

General Properties of Major Food Components

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Abstract

Food consists of major constituents or materials. Its composition will affect nutritional and sensory quality of food product, therefore elucidating the composition of food is very essential for food production chain. The major compositions of most foods are including water, lipid, protein, carbohydrate, and enzyme. Each component has its own physical and chemical characteristics which contribute to the final properties of food products. This chapter focuses on the structure, physicochemical properties, and functionality of water, lipid, protein, carbohydrate, and enzyme.

Introduction

Raw food products from plants and animals contains mostly water, lipid, protein, and carbohydrate as major components. Understanding the fundamental aspects such as the composition and physicochemical properties of raw food products during handling, processing, and storage will be very important.

Water is an essential constituent in which organisms' life processes occur. In food, water presents predominantly as an intracellular or extracellular component in plant and animal food products. Interaction of water with other food constituents results in controlling many chemical and physical reactions which significantly contributes to shelf life and quality values of food products (Luck 1981). For instance, removal of water from food by physical or chemical methods such as binding it with salt or sugar inhibits chemical and enzymatic reactions produced by microorganisms, resulting in shelf life improvement of food products (Lewin 1974; Luck 1981). On the other hand physical interaction of water with macromolecules may contribute to the physical appearance of food.

Food lipids are generally nonsoluble compounds referred to as fats (solid) or oils (liquid) indicating their physical state at ambient temperatures. Food lipids are also classified as nonpolar (e.g., triacylglycerol and cholesterol) and polar lipids (e.g., phospholipids) to indicate differences in their solubility and functional properties. Food lipids play an important role in food sensory quality by contributing to attributes such as texture, flavor, nutrition, and caloric density.

Proteins play a central role in biological systems and food as well. All biologically derived proteins can be used as food proteins which must be easily digestible, nontoxic, nutritionally adequate, functionally usable in food products, available in abundance, and sustainable agriculturally. The functional properties of proteins in foods are related to their structural and other physicochemical characteristics.

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Table 1 Physical properties of water

Water	Temperature (°C)					
	0	20	40	60	80	100
Vapor pressure (mm Hg)	4.58	17.53	55.32	149.4	355.2	760.0
Density (g/cm ³)	0.9998	0.9982	0.9922	0.9832	0.9718	0.9583
Specific heat (cal/g °C)	1.0074	0.9988	0.9980	0.9994	1.0023	1.0070
Heat of vaporization (cal/g)	597.2	586.0	574.7	563.3	551.3	538.9
Thermal conductivity (kcal/m ² h °C)	0.486	0.515	0.540	0.561	0.576	0.585
Surface tension (dynes/cm)	75.62	72.75	55.32	69.55	66.17	62.60
Viscosity (centipoises)	1.792	1.002	0.653	0.466	0.355	0.282
Refractive index	1.3338	1.3330	1.3306	1.3272	1.3230	1.3180
Dielectric constant	88.0	80.4	73.3	66.7	60.8	55.3
Coefficient of thermal expansion $\times 10^{-4}$	—	2.07	3.87	5.38	6.57	—

Source: De Man J M. (1999). Principle of Food Chemistry. Aspen Publisher. Gaithersburg, Maryland

Carbohydrates are organic compounds that are mostly distributed and abundant on earth. They consist of carbon, hydrogen, and oxygen and can be simple or complex in structure of molecules. In food processing, a carbohydrate has functional role in its physical and chemical properties which act as sweeteners, thickeners, stabilizers, gelling agents, fat replacers, and precursors for aroma and coloring substances, especially in thermal processing. Carbohydrates are commonly divided into monosaccharides, oligosaccharides, and polysaccharides.

Enzymes are proteins involved in chemical reactions related to metabolism. Generally, food enzymes can be classified as endogenous and exogenous. Endogenous enzymes are enzymes that exist and are synthesized by biological cells in all organisms and thus enhance or deteriorate food quality, while exogenous enzymes are enzymes that are added to foods to cause a desirable change (Damodaran et al. 2008). Inactivation or controlling the rate of enzymes is important to result in desirable changes in food products.

In this chapter, general properties of water, lipid, protein, carbohydrate, and enzyme such as their chemical structure, physical and chemical properties, and functional properties in food are discussed in different sections.

Water

Physical Properties of Water and Ice

Physical properties of water are shown in Table 1; much of this information will be obtained from De Man (1999). Table 2 shows physical properties of ice at various temperatures. Some of the physical properties of water and ice are exceptional; however, these exceptionally high values of the caloric properties of water would be important for food processing operations such as freezing and drying (Fennema 1973). In frozen food, density difference of water and ice may contribute in structural damage to foods. Structural change from solid to semisolid or vice versa as a result of fluctuating temperature will change also the density of ice, producing stresses and structural damage in frozen foods (Boutron et al. 1960; Vaclavik and Christian 2014).

Table 2 Physical properties of ice

Ice	Temperature (°C)						
	0	−5	−10	−15	−20	−25	−30
Vapor pressure (mm Hg)	4.58	3.01	1.95	1.24	0.77	0.47	0.28
Heat of fusion (cal/g)	79.8	–	–	–	–	–	–
Heat of sublimation (cal/g)	677.8	–	672.3	–	666.7	–	662.3
Density (g/cm ³)	0.9168	0.9171	0.9175	0.9178	0.9182	0.9185	0.9188
Specific heat (cal/g °C)	0.4873	–	0.4770	–	0.4647	–	0.4504
Coefficient of thermal expansion $\times 10^{-5}$	9.2	7.1	5.5	4.4	3.9	3.6	3.5
Heat capacity (joule/g)	2.06	–	–	–	1.94	–	–

Source: De Man J M. (1999). Principle of Food Chemistry. Aspen Publisher. Gaithersburg, Maryland

Interactions of Water

Water-Solute Interaction

Water-solute interaction results in alteration of the properties of food systems. These changes result from molecular interactions between water and the nature of the solute, particularly from ions or charged groups which interact with water through electrostatic forces. These interactions alter the geometric structure of water molecules found in hydrophilic groups of solutes which result in their mobility retardation and reactivity (Brady and Romanov 1960). In contrast, the hydrophobic groups of solutes interact weakly with adjacent water, due to their preference to nonaqueous surrounding environment (Ashbaugh et al. 2002). However, this weak interaction may result in instability and structural consequences.

Types of Water

Most natural fresh foods contain water up to 70 % of their weight or greater; fruits and vegetables contain water up to 95 % or greater (Vaclavik and Christian 2014). Water presents in food in the form of free, bound, and entrapped water (Fennema 1973; Schmidt 2004). Free water is water which can be removed easily from foods just by squeezing, grinding, or pressing, for instance, removing water from orange fruit just by squeezing it.

Bound water is water which cannot be extracted easily because it binds tightly onto water molecules (Fennema 1973). Thus, this type of water needs particular analysis methods to determine its value in the particular food. An example of bound water is the water present in cacti or pine tree needles; it cannot be squeezed or pressed out; even extreme desert heat or a winter freeze does not negatively affect bound water, and the vegetation remains alive.

Water may also present as entrapped water in foods such as water in pectin gel or in fruit or vegetable. Entrapped water is immobilized in matrixes, capillaries, or cells, but if released during cutting or damage, it flows freely. Entrapped water has properties of free water and no properties of bound water. Entrapped water in food is often associated with water holding capacity, a term that is frequently employed to describe the ability of a matrix of molecules, usually macromolecules present at low concentration, to physically entrap large amounts of water in a manner that inhibits exudation under the application of an external, often gravitational, force (Belitz et al. 2009; Damodaran et al. 2008; De Man 1999). Familiar food matrices that entrap water in this way include gels of pectin and starch and cells of tissues, both plant and animal.

Physically entrapped water does not readily flow from tissue foods, even when they are cut or minced. Nevertheless, this water behaves during processing with properties close to those of pure water. It is easily removed during drying, easily converted into ice during freezing, and readily available as a solvent. Thus, though its bulk flow is severely restricted, the movement of individual molecules is essentially similar to that of water molecules in a dilute salt solution (Fennema 1973, 1996).

Most of the water in tissues and gels can be categorized as physically entrapped, and impairment of this entrapment capability (water holding capacity) of foods has a profound effect on food quality. Examples of quality defects associated with impairment of water holding capacity are syneresis of gels, thaw exudation from previously frozen foods, and inferior performance of animal tissue in sausage resulting from the decline in muscle pH that accompanies normal physiological postmortem events. In all cases, the quality defect stems from the physical relocation of water molecules in space but does not necessarily reflect any significant change in the interactive properties of these molecules (De Man 1999; Schmidt 2004).

Water as Food Solvent and Dispersing Medium

Solutes in the form of food constituents can be either *dissolved*, *dispersed*, or *suspended* in water depending on their particle size and solubility. To form a solution, water should dissolve small molecules such as salts, sugars, or water-soluble vitamins which may be either ionic or molecular. An ionic solution is formed by dissolving substances that ionize in water, such as salts, acids, or bases. Sodium chloride contains sodium (Na⁺) and chloride (Cl⁻) ions held together by ionic bonds; the added water molecules reduce the attractive forces between the oppositely charged ions, the ionic bonds are loosened, and thus the water molecules surround the individual hydrated ions. Each ion is usually surrounded by six water molecules; the ions move independently of each other.

The surrounding concept of water molecules occurs also in polar molecules to form molecular solutions, for instance, sugars. When a sugar crystal is dissolved in water, predominant hydrogen bonds between the polar hydroxyl groups are loosened and replaced by hydrogen bonds between water and the sugar molecules. Therefore, the hydration occurs gradually until each sugar molecule is fully surrounded by water molecules. Temperature also affects the hydrogen bond disruption between polar hydroxyl groups of sucrose molecules, then facilitating the formation of hydrogen bonds between water and sucrose and hydration of sucrose molecules. Therefore, sucrose has much better solubility in hot water than in cold water. Solute dissolution in water will increase the boiling point of water which is practically important to be understood for food process application like in candy or jelly making through determination of the sucrose concentration by measuring the boiling point of sucrose solution (Fennema 1996).

Big molecules with a size range 1–100 nm are difficult to dissolve fully to form true solutions, but they can be dispersed to form colloidal dispersion. Examples of such molecules include hydrocolloids, starches, and some food proteins. Colloidal dispersions which mostly apply in food are often unstable systems; stabilization is necessary to maintain water-solute binding, thus phase separation can be prevented. They are particularly unstable to factors such as heating, freezing, or pH change. In food application, changing the conditions in a stable dispersion can cause the system to be unstable such as precipitation or gelation; however, this is desirable in some cases, for instance, when making pectin jellies (Belitz et al. 2009). Colloidal dispersion is essential to be understood in food processing as many convenient or packaged foods have colloidal dimensions and their stability and sensitivity to certain types of reactions.

Particles that are too large, usually >100 nm, will form a *suspension* when mixed with water. Suspension is much more unstable, which separates out over a period compared with colloidal dispersion. An example of a suspension is when native starch grains are suspended in water.

Table 3 Water activity of some foods

Food	aw
Leberwurst	0.96
Salami	0.82–0.85
Dried fruits	0.72–0.80
Marmalades	0.82–0.94
Honey	0.75

Source: Belitz HD, Grosch W, Schieberle P (2009). Food Chemistry. 4th revised and extended edition, Springer-Verlag Berlin Heidelberg

Water and Food Stability

Since water is a predominant compound in food, it has a significant role to control food stability. Stability of food includes its physical, chemical, and microbiological aspect associated with quality of food; these parameters will affect and relate to each other. Food instability can lead to food perishability which degrades food quality. It has long been recognized that there is a relationship between water content and food perishability. In some foods, water is an undesired compound. Concentration and dehydration processes are performed primarily for the purpose of decreasing the water content of a food, simultaneously increasing the concentration of solutes and thereby decreasing perishability (Scott 1957).

