



NETAJI SUBHAS OPEN UNIVERSITY

STUDY MATERIAL

**POST GRADUATE
ZOOLOGY**

**Paper : 7
Group : B**

**Endocrinology, Cell &
Tissue Structure,
Function**



PREFACE

In the curricular structure introduced by this University for students of Post-Graduate degree programme, the opportunity to pursue Post-Graduate course in a subject is introduced by this University is equally available to all learners. Instead of being guided by any presumption about ability level, it would perhaps stand to reason if receptivity of a learner is judged in the course of the learning process. That would be entirely in keeping with the objectives of open education which does not believe in artificial differentiation.

Keeping this in view, study materials of the Post-Graduate level in different subjects are being prepared on the basis of a well laid-out syllabus. The course structure combines the best elements in the approved syllabi of Central and State Universities in respective subjects. It has been so designed as to be upgradable with the addition of new information as well as results of fresh thinking and analysis.

The accepted methodology of distance education has been followed in the preparation of these study materials. Co-operation in every form of experienced scholars is indispensable for a work of this kind. We, therefore, owe an enormous debt of gratitude to everyone whose tireless efforts went into the writing, editing, and devising of a proper lay-out of the materials. Practically speaking, their role amounts to an involvement in 'invisible teaching'. For, whoever makes use of these study materials would virtually derive the benefit of learning under their collective care without each being seen by the other.

The more a learner would seriously pursue these study materials the easier it will be for him or her to reach out to larger horizons of a subject. Care has also been taken to make the language lucid and presentation attractive so that they may be rated as quality self-learning materials. If anything remains still obscure or difficult to follow, arrangements are there to come to terms with them through the counselling sessions regularly available at the network of study centres set up by the University.

Needless to add, a great deal of these efforts are still experimental—in fact, pioneering in certain areas. Naturally, there is every possibility of some lapse or deficiency here and there. However, these do admit of rectification and further improvement in due course. On the whole, therefore, these study materials are expected to evoke wider appreciation the more they receive serious attention of all concerned.

Prof. (Dr.) Subha Sankar Sarkar
Vice-Chancellor

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POST GRADUATE - ZOOLOGY

[1954]

PART II - CHOICE

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Supplement

It is the policy of the Board that the student should be required to take a minimum of two courses from the following list of subjects.

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Group – B

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Group - B

1	1. The structure shown in the figure is subjected to a horizontal load of 10 kN at the top. Determine the reaction forces at the supports.	10-15
2	2. A simply supported beam is subjected to a uniformly distributed load of 2 kN/m. Determine the reaction forces at the supports.	10-15
3	3. A simply supported beam is subjected to a point load of 10 kN at the center. Determine the reaction forces at the supports.	10-15
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5	5. A simply supported beam is subjected to a uniformly distributed load of 2 kN/m. Determine the reaction forces at the supports.	10-15
6	6. A simply supported beam is subjected to a point load of 10 kN at the center. Determine the reaction forces at the supports.	10-15
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8	8. A simply supported beam is subjected to a uniformly distributed load of 2 kN/m. Determine the reaction forces at the supports.	10-15
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11	11. A simply supported beam is subjected to a uniformly distributed load of 2 kN/m. Determine the reaction forces at the supports.	10-15
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13	13. A simply supported beam is subjected to a triangular load. Determine the reaction forces at the supports.	10-15

Unit 1 □ Hormone as Messenger and Their Role in Metabolic Regulation

Structure

1.1 The Endocrine System

1.2 Hormone : a signaling molecule

1.2.1 Steroid Hormone : Mechanism of action

1.2.2 Metabolic regulation

1.2.2.1 Regulation of Adrenal Steroids

1.2.2.2 Regulation of Sex steroids

1.2.3 Protein/peptide and Biogenic Amine Hormones : Mechanism of action

1.2.4 Metabolic regulation of Peptide/Amine hormone

1.1 The Endocrine System

The integration of body functions in humans and other higher organisms is carried out by the nervous system, the immune system, and the endocrine system. The foundations of the **endocrine system** are the hormones and glands. The endocrine system is composed of a number of tissues that secrete their products, **endocrine hormones**, into the circulatory system. Hormone is a chemical substance, usually a peptide, amine or steroid, produced by one tissue and conveyed by the bloodstream throughout the body to affect physiological activity, such as growth or metabolism and maintaining homeostasis. (Fig. 1)

Peptides and proteins include neuropeptides, pituitary and gastrointestinal hormones.

