Similarly, the viscosity or gelation viscosity, the mode of action, is like thickening and water binding. And it is again important in soups and gravy. The gelation involves the formation of the gel in the protein matrix, setting in meats, curd, cheese, etc. So, all these properties, like techno-functional properties, elasticity, emulsification, fat absorption, flavor bonding, foaming, etc. And there is a mode of action. Or food systems where these functional properties are important and that is very important, as provided here in this table. And it is very important; one should accordingly understand how this protein takes its structure, how its structure is changed during processing, etcetera, as it will influence various characteristics.



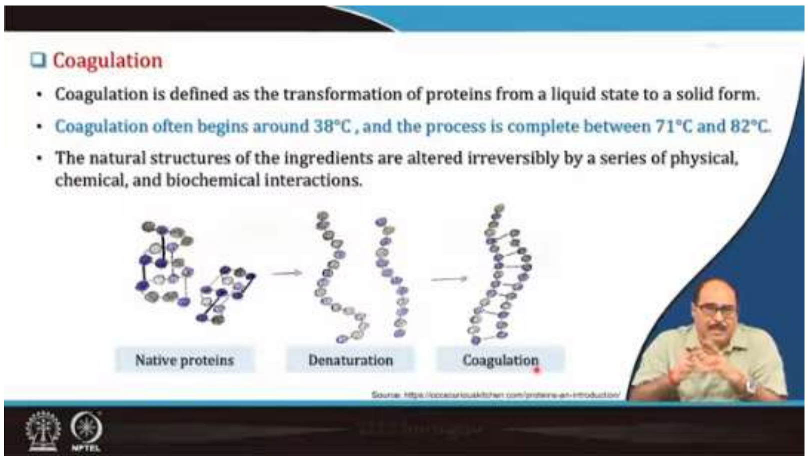
Then comes denaturation. It is a phenomenon wherein a well-defined native state of protein, formed under physiological conditions, is transformed into an ill-defined final state under non-physiological conditions using a denaturing agent. So, this is the native state, crystalline and active, and then it is the addition of urea or such other denaturing agents, etcetera. Then you can see here the organized structure is broken. It becomes an open structure, etcetera, or the three-dimensional conformation. Under most conditions, the denatured protein exists as a set of partially folded states; there will be an unfolding of the structure. Denaturation is usually, however, reversible; the process in which proteins regain their native structure is called renaturation. So, denaturation brings about many changes in a protein. Most rapidly available for hydrolysis, denatured protein decreases, and solubility decreases. For example, we discussed that while forming the three-dimensional protein. In the tertiary structure, all the polar R groups are towards the interior. It may happen when denaturation takes place, and then the organized structure changes.



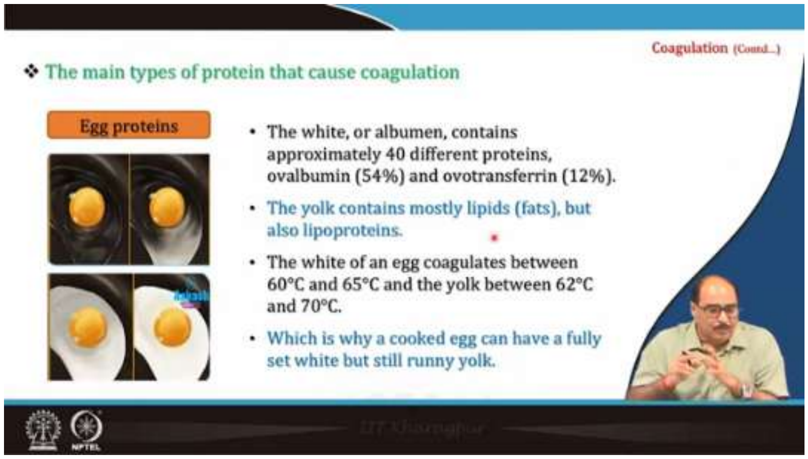
Then, maybe most of that is some of the polar R groups that were initially there on the exterior. They may go to the interior, and this may result in a decrease in solubility. There may be increased viscosity and optical rotation, also there may be a loss of biological properties.