Interestingly, it has also been investigated that various types of food with the same water content have different significant perishability. Therefore, it is evident that the indicator of perishability is not only the water content. Since water can interact with solute, the intensity binding might expect that water engaged in strong associations to lead food quality degradation mainly by microorganism growth and hydrolytic chemical reactions. The term “water activity” (aw) was introduced to reflect the intensity with which water associates with various solute constituents (Luck 1981; Scott 1957).

Although aw is not a totally reliable factor in food stability and safety, aw can give sufficient information regarding its correlation with rates of microbial growth and rates of many degradative reactions. Aw is considered high in living tissues of organisms because they require sufficient level of water to maintain cell metabolism. However, microorganisms such as bacteria, mold, and yeast multiply at high Aw (Labuza et al. 1972). Preservation techniques against spoilage because of these microorganisms take into account the controlling of water activity in the food. Less bacterial growth occurs if the water level is lowered to less than 0.85 according to FDA Model Food Code. Foods with aw values between 0.6 and 0.9 (examples in Table 3) are known as “intermediate moisture foods” (IMF) (Vaclavik and Christian 2014).

Aw is not the only factor that contributes to bacterial growth; other factors such as pH and environment would contribute also to food stability and safety. These foods are necessary to be protected against microbial spoilage. In food application, an option for decreasing water activity and thus improving the shelf life of food is to use additives with high water binding capacities, such as sucrose, salt, sorbitol, and glycerol, which act as humectants (Fennema 1978). For instance, jams, jellies, and dried fruits are prepared using high concentrations of sugar and brines, whereas hams, salami, and sausages contain high concentrations of salt to prolong their shelf life.

The storage quality of food does depend on the water activity (aw), not on the water content. The ratio of the moisture content of food and the relative humidity of the air surrounding it is known as the water activity. It is an important characteristic. Water activity (aw) is determined by (Vaclavik and Christian 2014)

$$Aw = P/P_0 = ERH \quad (1)$$

P = partial vapor pressure of food moisture at temperature T₀

P_0 = saturation vapor pressure of pure water at temperature T_0

T_0 = equilibrium temperature of the system

ERH = equilibrium relative humidity

A relationship between a_w and ERH is noteworthy. First, a_w is an intrinsic property of the sample, whereas %ERH is a property of the atmosphere established in steady state with the sample. Second, equality exists in Eq. 1 only if equilibrium has been established between the product and its environment. Equilibrium condition of the samples is a time-consuming process and almost impossible for large samples, especially at temperatures below 20 °C (Damodaran et al. 2008).

Role of Molecular Mobility in Food Stability

Even though a_w has become an important tool for the food industry, this should not preclude consideration of other approaches that can support a_w as a tool for predicting and controlling food stability and processability. Compelling evidence has accumulated to indicate molecular mobility. In the molecular mobility approach, attention is paid to the mobilities of the constituent molecules. Molecular mobility defined as rotational and translational mobilities is considered relevant. This consideration of mobilities implies that careful attention should be given to the diffusional aspects of many reactions, and in particular, the importance of diffusion-limited reactions to the quality in many foods such as glassy states, recrystallization, and collapse temperatures during freeze drying contributes to the properties of biological materials (Angibaud 1986).

Many of the basic concepts related to Mm in nonequilibrium systems consisting of synthetic amorphous polymers explained the important role of glassy and supersaturated states in food containing various sugars and suggested that the existence of these states had an important influence on the stability and processability of many foods (Ferry 1980; White and Cakebread 1966; White and Cakebread 1969; Williams et al. 1955). According to Duckworth et al. (1976) evidence of the relationship between Mm and food stability is important, since there is a relevance of Mm to rates of nonenzymatic browning and ascorbic acid oxidation.

The major concept regarding the relationship between molecular mobility and stability of foods is very simple. As a food is cooled, molecular mobilities decrease. The different molecular constituents of the food will give their own characteristic mobilities. Two possible mechanisms are proposed. First, as temperature is lowered, at some point the larger molecules' diffusion is highly restricted, and processes depending on their mobility will slow down as well. At some lower temperature, intermediate-size molecules also experience restricted motion that affects the properties of the system, and its reactions. This relationship exhibits temperature dependence, particularly in the temperature zone where restricted motion occurs (Boutron et al. 1986; Damodaran et al. 2008).

Second, as temperature is lowered, separation of new solid occurs. Ice solid phase would be more relevant to this mechanism. The principle is when ice separates out, concentration of solutes in the unfrozen aqueous phase increases; for this relationship it is known that molecular mobility is not solely a function of the temperature but also a function of the concentration, since at higher concentrations collisions and involvement become more likely. The combination of temperature and concentration prevail to a reduction in mobility with decreasing temperature, which is much more obvious than only driving force-temperature dependence. As previously, molecular size is a factor, with large molecules exhibiting severely restricted mobilities at higher temperatures than do smaller molecules (Damodaran et al. 2008; Duckworth et al. 1976; White and Cakebread 1966; White and Cakebread 1969).

In particular, Levine and Slade proposed the application of the Williams-Landel-Ferry (WLF) equation to food systems to describe interrelationships between WLF and molecular mobility. The WLF equation takes the form below (Damodaran et al. 2008):

$$\log \frac{\eta}{\eta_g} = \frac{-C_1(T - T_g)}{C_2 + (T - T_g)} \quad (2)$$

η = the viscosity at product temperature T (K)

η_g = the viscosity at product temperature T_g (K)

T_g (K) = product temperature (usually the glass transition temperature)

C_1, C_2 = constants

η can be replaced by $1/M_m$, the molecular mobility, or any other diffusion-limited relaxation process. This equation describes the dependence of system viscosity, and other diffusion-enabled processes, on the amorphous state behavior of a polymer. In polymer systems, universal values have been established for C_1 and C_2 . It is a topic of dispute as to whether these values can be usefully applied to systems of aqueous food glasses (Damodaran et al. 2008).

Diffusion-limited processes often play an important role in food stability, since the essential constituents considered in molecular mobility are water and the dominant solute or solutes; evidence implies that M_m is causatively related to diffusion-limited properties of foods which contain other substances besides water. Some types of these substances are substantial amounts of amorphous, primarily hydrophilic molecules, ranging in size from monomers to polymers, for example, starch-based foods, protein-based foods, boiled confections, intermediate-moisture foods, and dried, frozen, or freeze-dried foods (Slade and Levine 1995). When in a condition where M_m is greatly reduced, diffusion-limited properties become highly stable, changing very slowly or not at all with time. It is important to notice that while most processes of physical change are diffusion limited, not all processes of chemical change are so limited. Sometimes chemical reactivities are the dominant factor in food stability (Damodaran et al. 2008).

Food Lipids

Chemical Structure and Classification

Fats and oils are triglycerides, the major constituent of lipids. Overall, lipid is the umbrella term that includes the triglycerides, phospholipids, and sterols.

Glycerides

Glycerides include monoglycerides, diglycerides, and triglycerides. Glycerides have a glycerol molecule backbone joined to one or more fatty acid molecules (O'Keefe 2002). A monoglyceride contains glycerol esterified to one fatty acid molecule. Diglycerides are formed by esterification of two fatty acids to glycerol. If a triglyceride consists of three same fatty acids, it is called a simple triglyceride, otherwise if it contains two or three different fatty acids it is called a mixed triglyceride (O'Keefe 2002; Weiss 1983). The arrangement and specific type of fatty acids on the glycerol determine the chemical and physical properties of a fat.

In addition to glycerides and free fatty acids, lipids may contain small amounts of phospholipids, sterols, tocopherols, fat-soluble pigments, and vitamins (Nielsen 2003). Phospholipids are similar to triglycerides but consist of only two fatty acids esterified to glycerol. A polar group containing phosphoric acid and a nitrogen-containing group takes the place of the third fatty acid. Sterols contain a common steroid nucleus, an 8–10 carbon side chain, and an alcohol group (Giese 1996).

Fatty acids are long hydrocarbon chains with a methyl group (CH_3) at one end of the chain and a carboxylic acid group (COOH) at the other. Most natural fatty acids contain from 4 to 24 carbon atoms and an even number of carbon atoms in the chain; for instance, butyric acid is the smallest fatty acid, having

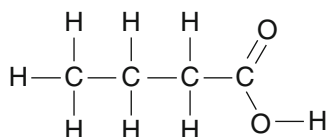


Fig. 1 Example of saturated fatty acid (butyric acid)

four carbon atoms. Fatty acids may be saturated, in which case they contain only single carbon-to-carbon bonds and have the general formula $\text{CH}_3(\text{CH}_2)_n\text{COOH}$ (Fennema 1996). Fatty acids also can be divided into monounsaturated fatty acids which contain only one double bond (e.g., oleic acid) and polyunsaturated fatty acids which contain two or more double bonds (e.g., linoleic acid) (Weiss 1983). Generally, unsaturated fats have low melting points and liquid form at room temperature (Marangoni and Narine 2002) (Fig. 1).

The double bonds in fatty acids have different isomer structures which occur either in *cis* or *trans* configuration. In the *cis* form, the hydrogen atoms attached to the carbon atoms of the double bond are located on the same side of the double bond. In the *trans* configuration of the isomer, the hydrogen atoms are located on opposite sides of the double bond, across from one another. This configuration of the double bonds affects both melting point and shape of a fatty acid molecule. The *trans* double bonds have a higher melting point than the *cis* configurations, and *trans* configurations do not significantly change the linear shape of the molecule, but a *cis* double bond forms coil structure in the chain (O’Keefe 2002).

Physical Properties

Crystal Formation

Fat molecules can bind each other to form crystals. When liquid fat is cooled, the molecular movement is reduced; the molecules will be attracted to each other by Van der Waals forces. These forces are weak and of minor significance in small molecules, but the effect is cumulative in large or long-chain molecules (O’Keefe 2002).

Crystal formation depends on symmetry of fat molecules and the similarity of fatty acid chain length (Marangoni and Narine 2002). Fats containing asymmetrical molecules and molecules containing coil structure of the double bonds align in more difficult manner, because they cannot pack together closely in space. Symmetrical fat molecules that align easily tend to form large crystals because they have high melting points resulting from less energy removed before they crystallize. On the other hand, asymmetrical molecules tend to form small crystals because more energy must be removed before they crystallize.

Polymorphism

Fat polymorphism is when fat can exist in different crystalline forms. A fat may crystallize in one of four different crystal forms, depending on the conditions during crystallization and on the composition of the fat. The smallest and least stable crystals are called α -crystals. They are formed when fats are chilled rapidly. Because of instability, they change readily to β' -crystals, which are small needle-like crystals approximately 1 μm long. Fats that can form stable β -crystals are good for use as shortenings, as they can be creamed easily and give a smooth texture. Unstable β' -crystals change to the intermediate crystal form, about 3–5 μm in size, and finally convert to coarse beta β -crystals, which can range from 25 to 100 μm in length (Timms 1991; Vaclavik and Christian 2014). These large crystals have the highest melting point.

Formation of small crystals is favored by rapid cooling with agitation. This allows formation of many small crystals, instead of slow growth of fewer large crystals (Akoh and Min 2002).