Steroids consist of adrenal and gonadal steroids and vitamin D, which is converted to a hormone. Steroids are lipid soluble (lipophilic).

Source : gland

- No contribution to specificity of target
- Synthesis/secretion

Distribution : blood stream

- Mostly Universal
- Importance of dilution

Non-target organ

- Metabolism

Target cell

- Receptor : source of specificity
- Responsiveness :
 - Number of receptors
 - Downstream pathways
 - Other ligands
 - Metabolism of ligand/receptor
 - All often regulated by ligand

Fig. 1. Regulation of endocrine signaling

Monoamines (modified amino acids) comprise of catecholamines, histamine, serotonin, and melatonin. Catecholamines (dopamine, noradrenaline and adrenaline) are derived from tyrosine and serotonin/melatonin from tryptophan by a series of enzymatic conversions. Monoamines and amino acid hormones are water soluble just as peptides.

The term *Hormone* comes from the Greek *hormao*, means to urge on or excite. The essence of hormone action is that the hormone affects substances other than itself, typically by causing regulation of a metabolic pathway. At their target tissue they act by binding to a specific receptor, itself a protein. For **peptide and protein hormones** this receptor is usually an integral protein of the cell membrane, while for **steroid hormones** it is within the cell. The hormone or hormone receptor complex enters the nucleus (or is formed in the nucleus) and affects DNA transcription, and thus synthesis of specific proteins. As the body's chemical messengers, hormones transfer information and instructions from one set of cells to another. Although many different hormones circulate throughout the bloodstream, each one affects only the cells that are genetically programmed to receive and respond to its message. Hormone levels can be influenced by factors such as stress, infection, and changes in the balance of fluid and minerals in blood. Because hormones are diffused throughout the body they need to be synthesized in enormous amounts. This synthesis usually occurs in specially designed cells. Another necessity is to travel in the blood stream and diffuse in effective

concentrations into tissues. The ability of hormones to diffuse through the extracellular space relates to the local concentration of hormone at target sites, which may rapidly decrease when glandular secretion of the hormone stops. Hormones diffuse throughout extracellular fluid quickly. Hence, hormonal metabolism can occur in specialized organs such as the liver and kidney in a way that can determine their effective concentrations in other tissues.

A gland is a group of cells that produces and secretes chemicals. A gland selects and removes materials from the blood, processes them, and secretes the finished chemical product for use somewhere in the body. Some types of glands release their secretions in specific areas. For instance, exocrine glands, such as the sweat and salivary glands, release secretions in the skin or inside the mouth. Endocrine glands, on the other hand, release more than 20 major hormones directly into the bloodstream where from they can be transported to cells in other parts of the body.

1.2 Hormone : a signaling molecule

Hormone is essentially a chemical messenger that transduce signal from one cell to another. In fact, hormonal signaling represents a special case of the more general process of signaling between cells. Even unicellular organisms like *Saccharomyces cerevisiae* secrete short peptide mating factors acting on receptors of other yeast cells. In a separate but related system, **exocrine** tissues secrete their products into ducts and then outside the body or to the intestinal tract.

The classical definition of hormone has begun to change as it is found that some secreted substances can act close to the cells that secrete them (**paracrine**), or act directly on the cell that secretes them (**autocrine**). Signals from one cell to adjacent, called paracrine signals, often trigger cellular responses that use the same molecular pathways used by hormonal signals. Because paracrine factors and hormones can share signaling mechanisms, hormones can, in some cases, act as paracrine factors. For example, Testosterone, besides being secreted into the blood stream, also acts locally to control spermatogenesis. Insulin like growth factor I (IGF-I), a hormone secreted into the blood stream from the liver and other tissues, also acts as a local paracrine factor to control cell proliferation in most tissues. Again, a single receptor can mediate the actions of a hormone (e.g. parathyroid hormone) and a paracrine factor (e.g. parathyroid hormone related protein). On the other hand, target cells respond similarly to signals that

reach them from the blood stream (hormones) or from the adjacent cell (paracrine factors); the cellular response machinery does not distinguish the sites of origin of signals. The major hormonal signaling programs are G protein-coupled receptors, tyrosine kinase receptors, serine/threonine kinase receptors, ion channels, cytokine receptors and nuclear receptors. (Fig. 2)