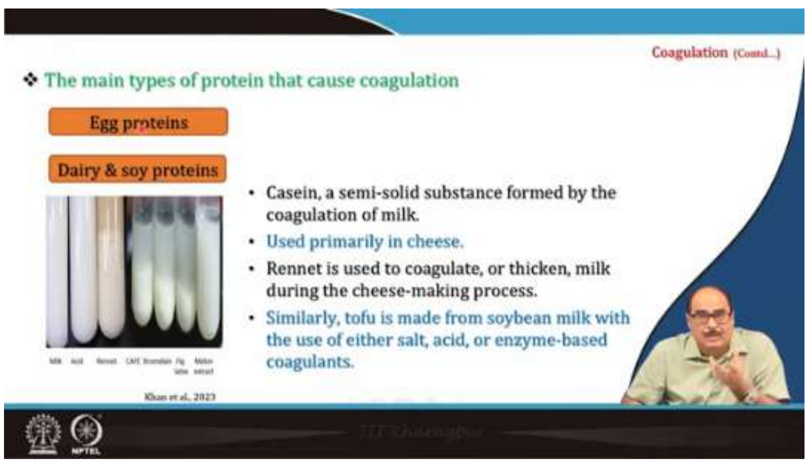
So, the various denaturing agents may be physical agents like heat, stirring, shaking, high pressure, ultraviolet radiation, etcetera. Chemical agents like pH 6 to 8 molar urea and guanidine hydrochloride and synthetic detergents like sodium dodecyl sulphate, SDS, etcetera are the denaturing agents. Then comes coagulation. Another important property of the protein is when the protein coagulates. You can see that it precipitates in the milk. That is when the milk is converted into curd or cheese, etcetera, the protein precipitates or the protein coagulates.



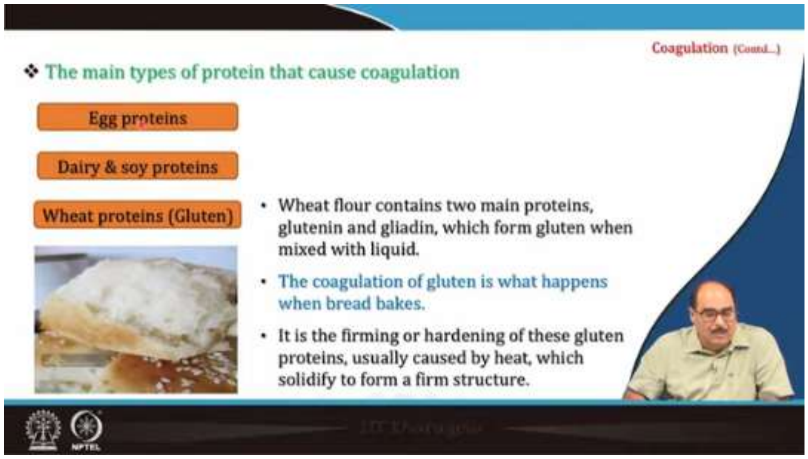
So, coagulation is defined as the transformation of protein from a liquid state to a solid form. Coagulation often begins around 38 degrees, and the process is complete between 71 to 82 degrees Celsius, and the natural structure of the ingredients is altered irreversibly by a series of physical, chemical, and biochemical alterations. As you can see here in the native protein, has an organized three-dimensional structure. In denaturation, these organized structures may change; that is denaturation. And then again, in coagulation, it means that there might be some rearrangement of this, and then it may again get into depending upon the SPI and other changes, etc. It may get precipitated or coagulated, like when you boil an egg or curdle milk, etc.



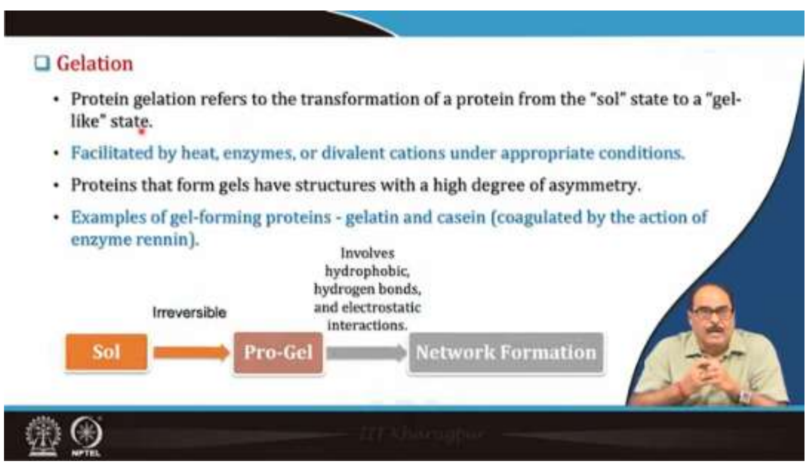
So, the main type of protein that coagulation equals is one good example is egg protein, which is when you heat the egg, and boil the egg. The white of the egg, or albumin, contains approximately 40 different proteins. Ova albumin is 54 per cent, and ovotransferrin is 12 per cent. The yolk contains mostly lipids, which are fat, but it also contains lipoproteins. So, the white of an egg coagulates between 60 to 65 degrees Celsius, whereas the yolk coagulates between 62 and 70 degrees Celsius. This is why a cooked egg can have a fully set white but still have a runny yolk. So, depending upon the temperature, etcetera, to what it has been heated or boiled, okay.