Formation of small or large crystals essentially depends on the cooling rate and homogeneity of fats (Marangoni and Narine 2002). Growth of large crystals occurs if cooling is slow and vice versa. The more heterogeneous the fat, the more likely that the molecules form small stable crystals. Large crystals are formed by homogeneous fats (e.g., lard), and small crystals are formed by heterogeneous fats (e.g., acetoglycerides). Increasing of the heterogeneity of the fatty acid composition prevents the formation of large crystals. Fats with small crystals are harder fats, have a smooth fine texture, and appear to be less oily because the oil is present as a fine film surrounding the crystals, whereas the reverse is true of fats with large crystals. Smaller crystals are desirable if a fat contributes aeration to a food.

Melting Points

The melting point is an index of the force of attraction between molecules. A strong attractive force indicates a good degree of fit between the molecules. Molecules that do not fit together well do not have strong attractive forces holding them together, and so they have lower melting points (Marangoni and Narine 2002).

The melting point range of fat or oil is based on the component fatty acids (Akoh and Min 2002). The melting point of a fat or oil is actually a range, not a sharply defined temperature. Each fat or oil contains triglycerides that melt at different temperatures, depending on their component fatty acids. The more heterogeneous of fatty acids will be less easy to fit together, thus they will have lower melting points. Some fats have a wide melting range, whereas others, such as butter or chocolate, have a narrow melting range. Chocolate has a narrow melting range that is close to body temperature, and this accounts for its characteristic melt-in-your-mouth property.

The melting point is also determined by length of fatty acid chain, number of double bonds, and isomeric configuration. The first factor is length of fatty acid chain: long-chain fatty acids have a higher melting point than short-chain fatty acids, because there is more potential for attraction between long chains than there is between short chains; for instance, butyric acid (4:0) has a melting point of 18 F (−7), whereas stearic acid (18:0) has a higher melting point of 157 F (69 °C). The second factor is number of double bonds: higher the number of double bonds, lower the melting point. A third influence on melting point is isomeric configuration. The *cis* double-bond configuration introduces a number of coil structures which are more difficult to pack together into the molecule than the *trans* configuration, thus it has lower melting point (Weiss 1983).

Chemical Reaction

Hydrolytic Reaction

Off-flavors in fat-based products are caused by hydrolysis of fatty acids from triacylglycerols (Akoh and Min 2002). Free fatty acids may produce off-flavor, reduce oxidative stability, cause foaming, and reduce smoke point (the temperature at which an oil begins to smoke). In hydrolytic rancidity, free fatty acids are liberated from the glycerol backbone resulting in the development of off-flavors. Free fatty acids produce off-aromas, and long-chain fatty acids produce soapy tastes (Min and Boff 2002). Triacylglycerol hydrolysis also occurs in frying oils during high-temperature processing, the water from fried food inducing the hydrolysis of triacylglycerol. As the free fatty acid content of the frying oil increases, smoke point and oxidative stability decrease and the tendency for foaming increases. Triacylglycerol hydrolysis will also occur at extreme pH values. However, short-chain free fatty acids sometimes contribute to desirable flavor profiles, such as in yogurt or cheese products.

Enzyme lipases play a role in free fatty acid liberation. Enzyme lipases present in living tissues of raw food materials for foods, and the activity can occur naturally such as in olive oil processing. Oils from subsequent pressing and oil extracted from the pomace have higher free fatty acid concentrations as the cellular matrix is further disrupted and the lipases have time to hydrolyze triacylglycerols (Rousseau and Marangoni 2002).

Oxidative Rancidity

Oxidative rancidity is the predominant type of rancidity. In this process, the unsaturated fatty acids are subjected to autoxidation. The more double bonds there are, the greater the opportunity for addition of oxygen to double bonds, increasing the risk that the fat or oil will become rancid (Zhuang et al. 2002).

Autoxidation is an oxidative complex reaction and is promoted by heat, light, certain metals (iron and copper), and enzymes known as lipoxygenases (Min and Boff 2002). There are three stages in the autoxidation reaction: initiation, propagation, and termination. The initiation stage of the reaction involves formation of a free radical. The free radical results if a hydrogen on a carbon atom adjacent to one carrying a double bond is displaced (Buettner 1993). This reaction is propagated which displaces another hydrogen from another unsaturated fatty acid, forming another free radical. The reaction repeats, and this stage is called propagation stage that yields activated peroxide. The liberated hydrogen unites with the peroxide to form a hydroperoxide. Hydroperoxides are very unstable and decompose into compounds with shorter carbon chains, such as volatile fatty acids, aldehydes, and ketones (Decker and McClements 2001). These are responsible for the characteristic odor of rancid fats and oils. The termination stage of the reaction involves the reaction of free radicals to form nonradical products. Elimination of all free radicals is the only way to stop the oxidation reaction.

Oxidation can be prevented or delayed by avoiding situations that would serve as catalysts for the reaction (e.g., high temperature, presence of light, oxygen, and water vapor) and addition of antioxidant (e.g., EDTA, tocopherols, BHA (butylatedhydroxyanisole), BHT (butylatedhydroxytoluene), TBHQ (tertiary-butyl hydroquinone), and propyl gallate (Buettner 1993).

Functional Properties in Foods

The functionality of triacylglycerol plays important roles in determining physical and sensory properties of food products, such as texture, appearance, and flavor.

Texture

Functionality of triacylglycerols in food texture is determined by the physical state of the lipid in the food matrix. For partially crystalline fats, such as chocolate, baked products, shortenings, butter, and margarine, the texture is mainly determined by the concentration, morphology, and interactions of the fat crystals (McGrady 1994; Pszczola 2000). In particular, the melting profile of the fat crystals plays a major role in determining properties such as texture, stability, spread ability, and mouthfeel.

The lipid concentration and behavior in the food matrix will also contribute to the overall texture; for example, oil-in-water (O/W) food emulsion is determined by the presence of fat droplets (e.g., creams, desserts, dressings, and mayonnaise). In these systems, the texture is represented by the viscosity of the overall system. In W/O food emulsions, the texture is represented by overall rheology of the system, which is largely determined by the rheology of the oil as dominant phase. The rheology of these products is determined by the morphology and interactions of the fat crystals present during crystallization and storage conditions. Formation of a three-dimensional network of aggregated fat crystals in the continuous phase provides fat product with spread ability (Moran 1994). On the other hand, interaction of lipids with other compounds in food (e.g., cookies, cakes, biscuits) impacts their texture by forming a network of interacting fat crystals that gives characteristics of firmness or snap (Marangoni and Narine 2002).

The W/O emulsion consists of water droplets embedded in a lipid phase that contains a network of aggregated crystals. The fat crystals formed are initially in the α polymorphic form but are converted to the more stable β' polymorphic form during the crystallization step. It is important to control the extent of this transformation during the manufacturing process since this determines the number and strength of the bonds formed between the fat crystals and therefore the rheology of the final product. On the other hand, it is also important to prevent the polymorphic transition from the β' form to the more stable β form during

storage, since this leads to the formation of large crystals ($>30\text{ }\mu\text{m}$) that are perceived as “grainy” or “gritty” in the mouth. This conversion can often be prevented by adding surfactants that interfere with the polymorphic transition, choosing lipids that will not form β crystals, or by appropriate blending of lipids to favor the β' -crystal habit (Lawler and Dimick 2002).

To obtain the desired functional characteristics in a particular product, it is important to choose a blend of fats and oils that gives the appropriate melting profile and polymorphic characteristics, then to process the fat using controlled cooling and shearing conditions to obtain the desired crystal type and structure (Ghotra et al. 2002). It is usually important that the lipid is partially crystalline at storage temperatures so that it maintains its structural integrity but melts during consumption to give a desirable mouthfeel.

Appearance

The characteristic appearance of many food products is represented by visual observation such as color and opacity. The color of bulk oils, such as cooking or salad oils, is mainly determined by the presence of pigment impurities that adsorb light, such as chlorophyll and carotenoids. The opacity of the fat depends on the concentration, size, and shape of the fat crystals present. Solid fats are usually optically opaque because of scattering of light by the fat crystals present, whereas liquid oils are usually optically clear. Food emulsions usually appear optically opaque because the light passing through them is scattered by the droplets (McClements 2002).

Instability problem associated with fat crystallization in lipid-based products such as chocolate can cause bloom. Bloom manifests itself as large grayish appearance on the surface of the product (Lonchampt and Hartel 2004). Fluctuating temperature during their storage causes the fat phase to melt and recrystallize (Erickson and Frey 1994). Bloom can often be retarded or prevented by using surfactants that limit the crystal transition or by carefully controlling the storage temperature to avoid fat polymorphic phase transitions (Erickson and Frey 1994; Lonchampt and Hartel 2004).

Flavor

Edible fats and oils contribute to the flavor of food. Different fatty acid composition in fats and oils has distinctive flavor profiles. The flavor of many food products is indirectly influenced by the lipid phase because flavor compounds can partition between oil, water, and gaseous regions within the food matrix according to their polarities and volatilities (McClements 2004). For this reason, the perceived aroma and taste of foods are often strongly influenced by the type and concentration of lipids present. Physical states of lipids also influence the mouthfeel of many food products (Walstra 2003), for example, oily mouthfeel produced by liquid oils and “grainy” or “sandy” mouthfeel produced by fat crystals (Moran 1994). The melting of fat crystals in the mouth causes a cooling sensation, which is an important sensory attribute of many fatty foods (Walstra 2003).

Food Proteins

Proteins are present in all living things and have a key role in many biological processes. The nutritional energy value of proteins is 4 kcal/g. Amino acids are required building blocks for protein biosynthesis. Damodaran (2008) has defined food proteins as “those that are easily digestible, nontoxic, nutritionally adequate, functionally useable in food products, available in abundance, and sustainable agriculturally.” Proteins contribute to the flavor of food, precursors for aroma compounds and colors formed during various processing of food. Proteins have ability to build or stabilize gels, foams, emulsions, and fibrillar structures, which is essential in certain food products. The proteins can be obtained from milk, meat, grain, oilseeds, legumes, algae, yeasts, and bacteria (single-cell proteins).

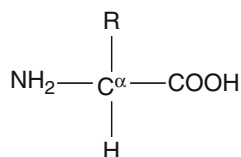


Fig. 2 General structure of amino acid

Table 4 Common amino acids found in proteins

Type	Name	Abbreviation (three and one letter symbols)	
Simple	Glycine	Gly	G
Aliphatic	Alanine	Ala	A
	Valine	Val	V
	Leucine	Leu	L
	Isoleucine	Ile	I
Heterocyclic	Tryptophan	Trp	W
	Histidine	His	H
	Proline	Pro	P
Aromatic	Phenylalanine	Phe	F
	Tyrosine	Tyr	Y
Hydroxy	Serine	Ser	S
	Threonine	Thr	T
Acidic	Aspartic acid	Asp	D
	Glutamic acid	Glu	E
Amide	Asparagine	Asn	N
	Glutamine	Gln	Q
Basic	Lysine	Lys	K
	Arginine	Arg	R
Sulphur containing	Cysteine	Cys	C
	Methionine	Met	M

Chemical Structure and Classification

There are 20 amino acids forming the building blocks of most proteins. Each amino acid contains a primary amine and carboxylic acid group, which is shown in Fig. 2. They link by peptide (amide) bonds formed between α -amino and α -carboxylic acid groups of neighboring amino acids in the polypeptide sequence. The amide linkage in proteins is a partial double bond.

In the simplest case, $\text{R} = \text{H}$ (aminoacetic acid or glycine). In other amino acids, R is aliphatic, aromatic, or heterocyclic residue and may incorporate other functional groups shown in Table 4.

Various side chains of the amino acids are involved in inter- and intramolecular interactions in proteins and classified into a number of ways, which is shown in Table 5.