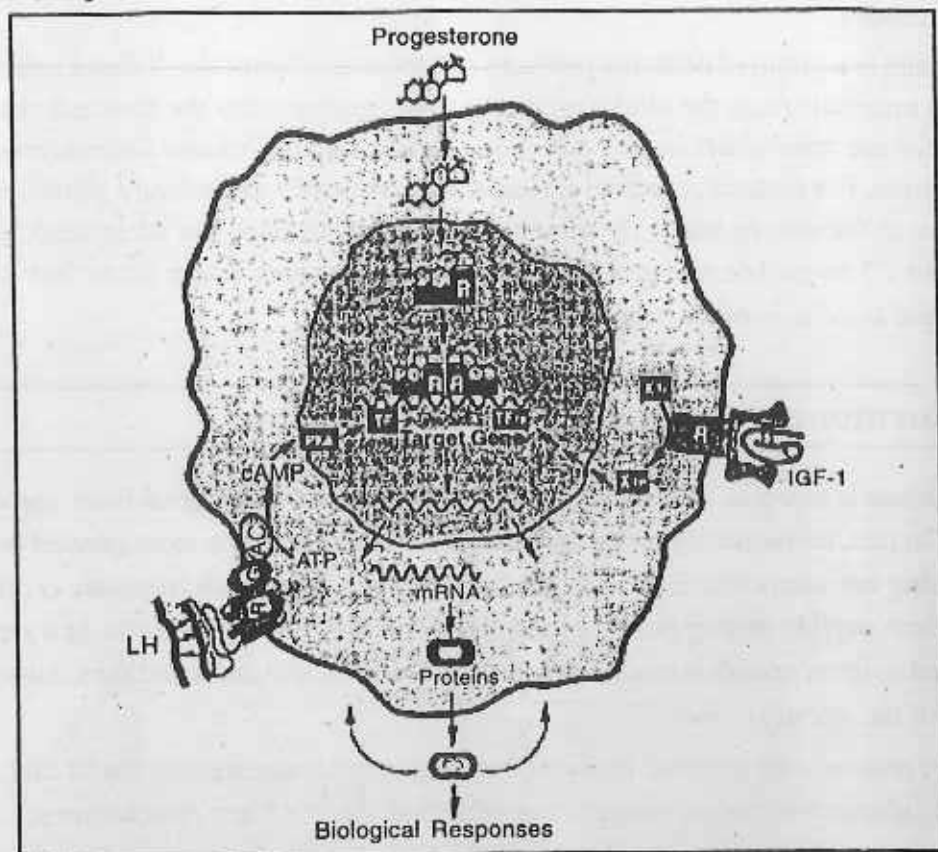


Fig. 2. Hormonal signaling by cell-surface and intracellular receptors. The receptors for the water-soluble polypeptide hormones, LH and IGF-I are integral membrane proteins located at the cell surface. They bind the hormone-utilizing extracellular sequences and transduce a signal by the generation of second messengers, cAMP for the LH receptor, and tyrosine-phosphorylated substrates for the IGF-I receptor. Although effects on gene expression are indicated, direct effects on cellular proteins, for example, ion channels, are also observed. In contrast, the receptor for the lipophilic steroid hormone progesterone resides in the cell nucleus. It binds the hormone and becomes activated and capable of directly modulating target gene transcription. (Tf = transcription factor; R = receptor molecule.) (Reproduced from Mayo K, In Conn PM, Melmed S (eds). *Endocrinology: Basic and Clinical Principles*. To-towa, NJ, Humana Press, 1997, p. 11.)