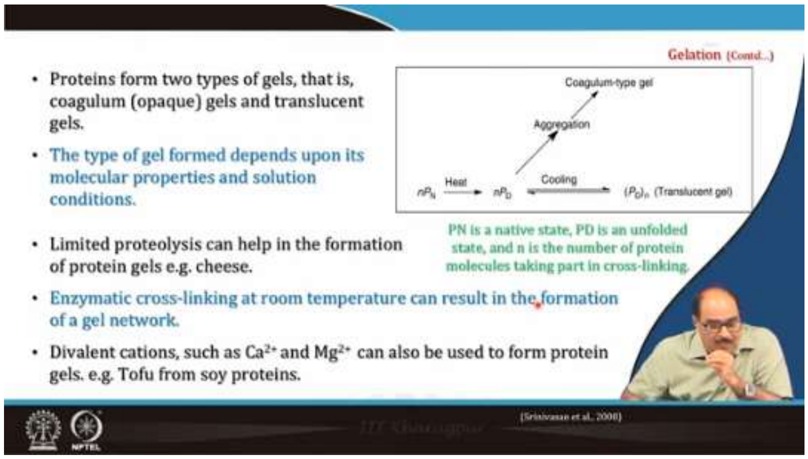
Then also the dairy and soya proteins, the casein, they told you. It is a semi-solid substance formed by the coagulation of milk. It is used primarily in cheese or curd, etc. That is, in cheese preparation, rennet, an enzyme, is used to coagulate the proteins or to thicken the milk during the cheese-making process. Similarly, tofu is made from soybean milk using either salt, acid, enzyme-based coagulation, etc. So, protein is basically precipitated and coagulates, becoming into the solid form.



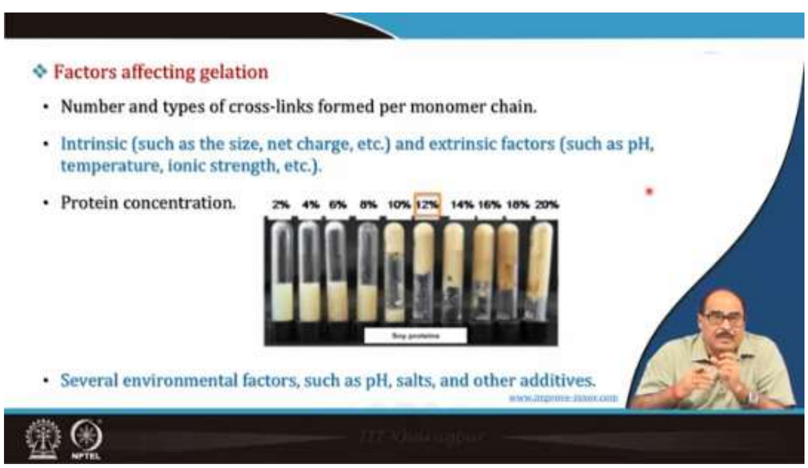
Similarly, the wheat protein gluten is formed from two main proteins found in wheat flour: glutenin and gliadin. When water is added to the wheat flour and mechanical force is applied through kneading, these proteins combine to create a coherent, three-dimensional network structure known as gluten. During baking, the coagulation of gluten occurs, which helps in forming the final structure of bread and other baked products in the oven. The gluten coagulates, and it is a soft dough that is converted into thick or thin or soft or little hard bakery products, depending upon the condition of baking and other agents present in the mixture. So, it is the forming or hardening of these gluten proteins, which is usually caused by heat and which solidifies to form a firm structure of the bakery products in breads, cakes, biscuits, cookies, pastries, etc.