Proteins are macromolecules whose name was derived from the Greek word *proteois*, which means of the first kind. Proteins contain 50–55 % carbon, 6–7 % hydrogen, 20–23 % oxygen, 12–19 % nitrogen, and 0.2–3.0 % sulfur on wt/wt basis. Protein synthesis occurs in ribosomes, and then subsequently some of them get modified by cytoplasmic enzymes (Damodaran 2008; Belitz et al. 2009). Proteins modified by enzyme or made complex with nonprotein components (prosthetic groups) are called conjugated (heteroproteins) proteins whereas modified proteins are known as homoproteins. Various proteins like glycoproteins, phosphoproteins, lipoproteins, metalloproteins, and nucleoproteins are some of the

Table 5 Base for classification of amino acids

Basis for classification	Amino acids
Charged side chains	Arginine, aspartic acid, glutamic acid, histidine, and lysine
Nonpolar, uncharged side chains	Methionine, glycine, alanine, valine, leucine, isoleucine, proline, phenylalanine, and tryptophan
Uncharged, polar side chains	serine, threonine, cysteine, tyrosine, asparagine, and glutamine
Essential amino acids	Valine, leucine, isoleucine, phenylalanine, tryptophan, methionine, threonine, histidine, lysine, and arginine
Nonessential amino acids	Glycine, alanine, proline, serine, cysteine, tyrosine, asparagine, glutamine, aspartic acid, and glutamic acid

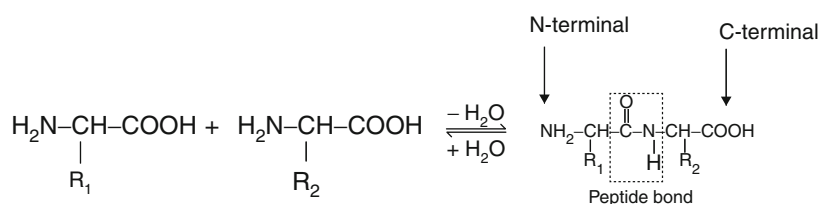


Fig. 3 Peptide bond with N- and C-terminal

examples of conjugated proteins. Moreover, based on structural organization, proteins can be classified as globular and fibrous proteins. Globular proteins exist in ellipsoidal or spherical shapes due to folding of a polypeptide chain on itself while fibrous proteins are rod-shaped molecules containing twisted linear polypeptide chains. Enzymes are globular proteins whereas collagen, keratin, and fibrin are fibrous proteins. Based on biological functions, proteins can further be classified as structural proteins, contractile proteins, transfer proteins, enzyme catalysts, storage proteins, protective proteins, hormones, and antibodies (Damodaran 2008).

Structure of Proteins

Amino acids are linked covalently through the α -carboxyl group of one amino acid and the α -amino group of another amino acid through an amide or peptide bond to form peptides, oligopeptides, polypeptides, and proteins (Ustunol 2015). Peptides are denoted by the number of amino acid residues as di-, tri-, tetrapeptides, etc., and the term “oligopeptides” is used for those with 10 or less amino acid residues. Higher molecular weight peptides are called polypeptides. The transition of “polypeptide” to “protein” is rather undefined, but the limit is commonly assumed to be at a molecular weight of about 10 kd; i.e., about 100 amino acid residues are needed in the chain for it to be called a protein. The amino acid residue with the free amino group is always placed on the left. The amino acids of the chain ends are denoted as N-terminal and C-terminal amino acid residues (Belitz et al. 2009) which are shown in Fig. 3.

Proteins are formed from amino acids through amide linkages. The structure of a protein is dependent on the amino acid sequence (the primary structure) which determines the molecular conformation (secondary and tertiary structures). Proteins sometimes occur as molecular aggregates which are arranged in an orderly geometric fashion (quaternary structure) (Belitz et al. 2009). Thus proteins have primary, secondary, tertiary, and quaternary structures, which are shown in Fig. 4.

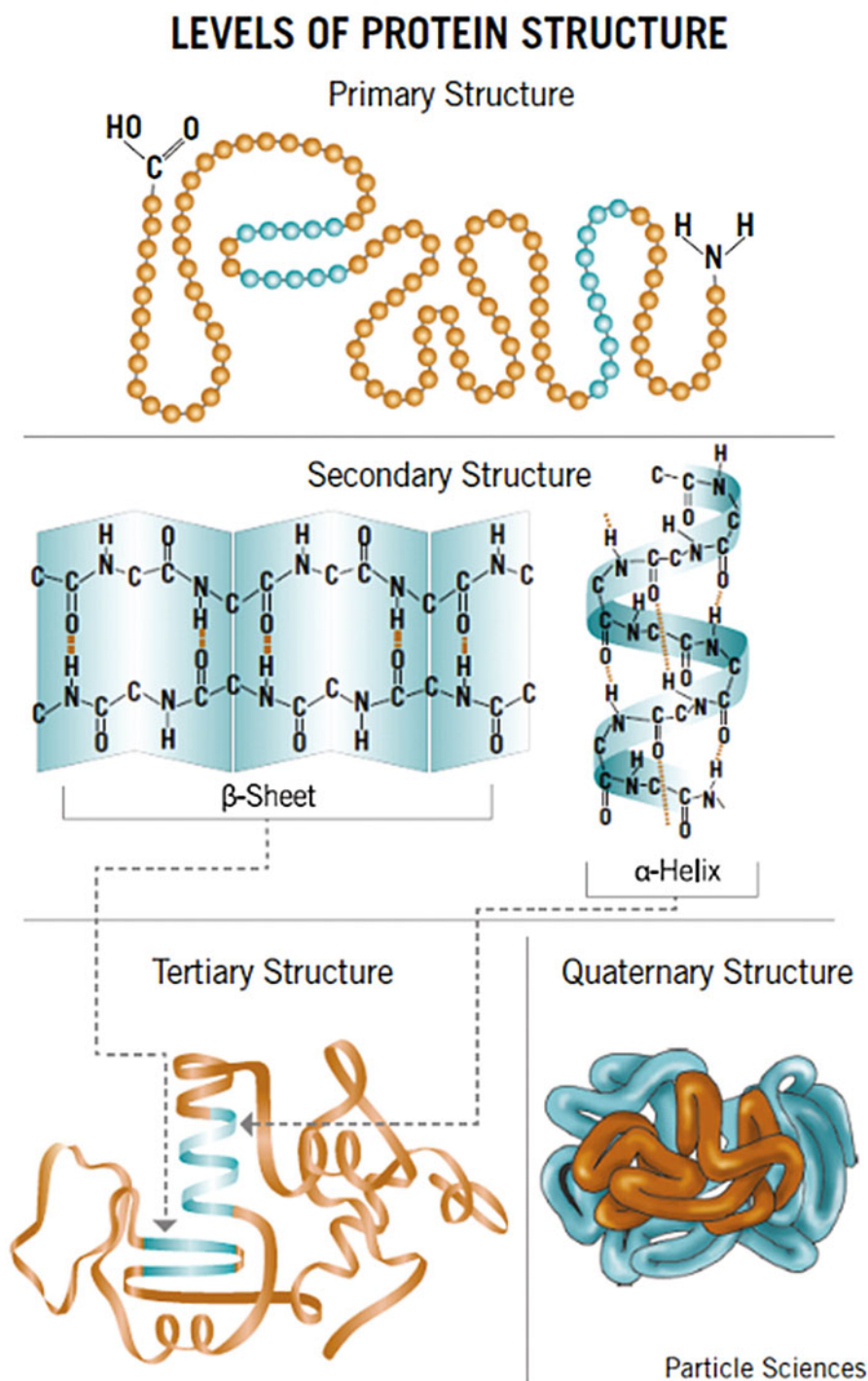


Fig. 4 Various levels of protein structures (Reprinted (adapted) with permission from Particle Sciences, Inc. Source: Protein Structure. Particle Sciences – Technical Brief: 2009: volume 8. Particle Sciences – Drug Development Services (www.particlesciences.com))

Primary Structure

It refers to the linear sequence in which the constituent amino acids are covalently linked through amide bonds, also known as peptide bonds. The primary structure is determined by its genetic code and post-translational covalent modifications. The primary structure of a protein determines the physicochemical and the functional properties of food protein (Damodaran 2008; Ustunol 2015).

Secondary Structure

The primary structure gives the sequence of amino acids in a protein chain while the secondary structure reveals the arrangement of the chain in space. Secondary structure may result from aperiodic (random coil) or periodic structures. In aperiodic structures consecutive amino acid residues possess different sets of dihedral angles whereas *helical* and *extended* structures are periodic structures which result from consecutive amino acid residues in a segment having the same recurring set of ϕ and ψ angles (Damodaran 2008; Ustunol 2015). The α -, 3_{10} -, and β -helices are the helical structures, but the right-handed α -helix is the most common and is also the most stable in food proteins. Protein helical structures are formed when the ϕ and ψ angles of consecutive amino acid residues are twisted to a same set of values. Stability to α -helix is provided by the hydrogen bonding of the N–H and C=O groups of the fourth preceding residue. The hydrogen bonds are oriented parallel to the helix axis. The α -helical structure found in proteins is amphiphilic in nature. The cyclic imino acid, proline, cannot form α -helices. Proline is considered to be an α -helix breaker. It cannot form hydrogen bond due to the lack of hydrogen on the nitrogen atom. Proteins containing high levels of proline residues will take random aperiodic structures. A β -casein and α_{s1} -casein possess about 17 % and 8.5 % proline of the total amino acid respectively. Proline residues are uniformly distributed, and α -helices are not present in these proteins (Damodaran 2008; Ustunol 2015). These caseins have only primary (random) structures, and hence casein is known as naturally denatured proteins. The β -sheet is an extended structure where C=O and N–H groups are positioned perpendicular to the direction of the polypeptide chain, which then allows for hydrogen bonding between the two segments or β -strands. Two β -strands of the same molecule interact via hydrogen bonds, forming a sheet-like structure known as β -pleated sheet. Depending on the direction of the polypeptide strands, parallel β -sheet or antiparallel β -sheet are formed. The β -sheet structure is generally more stable than the α -helix (Damodaran 2008).

Tertiary Structure

It refers to the spatial arrangement attained when a linear protein chain with secondary structure segments folds further into a compact three-dimensional form. Formation of tertiary structure involves hydrophobic, electrostatic, van der Waals, and hydrogen bonding between various groups of proteins. The folding of the protein into a tertiary structure defines the size and shape of that protein. Folding of proteins brings hydrophobic residues at the interior as well as hydrophilic and charged residues on the surface of the molecule (Damodaran 2008; Ustunol 2015). Presence of hydrophilic and hydrophobic residues in the polypeptide determines the shape of proteins. Globular proteins are abundant in hydrophobic residues while elongated or rod-shaped proteins are abundant in uniformly distributed hydrophilic residues (Nelson and Cox 2013).

Quaternary Structure

It refers to the spatial arrangement of a protein when it contains more than one polypeptide chain, which are also referred to as subunits or oligomers. Formation of quaternary structure is primarily driven by the thermodynamic requirement to bury exposed hydrophobic surfaces of subunits. The quaternary structure is further stabilized by noncovalent interactions such as hydrogen bonding and hydrophobic and electrostatic interactions (Damodaran 2008; Ustunol 2015).