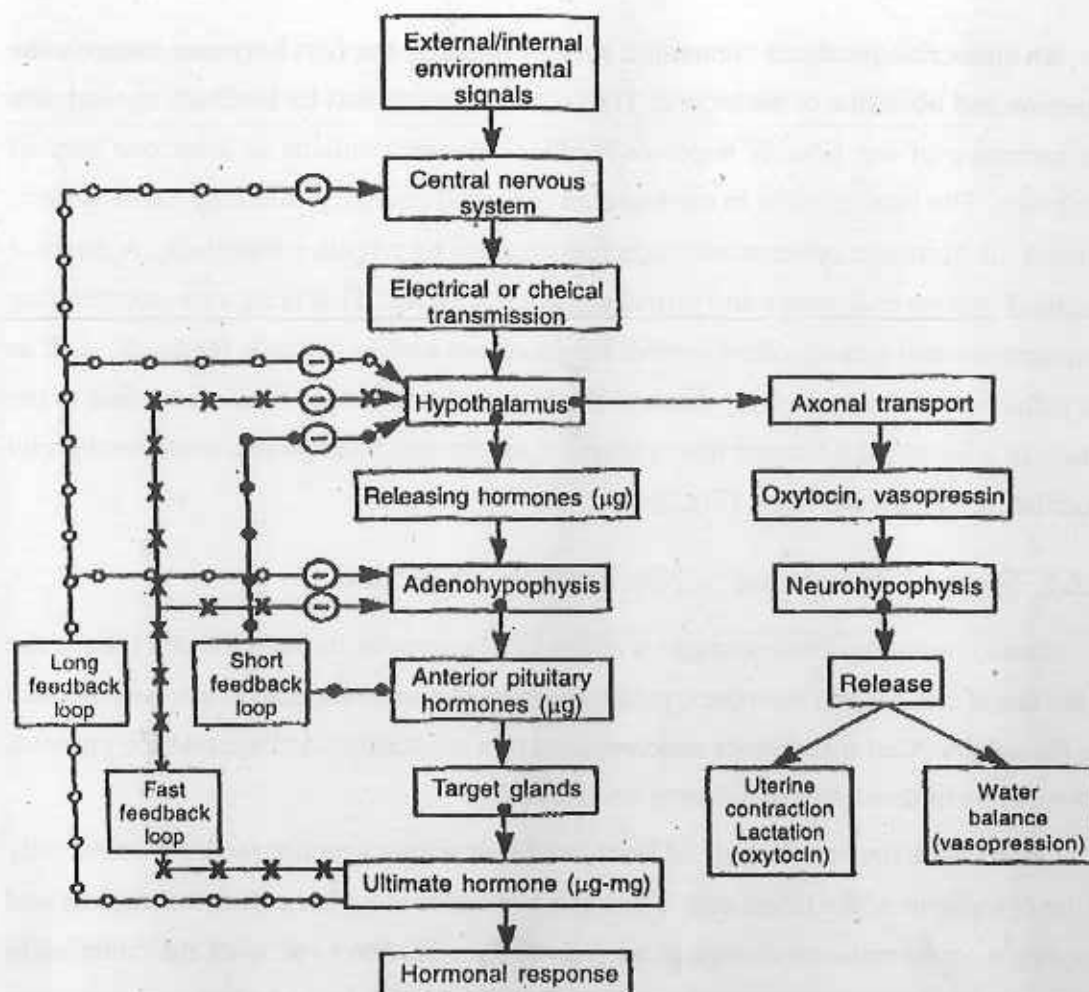


Fig. 3. Peripheral feedback mechanism and a million-fold amplifying cascade of hormonal signals. Environmental signals are transmitted to the central nervous system, which innervates the hypothalamus, which responds by secreting nanogram amounts of a specific hormone. Releasing hormones are transported down a closed portal system, pass the blood-brain barrier at either end through fenestrations, and bind to specific anterior pituitary cell membrane receptors to elicit secretion of micrograms of specific anterior pituitary hormones. These enter the venous circulation through fenestrated local capillaries, bind to specific target gland receptors, trigger release of micrograms to milligrams of daily hormone amounts, and elicit responses by binding to receptors in distal target tissues. Peripheral hormone receptors enable widespread cell signaling by a single initiating environmental signal, thus facilitating intimate homeostatic association with the external environment. Arrows with a black dot at their origin indicate a secretory process. (Reproduced from Normal AW, Litwack G. *Hormones*, 2nd edn. New York, Academic Press, 1997, p 14.)

An endocrine *feedback system* is a system whereby the first hormone controls the secretion and liberation of the second. The second hormone acts by feedback to modulate the secretion of the first. A *negative feedback system* contains at least one step of inhibition. The total effect is to minimise any external change introduced to the system. Almost all hormone systems maintain homeostasis by negative feedback. A *positive feedback system* exaggerates any primary change initiated. This is an auto-accelerating phenomenon and a rarity. *Short feedback systems* use a short distance feedback, such as the influence of the hypophysis back to the hypothalamus. *Auto-feedback* refers to the action of a liberated hormone that is secreted on the cell from where it comes thereby modulating its own secretion. (Fig. 3)

1.2.1 Steroid Hormone : Mechanism of action

Steroid hormones cause changes within a cell by passing through the cell membrane of the target cell. Steroid hormones, unlike non-steroid hormones, can do this because they are fat-soluble. Cell membranes are composed of a phospholipid bilayer which prevents fat-insoluble molecules from diffusing into the cell.