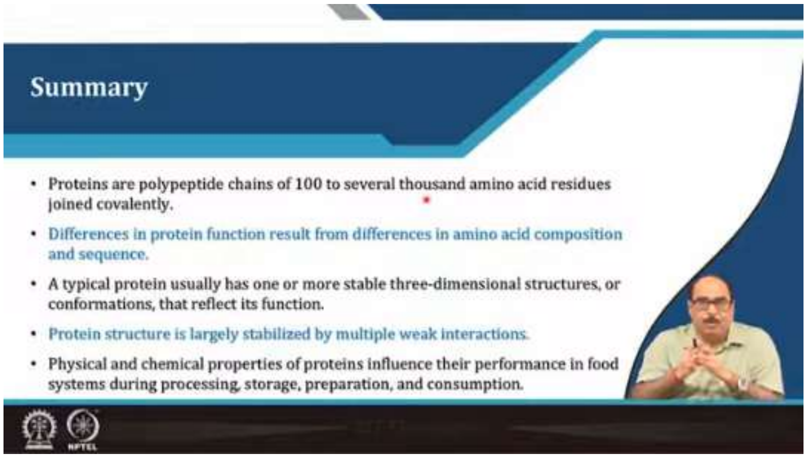
Another very important property of the protein is gelling or gelation. Protein gelation refers to the transformation of a protein from the solid state to a gel-like state. It is facilitated again by heat, enzymes, or divalent cations under appropriate conditions. Proteins that form gels have structures with a high degree of asymmetry. Examples of gel-forming proteins include gelatin and casein, which are coagulated by the action of the enzyme rennet. So, this is basically the salt. It is irreversible. It gives pro-gel that involves hydrophobic hydrogen bonds and electrostatic interactions. The network formation takes place, and protein is actually converted into a gel-like substance; there is a difference between the gel and a coagulant, etc. So, that is the gel.



So, the proteins basically form two types of gel: that is coagulum, which is an opaque gel, and a translucent gel. So, the type of gel formed depends upon its molecular properties and the cooling conditions. Limited proteolysis can help in the formation of protein gels, like in the case of cheese, etc. Enzymatic cross-linking at room temperature can result in the formation of a gel network and divalent cations such as calcium ions or magnesium ions can also be used to form protein gels, like tofu from soy protein or even if calcium, etc., is present, it gives a firm gel, etc., if there are calcium ions or calcium caseinate, etc., as it is there. So, it is shown here that nPN is the protein in its native state when it is given heat, then it becomes nPD, meaning denatured protein in an unfolded state, and it is the number of protein molecules taking part. Then it may be an aggregation coagulation type gel or, if you cool it, it becomes a translucent gel, different types of gels.



So, basically, the factors which affect gelation include the number of cross-linked polymers per monomer chain. The intrinsic factors such as size, net charge, etc., as well as extrinsic factors like pH, temperature, and ionic strength, all influence gelation. Gelation, gelling property, okay, and even the protein concentration, like what is the case with soy proteins, which form better gels at 12% concentration also. So, several environmental factors like pH, salt, and other additives, all will influence the gelling behaviour of the protein.



In summary, proteins are polypeptide chains consisting of 100 to several thousand amino acid residues covalently linked. Their functions vary based on differences in amino acid composition and sequence. Typically, a protein adopts one or more stable three-dimensional structures or conformations, which determine its functionality and properties. This functionality is largely derived from the organized structure of the protein. However, during processing or handling, factors such as heat, acid, physical and chemical influences, or radiation can alter this organized structure, a process known as denaturation. The protein structure is largely stabilized by multiple weak interactions. Properties such as gelation, denaturation, renaturation, and coagulation play a significant role in determining the functionality, characteristics, and nutritional value of proteins in food. Among the various amino acids present in proteins, there are about 8 to 10 essential amino acids that our bodies cannot synthesize. Hence, it is crucial to obtain these essential amino acids through dietary protein. Consuming a balanced form of protein ensures that we receive all the essential amino acids in the appropriate amounts for optimal health.

These are the references that were used in this lecture.

So, with this, thank you very much.

Thank you for your patient hearing.