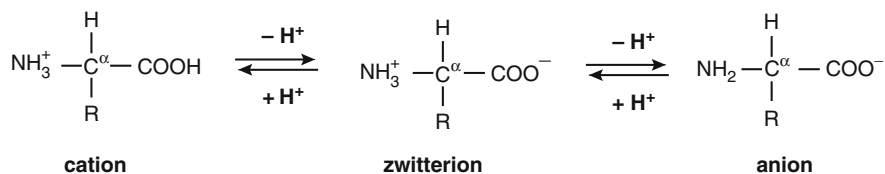


Fig. 5 Dissociation of amino acids

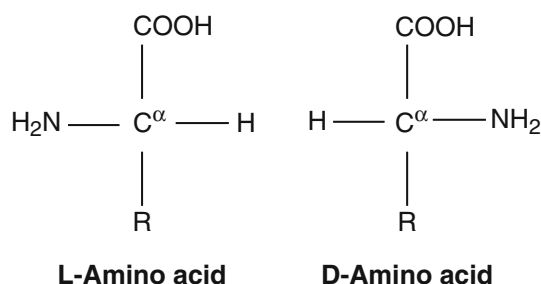


Fig. 6 L- and D- amino acids

The folding of a random polypeptide chain into its three-dimensional structure is a complex process, and various forces are involved. These forces may be grouped into two categories, i.e., (i) intermolecular interactions result from the surrounding solvent (i.e., hydrogen bonding, electrostatic and hydrophobic interactions), and (ii) intramolecular interactions result from forces intrinsic to the protein molecule (i.e., steric, van der Waals) (Damodaran 2008; Ustunol 2015).

Physical Properties

Dissociation/Acid–Base Properties

In aqueous solution amino acids are present, depending on pH, as cations, zwitterions, or anions, which are shown in Fig. 5. In amino acids the acidity of the carboxyl group is higher and the basicity of the amino group lower. Amino acids behave both as acids and bases, i.e., they are *ampholytes*. At around neutral pH, both the α -amino and α -carboxyl groups are ionized, and the molecule is a dipolar or a zwitterion. The pH at which the dipolar ion is electrically neutral is called the isoelectric point (pI) (Damodaran 2008; Belitz et al. 2009).

Configuration and Optical Activity Properties

Amino acids, except for glycine, have at least one chiral center (α -carbon atom) and, hence, are optically active. Isoleucine, threonine, and 4-hydroxyproline have two asymmetric C-atoms, thus each has four isomers (Belitz et al. 2009). The L- and D- amino acids are shown in Fig. 6.

All proteins found in nature contain only L-amino acids. D-amino acids also occur in nature, for example, in a number of peptides of microbial origin. The specific rotation of amino acids in aqueous solution is strongly influenced by pH. It passes through a minimum in the neutral pH range and rises after addition of acids or bases. The optical activity of proteins is due not only to asymmetry of amino acids but also to the chirality resulting from the arrangement of the peptide chain (Belitz et al. 2009).

Solubility

The solubilities of amino acids in water are highly variable. Proline is extremely soluble; hydroxyproline, glycine, and alanine are quite soluble, whereas cystine and tyrosine have low solubilities in water. Addition of acids or bases improves the solubility through salt formation. The extent of solubility of amino acids in protein hydrolysates is different than that observed for the individual components. The solubility in organic solvents is not very good because of the polar characteristics of the amino acids. All amino acids are insoluble in ether. Protein solubility is variable and is influenced by the number of polar and apolar groups and their arrangement along the molecule (Belitz et al. 2009).

UV Absorption

Aromatic amino acids such as phenylalanine, tyrosine, and tryptophan absorb in the UV range of the spectrum with absorption maxima at 200–230 and 250–290 nm. Tyrosine and tryptophan also exhibit fluorescence in the ultraviolet region (250–300 nm). Histidine, cysteine, and methionine absorb between 200 and 210 nm. Absorption readings at 280 nm are used for the determination of proteins and peptides (Damodaran 2008; Belitz et al. 2009).

Sensory Properties

While the taste quality of amino acids does depend on configuration, peptides, except for the sweet dipeptide esters of aspartic acid, are neutral or bitter in taste with no relationship to configuration. The taste intensity is influenced by the hydrophobicity of the side chains. The taste intensity does not appear to be dependent on amino acid sequence. Bitter-tasting peptides can occur in food after proteolytic reactions (Belitz et al. 2009).

Chemical Reactivity of Amino Acids

Amino acids show the usual reactions of both carboxylic acids and amines. Reaction specificity is due to the presence of both carboxyl and amino groups and other reactive groups such as amino, carboxyl, sulfhydryl, phenolic, hydroxyl, thioether (Met), imidazole, and guanyl in free amino acids and proteins. Reactions occurring at 100–220 °C, such as in cooking, frying, and baking, are particularly relevant to food chemistry (Damodaran 2008; Belitz et al. 2009). Various type reactions which involve (i) amino groups (e.g., reductive alkylation, guanidation, arylation, acetylation, succinylation, thiolation, deamination), (ii) carboxyl groups (e.g., esterification, reduction, decarboxylation), (iii) sulfhydryl group (oxidation, blocking), (iv) serine and threonine (e.g., esterification), and (v) methionine (e.g., alkyl halides, β -propiolactone) take place. Some of the reactions can be used to alter the hydrophilic and hydrophobic properties and the functional properties of proteins and peptides as well as quantify amino acids and specific amino acid residues in proteins (Damodaran 2008; Belitz et al. 2009). For further details on various reactions, readers are advised to refer to some books like Damodaran (2008) and Belitz et al. (2009).

Denaturation of Proteins

Protein denaturation refers to changes in the secondary and tertiary structure of the protein. The primary structure (the amino acid sequence) of a protein remains unchanged. The denaturation is a reversible or irreversible change of native conformation without cleavage of covalent bonds. Denaturation does not involve any chemical changes in the protein. Any treatment that cleaves hydrogen bridges or ionic or hydrophobic bonds is responsible for denaturation. This can be accomplished by: changing the temperature, adjusting the pH, increasing the interface area, or adding organic solvents, urea, salts, guanidine hydrochloride, or detergents such as sodium dodecyl sulfate. Denaturation is generally reversible when the peptide chain is stabilized in its unfolded state by the denaturing agent and the native conformation can be reestablished after removal of the agent. Irreversible denaturation occurs when the unfolded peptide

chain is stabilized by interaction with other chains (as occurs, for instance, with egg proteins during boiling). During unfolding reactive groups, such as thiol groups, that were buried or blocked may be exposed. Their participation in the formation of disulfide bonds may also cause an irreversible denaturation (Belitz et al. 2009). Consequences of denaturation of a protein are that it loses its biological and enzymatic activity as well as solubility, gets aggregated, improves digestibility, inactivates antinutritional factors as well as deteriorative enzymes, and improves functional properties of food proteins that are used as ingredients in processed foods (Ustunol 2015).

Functional Properties in Foods

Proteins possess a range of dynamic functional properties and represent a most important class of functional ingredients. Functionality of food proteins refers to the physical and chemical properties that influence the performance of proteins in food systems during processing, storage, preparation, and consumption (Damodaran 2008). Functional properties of protein depend on physicochemical properties like shape, size, composition and sequence of amino acid, distribution of charges, structural levels of proteins, hydrophobicity/hydrophilicity ratio, molecular flexibility, and ability to react/interact with other components (like lipids, sugars, polysaccharides, salts, and minor components). Various functional properties like organoleptic (flavor, odor, color), hydration (gelling, syneresis, swelling, thickening, solubility, wettability, water sorption, viscosity, gelation), kinesthetic (texture, grittiness, mouthfeel, smoothness), rheological/textural (aggregation, cohesiveness, chewiness, elasticity, adhesiveness, network formation, dough formation, texturizability, extrudability), and surface (foaming, emulsification, film formation) are commonly possessed by proteins. Proteins show versatility during processing. They can form networks and structures and provide essential amino acids. Moreover, they interact with other components and improve quality attributes of foods (Kinsella et al. 1994).

Solubility of Proteins

Protein solubility is variable. The solubility of proteins is considered as that proportion of nitrogen in a protein product which is in the soluble state under specific conditions. Proteins can be partly or completely soluble or completely insoluble in water. Protein solubility provides useful information on foams, emulsions, and gels. Protein solubility is influenced by sequence and composition of amino acid, molecular weight, and conformation and content of polar and nonpolar groups in amino acids. Water molecules bind to charged groups, backbone peptide groups, the amide groups of glutamine and asparagines, hydroxyl groups of threonine, serine and tyrosine residues, and nonpolar residues in the proteins. Ionic strength, type of solvent, pH, temperature, and processing conditions affect the solubility of proteins. Solubility is increased if electrostatic repulsion between the molecules is higher than hydrophobic interactions. At the isoelectric point (pI), proteins have a net zero charge, attractive forces predominate, and molecules tend to associate, resulting in insolubility. Above the pI, the net charge is negative and solubility is enhanced. Protein-water interactions increase at pH values higher or lower than the pI because protein carries a positive or negative charge. At low ionic strengths, the solubility rises with increase in ionic strength. Neutral salts have a twofold effect on protein solubility. At low concentrations they increase the solubility ("salting in" effect) by suppressing the electrostatic protein-protein interaction (binding forces). Protein solubility is decreased ("salting out" effect) at higher salt concentrations due to the ion hydration tendency of the salts. Solubility of various proteins decreases variously with temperature and time of heating (Zayas 1997).

Water Holding Capacity of Proteins

Water hydration and holding, water retention, water binding, water imbibing, and water adsorption are some of the terms used interchangeably for interaction of proteins with water. The water holding capacity

(WHC) of foods can be defined as the ability to hold its own and added water during the application of forces, pressing, centrifugation, or heating. WHC plays a major role in the formation of food texture, especially in comminuted meat products and baked doughs. Swelling is an important protein functional property as it is the first step in their solvation and can be defined as the spontaneous uptake of water by a protein matrix. Water retention is a critical factor in protein functionality because it affects the texture, color, and sensory properties of products. Water binding depends on the composition and conformation of the protein molecules. Water interacts with proteins in a number of ways, and significant amounts of water bounded by proteins are retained by hydrogen bonding. Interactions between molecules of water and hydrophilic groups of the protein side chains occur via hydrogen bonding. Structural water is held by hydrogen bonding between polypeptide groups of the proteins. Binding of water to proteins is related to the polar hydrophilic groups, such as imino, amino, carboxyl, hydroxyl, carbonyl, and sulfhydryl groups. The capacity of proteins to retain moisture is affected by the type and number of these polar groups in the protein polypeptide chain. The binding of water is due to the dipolar character of water. Proteins that contain numerous charged amino acids will tend to bind large amounts of water. Water binding of proteins can be predicted from their amino acid composition. The absorbed water is tightly bound to the protein molecules. Water binding of a protein is influenced by protein concentration; pH; ionic strength; temperature; presence of other components of foods such as hydrophilic polysaccharides, lipids, and salts; rate and length of heat treatment; and conditions of storage (Zayas 1997; Belitz et al. 2009).

Foam Formation and Foam Stabilization

Proteins function as foam-forming and foam-stabilizing components in many foods, e.g., baked goods, sweets, desserts, and beer. The most widely used protein foaming agents are egg white, gelatins, casein, other milk proteins, soy proteins, and gluten. Serum albumin foams very well, while egg albumin does not. Foams consist of an aqueous continuous phase and a gaseous (air) dispersed phase. Foam can be defined as a two-phase system consisting of air cells separated by a thin continuous liquid layer called the lamellar phase. Proteins stabilize by forming flexible, cohesive films around the gas bubbles. Protein is adsorbed at the interface via hydrophobic areas followed by partial unfolding. Protein adsorption facilitates the formation of new interfaces by reducing surface tension. The more quickly a protein molecule diffuses into interfaces and the more easily it is denatured there, the more it is able to foam. Foam stability refers to the ability of protein to stabilize foam against gravitational and mechanical stresses. Foams collapse because large gas bubbles grow at the expense of smaller bubbles (disproportionation). The protein films counteract this disproportionation. That is why the stability of a foam depends on the strength of the protein film and its permeability for gases. Film strength depends on the adsorbed amount of protein and the ability of the adsorbed molecules to associate. An ideal foam-forming and foam-stabilizing protein is characterized by a low molecular weight, high surface hydrophobicity, good solubility, a small net charge in terms of the pH of the food, and easy denaturability (Zayas 1997; Belitz et al. 2009).