Once inside the cell the steroid hormone binds with a specific receptor found only in the cytoplasm of the target cell. The steroid receptor complex enters the nucleus and initiates a conformational change that involves dimerization to activate the complex to interact with specific regions on cellular DNA referred to as hormone responsive elements (HRE). Once bound to the chromatin, this steroid hormone-receptor complex calls for the production of messenger RNA (mRNA) molecules through a process called transcription. The mRNA molecules are then modified and transported to the cytoplasm. The mRNA molecules code for the production of proteins through a process called translation. These proteins regulate cell function, growth differentiation, etc. So it is the process of expression of proteins that these hormones regulate.

The steroid hormone mechanism of action can be summarized as follows :

1. Steroid hormones pass through the cell membrane of the target cell.
2. The steroid hormone binds with a specific receptor in the cytoplasm.

3. The receptor bound steroid hormone travels into the nucleus and binds to another specific receptor on the chromatin.
4. The steroid hormone-receptor complex calls for the production of messenger RNA (mRNA) molecules, which code for the production of proteins.

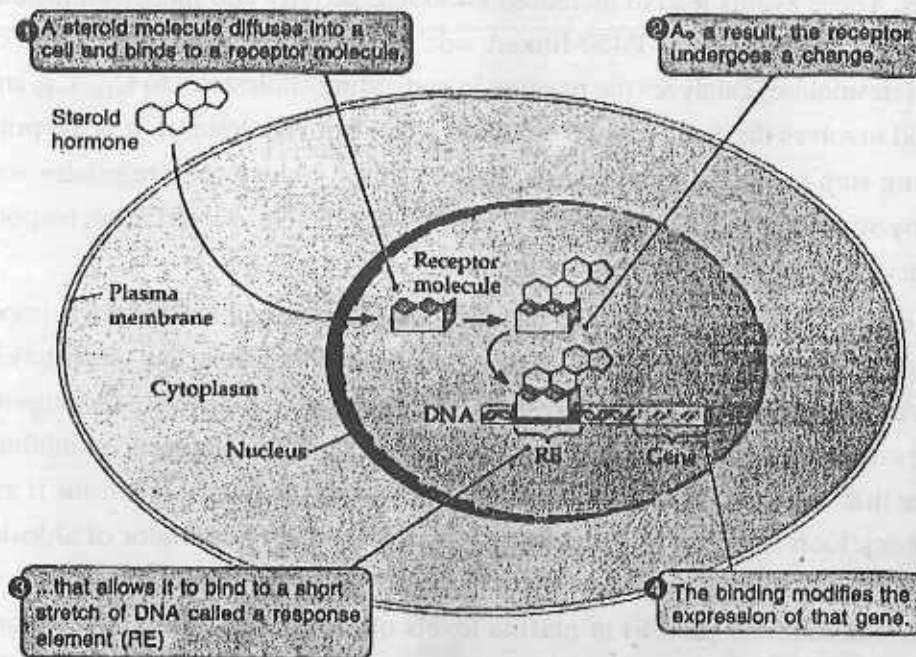


Fig. 4. Steroid hormone : mechanism of action.

1.2.2 Metabolic regulation

1.2.2.1 Regulation of Adrenal Steroids

Adrenocorticotrophic hormone (ACTH) of the anterior pituitary regulates the hormone production of the zona fasciculata and zona reticularis. ACTH receptors in the plasma membrane of the cells of these tissues activate adenylate cyclase with production of the second messenger, cAMP. The effect of ACTH on the production of cortisol is particularly important, because a classic feedback loop is prominent in regulating the circulating levels of corticotropin releasing hormone (CRH), ACTH, and cortisol.

Mineralocorticoid secretion from the zona glomerulosa is stimulated by an entirely different mechanism. Angiotensins II and III, derived from the action of the kidney protease, renin on liver-derived angiotensinogen, stimulate zona glomerulosa cells by binding a plasma membrane receptor coupled to phospholipase C. Thus, angiotensin II and III binding to their receptor leads to the activation of PKC and elevates intracellular Ca^{2+} levels. These events lead to increased P450SCE activity and increased production of aldosterone. P450SCE or P450-linked side chain cleaving enzyme (also called cholesterol desmolase) catalyzes the reaction in converting cholesterol to C_{18} , C_{19} and C_{21} steroids and involves the cleavage of a 6-carbon group from cholesterol. It is the principal rate-limiting step in steroid biosynthesis. In the kidney, aldosterone regulates sodium retention by stimulating gene expression of mRNA for the Na^+/K^+ -ATPase, responsible for the reaccumulation of sodium from the urine.