Gel Formation

A gel is an intermediate phase between a solid and a liquid. Gel is a substantially diluted system that exhibits no steady-state flow. Gelation is a basic process in the processing of various foods, milk gels, comminuted meat and fish products, other meat products, fruit jellies, bread doughs, pie and cake fillings, coagulated egg white, and others. Protein gels may be utilized to simulate the textural properties and mouthfeel of lipids. Gels are formed when partially unfolded proteins develop uncoiled polypeptide segments that interact at specific points to form a three-dimensional cross-linked network. Partial unfolding of proteins with slight changes in secondary structure is required for gelation (Zayas 1997; Belitz et al. 2009).

Emulsifying Effect

Emulsions are disperse systems of one or more immiscible liquids. They are stabilized by emulsifiers – compounds which form interface films and thus prevent the disperse phases from flowing together. The adsorption of a protein at the interface of an oil droplet is thermodynamically favored because the hydrophobic amino acid residues can then escape the hydrogen bridge network of the surrounding water molecules. In addition, contact of the protein with the oil droplet results in the displacement of water molecules from the hydrophobic regions of the oil–water boundary layer. Therefore, the suitability of a protein as an emulsifier depends on the rate at which it diffuses into the interface and on the deformability of its conformation under the influence of interfacial tension (surface denaturation). The diffusion rate depends on the temperature and the molecular weight, which in turn can be influenced by the pH and the ionic strength. A protein with ideal qualities as an emulsifier for an oil-in-water emulsion would have a relatively low molecular weight; a balanced amino acid composition in terms of charged, polar, and nonpolar residues; good water solubility; well-developed surface hydrophobicity; and a relatively stable conformation. The β -casein molecule meets these requirements because of less pronounced secondary structures and no cross-links due to the lack of SH groups (Belitz et al. 2009).

Food Carbohydrates

Chemical Structure and Classification

Carbohydrate in nature has a general elemental composition, namely, $C_x(H_2O)_y$, which signifies molecules containing carbon atoms along with hydrogen and oxygen atoms in the same ratio as they occur in water (Fennema 1996). However, the great majority of natural carbohydrate compounds produced by living organisms do not have this simple empirical formula (Vaclavik and Christian 2014). Rather, most natural carbohydrates are classified as simple sugars (mono- and disaccharides), oligomers (oligosaccharides), and polymers (polysaccharides). However, this chapter begins with a presentation of simple sugars and builds from there to larger and more complex structures.

Monosaccharides

Monosaccharides are simple carbohydrates containing three to eight carbon atoms, but only those with five or six carbon atoms are common. Two of the most important ones in foods are the six-carbon sugars, glucose and fructose, which have the general formula $C_6H_{12}O_6$ (Fennema 1996).

Glucose is categorized as an aldose sugar due to an aldehyde group (CHO) located on the first carbon atom of the chain. It is conventional to number the carbon atoms along the chain so that the carbon atom with the highest number is farthest away from the aldehyde (or functional) group. The aldehyde group therefore is located on carbon one in glucose (and in all other aldose sugars) (Belitz et al. 2009; Vaclavik and Christian 2014).

In nature, two isomers of glucose exist, which are mirror images of each other: D-glucose and L-glucose. D-glucose is the isomer that occurs naturally. In fact, there are two series of aldose sugars, known as the d-series and the l-series, in which each isomer is formed by adding CHOH groups to build the carbon chain, starting from the smallest aldose sugar, which is D- or L-glyceraldehyde (Cho et al. 1999).

As shown in Fig. 7, each H–C–OH group within the chain is asymmetrical (since the H and OH groups are different). The highest-numbered asymmetric carbon atom of each d-series sugar has the same configuration as D-glyceraldehyde, rather than its l-isomer. In glucose, the highest-numbered asymmetric carbon atom is carbon-5, which is termed the reference carbon atom, due to structure configuration determination if the sugar is known as the d series or l series. The hydroxyl group attached to it is called the reference hydroxyl group, which is always on the right side in a d-series sugar (Stick and Williams 2009).

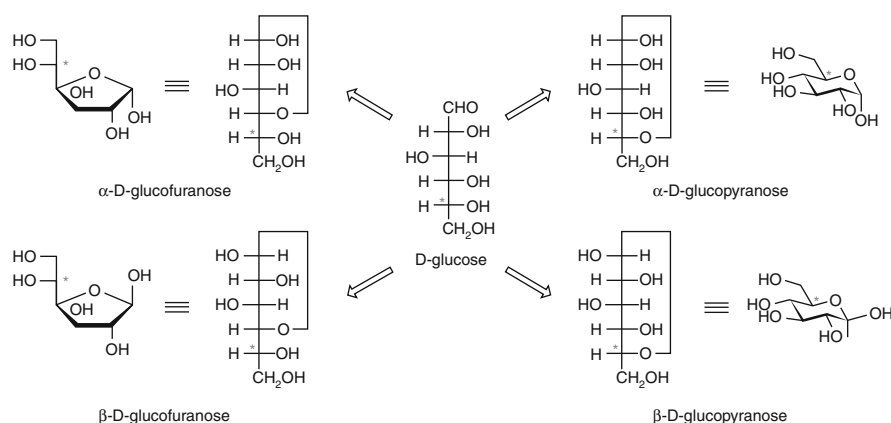


Fig. 7 The main isomers of D-glucose (Fischer projections) (Reprinted (adapted) with permission from Withers (2015)). Anomeric centre (alpha and beta) in CAZypedia, available at URL [http://www.cazypedia.org/index.php/Anomeric_centre_\(alpha_and_beta\)](http://www.cazypedia.org/index.php/Anomeric_centre_(alpha_and_beta))

Oligosaccharides

The reducing group of one monosaccharide can connect to one of the hydroxyl groups on another through glycosidic bond, to form disaccharides. More connections of glycosidic bonds will give rise to trisaccharides, tetrasaccharides, etc., categorized as oligosaccharides and ultimately polysaccharides. The glycosidic bond is the result of the condensation of the hydroxyl of the hemiacetal group of C-1 with the hydroxyl of an alcohol. When a glycosidic linkage is established only between the lactol groups of two monosaccharides, then a nonreducing disaccharide is formed, and when one lactol group and one alcoholic HO group are involved, a reducing disaccharide results (Belitz et al. 2009).

Polysaccharides

When oligosaccharides have more than ten monosaccharides the unit is known as polysaccharide. Polysaccharides consist of monosaccharide units bound to each other by glycosidic linkages. Their complete acidic hydrolysis yields monosaccharides. Partial chemical and enzymatic hydrolysis giving rise to them is important for structural elucidation, the analysis of which elucidates monosaccharide sequences and the positions and types of linkages (Stephen 1995; Whistler and BeMiller 1993).

Polysaccharides (glycans) can have only a type of sugar structural unit (homoglycans) or several types of sugar units (heteroglycans). Polysaccharides may have a linear pattern (as in cellulose and amylose) or a branched fashion (amylopectin, glycogen, guaran) of monosaccharide unit linkage. The frequency of branching sites and the length of side chains can vary greatly (glycogen, guaran). The monosaccharide residue sequence may be periodic, one period containing one or several alternating structural units (cellulose, amylose, or hyaluronic acid), the sequence may contain shorter or longer segments with periodically arranged residues separated by nonperiodic segments (alginate, carrageenans, pectin), or the sequence may be nonperiodic all along the chain (as in the case of carbohydrate components in glycoproteins). The monosaccharide structural unit conformation and the positions and types of linkages in the chain determine the chain conformation of a polysaccharide (Fennema 1996; Stephen 1995).

Physical Properties

Hygroscopicity of sugar in crystallized form is the ability of moisture uptake by sugars. The hygroscopicity varies and depends on the sugar structure, isomers present, and sugar purity (Belitz et al. 2009).

Monosaccharides tend to be soluble in polar solvent; they are also soluble to a small extent in ethanol but not soluble in organic solvents such as benzene, chloroform, and ether. When the crystal sugars cake

together, the solubility will decrease. Sugar solution in high concentrations, e.g. glucose syrup, is used in the baking industry to retain food moisture. The solubility of mono- and oligosaccharides in water is good. However, anomers may differ substantially in their solubility, as exemplified by α - and β -lactose (De Man 1999). The physical and sensory properties of oligosaccharides are covered by monosaccharides since oligosaccharides consist of not more than 10 sugar molecules.

While sugars form true solutions, polysaccharides form colloidal solutions and are, therefore, difficult to purify. The polysaccharides are tasteless and amorphous. Polysaccharides can be classified as (a) homoglycans: single monosaccharides linked together – starch, cellulose, and glycogen; (b) heteroglycans: two or more different constituents – hemicelluloses, mucilages, pectins, and resins; and (c) conjugated compounds made up of saccharides, proteins, or lipids (Stephen 1995; Whistler and BeMiller 1993).

Isolated polysaccharides are utilized to a great extent in food processing, either in native or modified form, such as thickening or gel-setting agents (starch, alginate, pectin, guaran gum), stabilizers for emulsions and dispersions, film-forming, coating substances to protect sensitive food from undesired change, and inert fillers to increase the proportion of indigestible substances in a diet.

Chemical Reactions

Carbohydrates can perform wide chemical reactions with other compounds because besides having hydroxyl groups, some monosaccharides and sugars also have carbonyl groups available for reaction. This section will focus on two most common reactions of carbohydrates in food processing, Maillard and caramelization.

Maillard Reaction

Maillard is categorized as nonenzymatic browning and plays an important role in improving appearance and taste of cooked food, particularly roasting, toasting, and baking food. The compounds that contribute to Maillard reaction were sugars and amino acids in water, which was first reported in 1912 by Louis-Camille Maillard. The chemistry underlying the Maillard reaction is very complex. It encompasses not one reaction pathway but a whole network of various reactions. The original comprehensive reaction scheme of Hodge (Fig. 8) has been developed and elaborated by food technologists ever since, so the understanding of the reaction is advancing steadily.

In the early stage of Maillard, a reducing sugar, like glucose, reacts with a compound possessing a free amino group (of an amino acid or in proteins mainly the ϵ -amino group of lysine but also the α -amino groups of terminal amino acids) resulting in a condensation product N-substituted glycosilamine. This product will lead to form the Amadori rearrangement product (ARP). The subsequent degradation of the Amadori product is dependent on the pH of the system. At pH 7 or below, it undergoes mainly 1,2-enolization with the formation of furfural when pentoses are entangled or hydroxymethylfurfural (HMF) when hexoses are entangled. At pH >7 the degradation of the Amadori compound is thought to involve mainly 2,3-enolization and formation of reductones, such as 4-hydroxy-5-methyl-2,3-dihydrofuran-3-one (HMF^{one}), and a variety of fission products, including acetol, pyruvaldehyde, and diacetyl as well. All these compounds are highly reactive and take part in further reactions. Carbonyl groups will condense with free amino groups, which results in the incorporation of nitrogen into the reaction products. Dicarbonyl compounds will react with amino acids with the formation of aldehydes and α -aminoketones known as the Strecker degradation. Subsequently, in an advanced stage, a range of reactions takes place, including cyclizations, dehydrations, retroaldolizations, rearrangements, isomerizations, and further condensation. In the final stage, melanoidins were formed, which are brown nitrogenous polymers and copolymers (Martins et al. 2001).

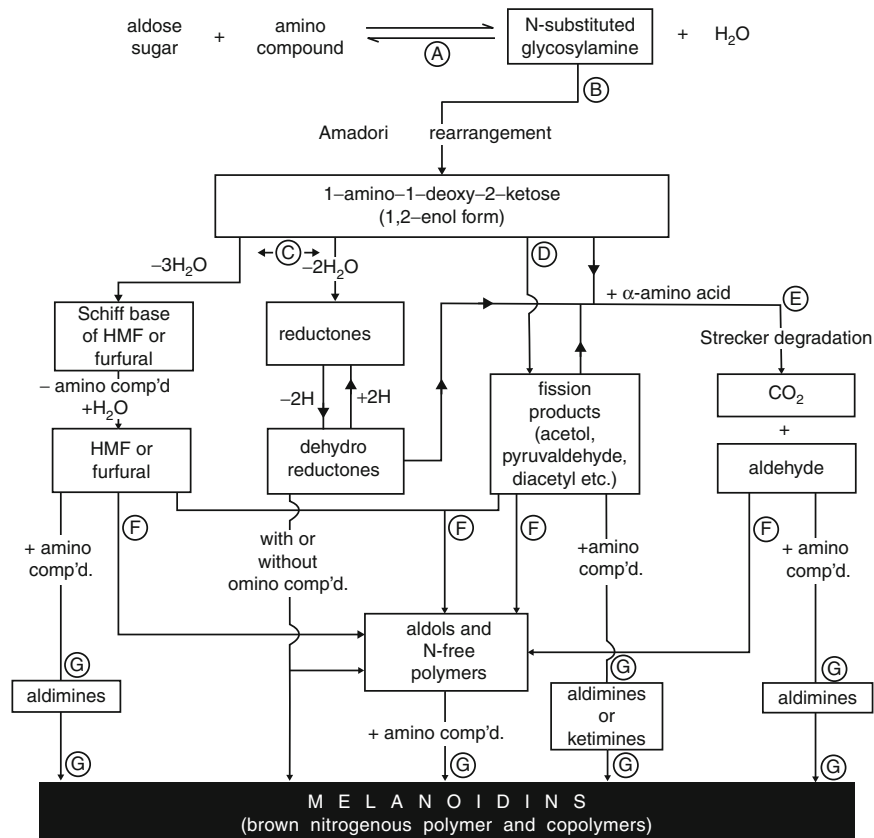


Fig. 8 Maillard reaction (Hodge) scheme (Reprinted (adapted) with permission from Hodge (1953). Chemistry of Browning Reactions in Model Systems. *J Agric Food Chem* 1: 928–943. Copyright (1953) American Chemical Society)

Caramelization

Although it produces the same brown color, caramelization is different from Maillard. In caramelization, sugar decomposition occurs at high temperature and produces brown color; this reaction does not involve proteins and produces different variety of compounds than Maillard, including organic acids, aldehydes, and ketones. Reaction is facilitated by the presence of an acid, base, or salt. Heating causes dehydration of the sugar molecule with introduction of double bonds or formation of anhydro rings. As in Maillard browning, intermediates such as 3-deoxyosones and furans are formed. The unsaturated rings may condense to form useful, conjugated double-bond-containing, brown-colored polymers. Catalysts increase the reaction rate and are used to direct the reaction to specific types of caramel colors, solubilities, and acidities. Caramel served as colorant and flavor in cola, acidic beverages, baked goods, syrups, candies, and dry seasoning (Damodaran et al. 2008).

Functional Properties in Foods

In food, simple forms of carbohydrates have main role as sweeteners in candies and many other food products. The most obvious sensory property of sugars such as glucose, fructose, and sucrose is their sweetness, which varies depending on the specific sugar. Lactose, which is commonly found as dominant sugars in milk, is the least sweet, whereas fructose is the sweetest sugar. In addition, sugars can form solution because they are soluble in water and form syrups when the concentration in water is high. In syrup production, water is evaporated to lead to crystal formation, thus the molecular solutions are formed because of hydrogen-bond interchange. When sugar is placed in water, the water molecules immediately form hydrogen bonds with the sugar molecules, thus hydrating them and removing them from hydrogen

Table 6 Application of polysaccharides in food

Area of application/food	Suitable polysaccharides
Stabilization of emulsions/suspensions in condensed milk and chocolate milk	Carrageenan, algin, pectin, carboxymethylcellulose
Stabilization of emulsions in coffee whiteners, low-fat margarines	Carrageenan
Stabilization of ice cream against ice crystal formation, melting, phase separation; improvement of consistency (smoothness)	Algin, carrageenan, agar, gum arabic, gum tragacanth, xanthan gum, guaran gum, locust bean flour, modified starches, carboxymethylcellulose, methylcellulose
Water binding, improvement of consistency, yield increase of soft cheese, cream cheese, cheese preparations	Carrageenan, agar, gum tragacanth, karaya gum, guaran gum, locust bean flour, algin, carboxymethylcellulose
Thickening and gelation of milk in puddings made with and without heating, creams; improvement of consistency	Pectin, algin, carrageenan, guaran gum, locust bean flour, carboxymethylcellulose, modified starches
Water binding, stabilization of emulsions in meat products (corned beef, sausage)	Agar, karaya gum, guaran gum, locust bean flour
Jellies for meat, fish, and vegetable products	Algin, carrageenan, agar
Stabilization and thickening, prevention of syneresis, freeze-thaw stability of soups, sauces, salad dressing, mayonnaise, ketchup; obtaining “body” in low-fat and low-starch products	Gum tragacanth, algin, karaya gum, xanthan gum, guaran gum, locust bean flour, carboxymethylcellulose, propylene glycol alginate, modified starches
Stabilization of protein foam in beer, whipped cream, meringues, chocolate marshmallows	Algin, carrageenan, agar, gum arabic, karaya gum, xanthan gum
Prevention of starch retrogradation in bread and cakes, water binding in dough	Agar, guaran gum, locust bean flour, carrageenan, xanthan gum
Thickening and gelation of fruit pulp (confiture, jams, jellies, fruit pulp for ice cream and yoghurt)	Pectin, algin
Gelation of jelly candies, jelly beans, glaze, icing, water-dessert jellies	Pectin, algin, carrageenan, agar, gum arabic, modified starches
Sediment stabilization in fruit juices, obtaining “body” in beverage powders	Algin, pectin, propylene glycol alginate, gum arabic, xanthan gum, guaran gum, methylcellulose
Stabilization of powdery aroma emulsions, encapsulation of aroma substances	

Source: Belitz HD, Grosch W, Schieberle P (2009). Food Chemistry. 4th revised and extended edition, Springer-Verlag Berlin Heidelberg

bonds between the sugar crystals. At high concentrations, sugars act as a food preservative which prevents food spoilage by growth of microorganisms. This mechanism is related to reducing the water activity in food to a level below which bacterial growth cannot be supported. Examples of foods preserved in this way include jams and candied fruit (Lee 1983; Vaclavik and Christian 2014).

Mono- and polysaccharides in appropriate concentration or proportion contribute to the viscosity of foods, thus giving mouthfeel to foods. This functionality related the binding capacity of the molecules particularly with water; if they are replaced by a chemically sweetening additive such as aspartame or saccharin, it doesn't affect the consistency of the food. Another substance will be added to give the expected body or mouthfeel to the food, for example, hydrocolloids to the desired consistency without addition of natural sugar (Belitz et al. 2009; Fennema 1996). Table 6 shows the application of polysaccharides in food industry.

The outlined functions of polysaccharides depend on their highly variable properties. They may vary from insoluble (cellulose) to those with good swelling power and solubility at different temperatures of solvent (starch, guaran gum). The solutions may have low viscosities even at very high concentrations

(gum arabic) or may have exceptionally high viscosities even at low concentrations (guaran gum). Some polysaccharides, even at a low concentration, set into a thermoreversible gel (alginates, pectin). While most of the gels melt at elevated temperatures, some cellulose derivatives set into a gel.

Food Enzymes

Classification

The systematic classification and designation of enzymes based on reaction specificity are based on the Nomenclature Committee of the International Union of Biochemistry and Molecular Biology (IUBMB)–adopted rules last amended in 1992. All enzymes can be classified into six major classes (Belitz et al. 2009):

1. Oxidoreductases: catalyzing oxidation-reduction reactions
2. Transferases: transferring a group from one compound to another
3. Hydrolases: catalyzing the hydrolytic cleavage of C-O, C-N, C-O, and some other bonds
4. Lyases: cleaving C-C, C-O, C-N, and other bonds by elimination
5. Isomerases: catalyzing geometric or structural changes within one molecule
6. Ligases or synthetases: catalyzing the joining together of two molecules coupled with the hydrolysis of a pyrophosphate bond in ATP or a similar triphosphate

Some other enzymes without the suffix “-ase” terminology are trypsin, rennin, and ficin.

Each enzyme has a systematic name and number derived from the six classes above. Each class can be subdivided into subclasses which more specifically denote the type of reaction, e.g., by naming the electron donor of an oxidation-reduction reaction or by naming the functional group carried over by a transferase or cleaved by a hydrolase enzyme. Moreover, each subclass is further divided into sub-subclasses. For example, sub-subclasses of oxidoreductases are denoted by naming the acceptor which accepts the electron from its respective donor (Belitz et al. 2009). An example is the enzyme ascorbic acid oxidase. Its systematic name is L-ascorbate: oxygen oxidoreductase, and its systematic number is E.C. 1.1.10.3.3. It is essential to mention the origin of the enzymes, particularly the type of organism and subcellular fraction of origin (cytoplasmic, mitochondrial, or peroxisomal), for example, ascorbate oxidase (E.C. 1.1.10.3.3) from cucumber.

E.C.	1.	10.	3.	3.
Enzyme commission	Oxidoreductase	Subclass of oxidoreductase (donor naming diphenols or ascorbic acid)	Sub-subclass (naming the acceptor: oxygen)	Serial number of the enzyme within the sub-subclass

Catalytic Actions

Catalytic actions of enzymes depend on their properties such as enzyme kinetics and specificity. Enzyme kinetics are affected by enzyme concentration and enzyme inhibition. The concentration of an enzyme in an enzyme-catalyzed reaction is directly proportional to the rate of the reaction (Cornish-Bowden 1995).

Michaelis and Menten (1913) were the first to introduce mathematical analysis of the velocity of enzyme-catalyzed reactions as affected by the substrate concentration (Fig. 9). It is assumed that an intermediate enzyme-substrate complex is formed, which is the important feature of this theory. In addition, the assumption is made that the conversion rate of the enzyme-substrate complex to products

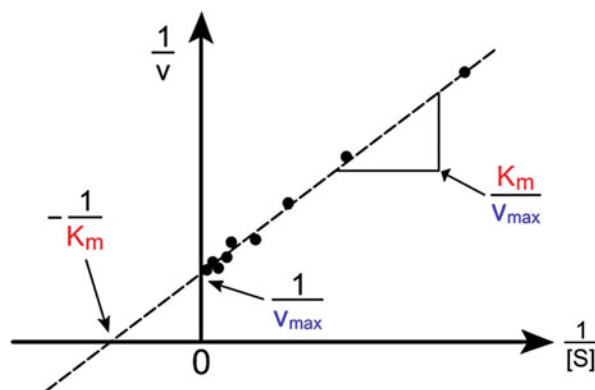


Fig. 9 Linear plots of the Michaelis–Menten equation (Source: Diberri (<http://commons.wikimedia.org/wiki/User:Diberri>))

of the reaction and the enzyme determines the conversion rate of the substrate to the reaction products. This equation is expressed as follows:

$$v = \frac{V [S]}{K_m + [S]} \quad (3)$$

where v = initial velocity, V = maximal velocity, $[S]$ = total concentration of substrate, K_m = Michaelis-Menten constant.

$$\frac{1}{v} = \frac{K_m}{V} \frac{1}{[S]} + \frac{1}{V} \quad (4)$$

If one plots $1/v$ versus $1/[S]$, K_m/V is the slope, and intercept on $1/v$ axis is $1/V$. One gets a straight line rather than a sigmoid curve as in Michaelis-Menten. It is possible to calculate K_m (Fig. 9).