The interplay between renin from the kidney and plasma angiotensinogen is important in regulating plasma aldosterone levels, sodium and potassium levels, and ultimately blood pressure. Among the drugs most widely used to lower blood pressure are the angiotensin converting enzyme (ACE) inhibitors. These compounds are potent competitive inhibitors of the enzyme that converts angiotensin I to the physiologically active angiotensins II and III. This feedback loop is closed by potassium, which is a potent stimulator of aldosterone secretion. Changes in plasma potassium of as little as 0.1 millimolar concentration can cause wide fluctuations ($\pm 50\%$) in plasma levels of aldosterone. Potassium increases aldosterone secretion by depolarizing the plasma membrane of zona glomerulosa cells and opening a voltage-gated calcium channel, with a resultant increase in cytoplasmic calcium and the stimulation of calcium-dependent processes.

Although fasciculata and reticularis cells have the capability of synthesizing androgens and glucocorticoids respectively, but normally the fasciculate glucocorticoids production. However, when genetic defects occur in the enzyme complexes leading to glucocorticoid production, or in case of tumour, large amount of androgen, dehydroepiandrosterone (DHEA) is produced and lead to hirsutism and other masculinizing changes in secondary sex characteristics.

1.2.2.2 Regulation of Sex steroids

Although many steroids are produced by the testes and the ovaries, the two most important sex hormones are testosterone and estradiol- 17β . These compounds are under

tight biosynthetic control, with short and long negative feedback loops that regulate the secretion of follicle stimulating hormone (FSH) and luteinizing hormone (LH) by the pituitary and gonadotropin releasing hormone (GnRH) by the hypothalamus. Low levels of circulating sex hormone reduce feedback inhibition on GnRH synthesis (the long loop), leading to elevated FSH and LH. The latter peptide hormones bind to gonadal tissue and stimulate P450SCE activity, resulting in sex hormone production via cAMP and PKA mediated pathways. The roles of cAMP and PKA in gonadal tissue are the same as that described for glucocorticoid production in the adrenals, but in this case adenylate cyclase activation is coupled to the binding of LH to plasma membrane receptors.

The biosynthetic pathway to sex hormones in male and female gonadal tissue includes the production of androgens, androstenedione and dehydroepiandrosterone. Testes and ovaries contain an additional enzyme, a 17β -hydroxysteroid dehydrogenase that enables androgens to be converted to testosterone.

In males, LH binds to Leydig cells, stimulating production of the principal Leydig cell hormone, testosterone. Testosterone is secreted to the plasma and also carried to Sertoli cells by androgen binding protein (ABP). In Sertoli cells the $\Delta 4$ double bond of testosterone is reduced, producing dihydrotestosterone. Testosterone and dihydrotestosterone are carried in the plasma, and delivered to target tissue, by a specific gonadal-steroid binding globulin (GBG). In a number of target tissues, testosterone can be converted to dihydrotestosterone (DHT). DHT is the most potent of the male steroid hormones, with an activity that is 10 times that of testosterone. Because of its relatively lower potency, testosterone is sometimes considered to be a prohormone. Testosterone is also produced by Sertoli cells but in these cells it is regulated by FSH, again acting through a cAMP- and PKA-regulatory pathway. In addition, FSH stimulates Sertoli cells to secrete androgen-binding protein (ABP), which transports testosterone and DHT from Leydig cells to sites of spermatogenesis. There, testosterone acts to stimulate protein synthesis and sperm development.

Aromatase activity is also found in granulosa cells, but in these cells the activity is stimulated by FSH. Normally, thecal cell androgens produced in response to LH diffuse to granulosa cells, where granulosa cell aromatase converts these androgens to estrogens. As granulosa cells mature they develop competent large numbers of LH receptors in the plasma membrane and become increasingly responsive to LH, increasing the quantity of estrogen produced from these cells. Granulosa cell estrogens are largely, if

not all, secreted into follicular fluid. Thecal cell estrogens are secreted largely into the circulation, where they are delivered to target tissue by the same globulin (GBG) used to transport testosterone.