The Michaelis-Menten equation can be analyzed by the effects of enzyme inhibitor on the reaction kinetics. There are three classes of enzyme inhibition: competitive, noncompetitive, and uncompetitive. All of these are reversible. In competitive inhibition, another substance related to the substrate competes with the substrate to bind at the active site of the enzyme. This can inhibit the activity of the enzyme in the formation of the complex with the normal substrate. In noncompetitive inhibition, the inhibitors do not bind at the active site of the enzyme but at another site that frequently alters the enzyme as a result. In uncompetitive inhibition, an inactive enzyme-substrate-inhibitor complex is formed by the combination with the enzyme-substrate complex, which is usually formed. This inhibitor itself does not react with the enzyme to form a complex. In irreversible inhibition, some agents are able to alter permanently and covalently a functional group of certain enzymes that is necessary for catalysis, resulting in irreversible inactivation of the enzyme (Copeland 2000; Cornish-Bowden 1995).

As particular enzyme only fits with very specific substrate, lock-and-key theory has been suggested by Fischer (1894) to describe the relationship. However, the lock needs some adjustment, thus allowing the key to combine with the lock with varying degrees of specificity, from highly specific to only moderately so. Urease, highly specific, will act on urea only and on no other known compound. Some enzymes act on a definite stereoisomeric structure. For example, racemic compounds have been separated by means of enzymes because a specific enzyme was found to act only on the dextro form, leaving the levo form undisturbed. Some enzymes are intermediate in specificity, for instance, invertase, which hydrolyzes sucrose and other β -fructosides. Lipases are enzymes of low specificity, which hydrolyze not only triacylglycerols to fatty acids and glycerol but also simpler esters to alcohols and acids (Pleiss et al. 1998).

Enzymes act only in the specific area due to the molecular size of enzymes, known as the active site. In order for this reaction to proceed asymmetrically, the enzyme and substrate must have a specific spatial relationship. The enzyme-cofactor complex that is catalytically active is known as the holoenzyme. The protein remaining after the removal of the cofactor is known as the apoenzyme, which is, by itself, catalytically inactive. However, the holoenzyme has the ability to combine with the substrate, yielding the final products (Gutfreund 1972).

Rate of Reaction

The rate of enzymatic reaction is referred to as the number of molecules of a substrate decomposed by a molecule of a given enzyme per minute. As an example, catalase decomposes 5,000,000 molecules of H_2O_2 in a minute. If the molecular weight of the enzyme is not known or if the material employed is not pure, it is internationally accepted that one unit of the enzyme material used will catalyze the reaction 1 μmol of substrate per minute under controlled conditions. Frank A. Lee (1983) describes some factors that considerably affect the rate of an enzyme reaction, as the following:

1. Temperature

Enzymes are denatured at high temperatures. Temperature can increase the rate of the reaction when the optimum temperature is selected, whereas if the temperature reaches the denaturation point of enzyme, it can decrease the rate of reaction. The bulk of enzymes are most active around 30^o-40 °C. Denaturation begins around 45 °C, and the activity of the enzyme starts to decline. Some enzymes are more heat stable. The temperature coefficient, Q_{10} , is used as an expression of the change in rate of reaction for a 10 °C change in temperature. The value of Q_{10} for many enzyme-mediated reactions is about 2. The Q_{10} value is determined by dividing the reaction rate at a given temperature plus 10 °C by the reaction rate at that given temperature.

2. Regeneration (Renaturation)

It is reported that the enzyme trypsin can recover its enzyme activity when it is cooled following denaturation by heat (Northrop 1932). Also, it is well known that peroxidase in vegetables which has been inactivated by blanching can recover at least part of its enzyme activity during frozen storage.

3. pH

pH can be used to control the rate of enzymatic reaction since the hydrogen ion concentration of the medium affects significantly the activity of the enzyme. The pH is controlled either to inhibit the enzyme activity or to increase the maximum enzyme activity. The pH can be lowered in fruit products by the addition of such compounds as phosphoric or citric acids.

4. Activators

Enzymes such as pyruvate kinase and enolase require either Mn^{2+} or Mg^{2+} to be activated. Bisulfite ion or cysteine can prevent inactivation of papain, bromelin, and ficin, plant proteolytic enzymes, when exposed to oxygen. These reducing compounds maintain the sulfhydryl groups in the enzyme protein.

5. Active Sites of Enzymes

Great catalytic efficiency depends on precise location of the substrate at the catalytic group of the active site of the enzyme. Of the enzymes that contain only amino acids it must be noted that not all are involved as part of the active site. In certain enzymes large parts of the protein can be removed with no change in the activity of the enzyme.

From the classification scheme given earlier, it is stated that enzymes are classified by the kinds of reactions they catalyze. Those that bring about hydrolysis and those active in oxidation and reduction are

of particular interest in dealing with foods. Various types of enzyme with their specific catalytic actions are given below (Belitz et al. 2009; Lee 1983):

1. Esterases, among others, are able to bring about hydrolysis, or reversibly, synthesis, of esters.
2. Lipase hydrolyzes fats and oils to glycerol and fatty acids. Lipase is also able to hydrolyze the ethyl esters of long-chain fatty acids.
3. Glycosidases, the enzymes effective in the synthesis and breakdown of carbohydrates, belong to the general group of hydrolases.
4. Pectinesterases hydrolyze the methyl ester groups naturally occurring in pectin. They are used in the production of low-ester pectins which, in turn, are used for the manufacture of jellies and jams of low sugar content for which products the ordinary pectin will not produce a gel.
5. Amylases have the ability to hydrolyze starch and glycogen. Three types of amylases are considered: α -amylases, β -amylases, and amyloglucosidases.
6. Phosphatases are able to split phosphoric acid from some types of organic phosphates.
7. Proteinases, otherwise known as proteolytic enzymes, include papain, ficin, trypsin, pepsin, and others and have the ability to cleave the CO-NH (peptide) bond.
8. Peroxidases catalyze reactions in which hydrogen emulsifying the fatty material increases the speed at which this reaction takes place.

Applications in Foods

In vegetable processing, the main purpose of enzyme inactivation is to prevent the quality deterioration of vegetables. Blanching or steaming vegetables before low-temperature storage can prevent their deterioration. Lee (1958) describes the liberation of fatty acids as a result of peroxidases found in unblanched peas during storage at -18°C , whereas the compounds were not formed in the blanched peas. On the other hand, blanching vegetables before drying process can eliminate the development of haylike flavor and aroma. While low water content protects food from spoilage by microbial action, it does not stop deterioration as a result of enzyme activity. An increase in the moisture content can result in an increase in enzyme activity.

In beverage industry, pectic enzymes are used to increase the yields of juice and to extract completely the pigments from fruits. In alcoholic beverages, microorganisms produce some enzymes that convert sugars to alcohol (Whitehurst and Law 2002).

Proteolytic enzymes are used to make meat tender. Wrapping meat with papaya leaves has been applied to tenderize meat since long time ago. These leaves contain proteolytic enzymes. In modern practice, allowing the carcass to hang at a low temperature (4°C) for several weeks improves the activity of tenderness enzyme. Another method of tenderizing is achieved by injecting small amounts of proteolytic enzymes into the animal just prior to slaughter. In dairy processing, cheese production is achieved by curdling milk with rennet, an enzyme produced by calf stomachs (Nagodawithana and Reed 1993; Whitehurst and Law 2002).

Enzymes are frequently isolated from parts of organisms and microorganisms. In enzyme isolation, the richest available source should be used in order to reduce the amount of work necessary to prepare the enzyme. The extraction should not be done in extreme temperature, pH, and ionic strength, which causes enzyme instability and inactivity. The isolation can be done by chromatography with some media such as Sephadex, cross-linked polyacrylamide, and ion-exchange, or another recent technique involves the use of isoelectric focusing (Nagodawithana and Reed 1993).

Enzymes can be advantageous because of the following characteristics. (a) They are efficient catalysts. (b) The reaction can be stopped by applying heat sufficient to destroy the enzymes. (c) Temperature, pH,

and time can be used to control the reactions. (d) Enzyme activity can be standardized. (e) They are nontoxic and can be left in the product unless it is necessary to destroy them (Whitehurst and Law 2002).

Conclusion and Future Directions

Water molecule structure accounts for its special behavior which determines its interaction with other compounds. Since water can determine the shelf life of food because of its interaction with food components, water activity is important. Water activity is the ratio of the moisture content of a food and the relative humidity of the air surrounding. Besides, physical and chemical properties of water affect and control food stability. Stability of food is associated with quality of food. Food instability can lead to food perishability which degrades food quality. A combination between rapid techniques to detect water content in food and novel methods to control physicochemical properties of water will be a focus to improve food quality in the future. Some novel techniques both for entrapping and eliminating water from the system will be interesting research to be developed in the future, such as eliminating water with minimized effect on the physical and chemical changes of food or entrapping water in the gel structure using food-grade biopolymer.

Lipids in food play an important role in food sensory attributes such as texture, flavor, nutrition, and caloric density. Lipids enhance and modify flavor, aerate doughs, contribute flakiness and tenderness, emulsify, transfer heat, and provide satiety. They are composed of a glycerol molecule with one, two, or three fatty acids attached creating mono-, di-, or triglycerides, respectively. Since lipids produce much calories, food scientists and manufacturers will need to modify the physical and chemical properties of food lipids in order to produce healthy foods with high consumer acceptability. In other words, the content of unhealthy lipids (e.g., saturated fats and trans fatty acids) will be reduced or replaced in food without changing much food texture or flavor.

Proteins have a key role in many biological processes as well as foods. Amino acids are required building blocks for protein biosynthesis. A protein containing all of the essential amino acids is considered a complete protein and will have a high biological value. Major animal proteins generally have high biological value as compared to plant proteins due to deficiency in some of the essential amino acids in plant foods. Food proteins are responsible for flavor, color, and texture as well as gel and foam formations. The functional properties of proteins in foods are related to their structural and other physicochemical characteristics. Food proteins can be powerful allergens for some people and have adverse effects in the diet. Food processing can alter the nutritional value and functional properties of proteins.

Food carbohydrates are differentiated by their sugar molecules, chemical structures, and physicochemical properties. Each carbohydrate has its own characteristics for various specific applications in food products. Microstructure manipulation of polymeric assembly of carbohydrates can have great potential in developing novel food. This polymer can be used as food texturing, encapsulant, emulsifier, and gelation agent.

Enzymes are classed as proteins, and the classification of enzymes is based on the reactions they catalyze. Enzymes act by combining with the substrate at a small area of activity which is known as the active site. The efficiency of an enzyme is known as the molecular activity. This is the number of molecules of a substrate which are decomposed by a molecule of a given enzyme in specific time. Enzymes are important in a number of industrial processes involving foods. In future food application, increasing food product quality through enzyme inactivation, isolation, and optimization will still become a main concern for food research and development.

Cross-References

- [Chemical Composition of Fat and Oil Products](#)
- [Nutritional and Toxicological Aspects of the Chemical Changes of Food Components and Nutrients During Heating and Cooking](#)

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