1.2.3 Protein/peptide and Biogenic Amine Hormones: Mechanism of action

Such water-soluble hormones (first messengers) bind to hormone receptors on the lipid-rich plasma membrane. Peptide hormone and catecholamine receptors are membrane receptors with a binding domain located extracellularly and an effector domain intracellularly.

The second messengers involved are cyclic adenosine monophosphate (cAMP), cyclic guanosine monophosphate (cGMP), inositol trisphosphate (IP_3), Ca^{2+} , diacylglycerol (DAG) etc. The Ca^{2+} -ion is an important second messenger. The Ca^{2+} -influx to the cytosol

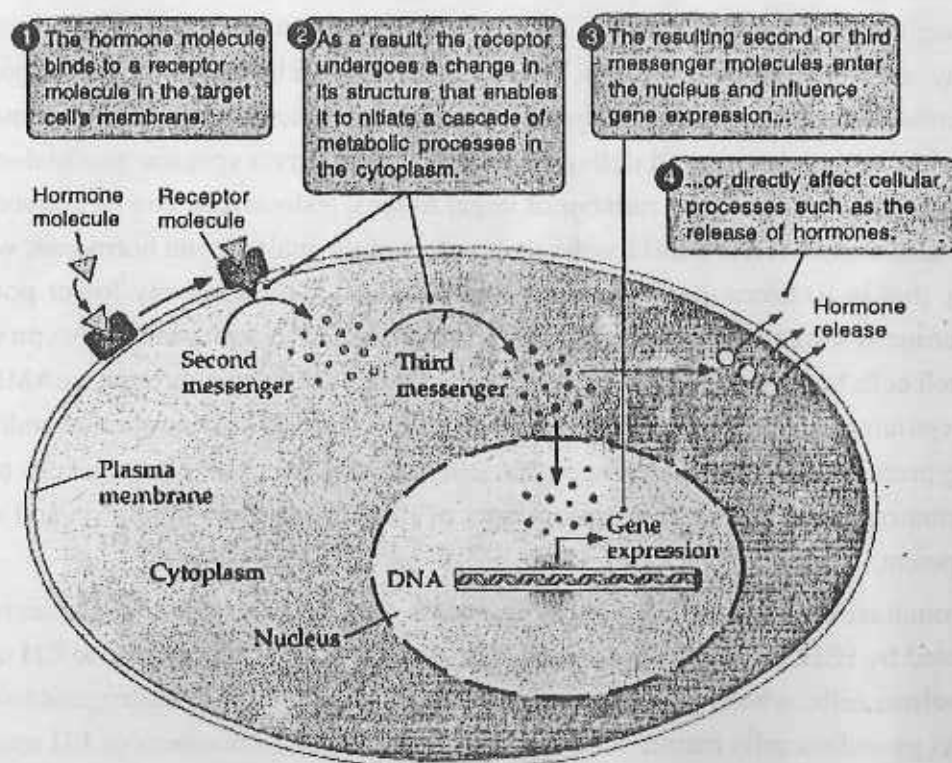


Fig 5. Peptide/Amine hormone : mechanism of action.

is controlled by hormone receptor binding, neural stimuli or modified by other second messengers. Sutherland received Nobel Prize in 1971 for discovering cAMP and demonstration of its role as a second messenger in mediating body functions.

1.2.4 Metabolic regulation of Peptide/Amine hormone

Increased activity of the sympathetic nervous system including release of adrenaline triggers fight-or-flight reactions. In the heart, adrenaline molecules diffuse to the myocardial cells, where they bind to membrane β -receptors. A stimulatory signal is hereby transmitted to an associated enzyme called adenylcyclase. This enzyme catalyses the conversion of ATP to cAMP. The importance of cAMP is that it activates protein kinase A, which, among many other functions, phosphorylates the Ca^{2+} -channel protein. This activation is correlated with an increase in the magnitude of the Ca^{2+} -influx, the force of contraction, and the heart rate.

The parasympathetic system counteracts the sympathetic by slowing the heart rate and decreasing the force of contraction. Acetylcholine is bound to another set of specific membrane receptors located on the heart cell membrane. Acetylcholine reduces the Ca^{2+} -influx that was increased by adrenaline.

Most hormones have a blood concentration of approximately 10^{-10} mol per l. One molecule bound to a cell receptor releases 10 000 times more cAMP in the cell. Hence, cAMP works as an amplifier of the hormone signal. Phosphodiesterase (PDE) destroys cAMP. PDE enhances hydrolysis of cAMP to the inactive 5'-AMP by a highly exergonic process. Inhibitors of the PDE (theophylline and caffeine) act synergistically with hormones that use cAMP as a second messenger. cAMP stimulates catabolic processes such as lipolysis, glycogenolysis (glucagon), gluconeogenesis, and ketogenesis. The cAMP also stimulates amylase liberation in the saliva by the parotid gland, the HCl secretion by the parietal cells, the insulin release by the β -cells in pancreas, and the increased ion permeability of many cell membranes. When the glucose concentration increases in the arterial blood and close to the β -cells of the pancreatic islets of Langerhans, it triggers an increase in Ca^{2+} -influx to the cell. The initial surge in insulin secretion is caused by calmodulin-dependent protein kinases.

The high cytosolic $[\text{Ca}^{2+}]$ activates the membrane phospholipase A_2 and C. Phospholipase A_2 releases arachidonic acid (AA) which stimulates insulin secretion. Phospholipase C catalyses the formation of IP_3 and DAG. The IP_3 releases more Ca^{2+} from the

endoplasmic reticulum, and DAG activates protein kinase C. The decrease in insulin secretion after the initial surge and its subsequent increase can be explained by the action of protein kinase C.

Initially, the active protein kinase C stimulates the Ca^{2+} -pump in the plasma membrane, reduces cytosolic $[\text{Ca}^{2+}]$ and thus reduces the initial calmodulin-dependent insulin secretion. Later, protein kinase C stimulates the formation of cAMP and amplifies the induction of calmodulin-dependent protein kinase thereby causing a gradual increase in insulin secretion. Prolonged glucose stimulation probably leads to down-regulation of protein kinase C. An abnormally prolonged glucose stimulation may render b-cells glucose blind and thus spoil their function.

Insulin secretion is not only stimulated by glucose, but also potentated by acetylcholine via phospholipase C and by glucagon via activation of adenylcyclase. b-Agonists stimulate b-receptors on the glucagon producing a-cells, whereas a-agonists inhibit insulin secretion via α_2 -receptors on the b-cells. Acetylcholine and glucagon react by activating protein kinase C and cAMP dependent protein kinase A, respectively. Both mechanisms potentate the Ca^{2+} -triggered insulin secretion.

Transcription in the cell nucleus produces a precursor messenger RNA molecule complementary to part of a DNA. The precursor is processed into messenger RNA and transported through the nuclear membrane into the cytoplasm. Translation produces big precursor molecules (pre-pro-hormones). Precursors have a signal peptide that contains processing information to ensure that the protein enters the rough endoplasmic reticulum. Here enzymes split the precursor into a signal molecule and a prohormone. Finally, peptide hormones undergo post-translational processing (for eg, thyroid stimulating hormone, TSH, and gonadotropins are glycosylated; insulin forms a zinc-complex). The hormones reach the Golgi complex, where they are packed into secretory granules that migrate to the cell surface.

Roger Guillemin synthesized brain peptides that regulate the pituitary secretion in vitro. He received the Nobel Prize in 1977.

Unit 2 □ Thyroid Biosynthesis and Function

Structure

2.1 Thyroid Hormone Synthesis

2.1.2 Iodine availability and transport

2.1.3 Uptake of iodine by the thyroid

2.1.4 Thyroperoxidase (TPO)

2.1.5 H_2O_2 Generating system

2.1.6 Thyroglobulin (Tg)

2.1.7 Thyroglobulin Iodination and Hormone Synthesis

2.1.8 Thyroglobulin Endocytosis

2.1.9 Proteolytic Cleavage of Thyroglobulin

2.1.10. Control of Hormone Synthesis

2.2 Thyroid : Function

2.2.1 Thyroid Hormone Secretion

2.2.2 Cellular Action of Thyroid Hormone

2.1 Thyroid Hormone Synthesis

Thyroid hormone synthesis requires the uptake of iodide by active transport, thyroglobulin biosynthesis, oxidation and binding of iodide to thyroglobulin, and within the matrix of this protein, oxidative coupling of two iodotyrosines into iodothyronines. All these steps are regulated by the cascades of enzymes.

The thyroid contains two hormones, L-thyroxine (tetraiodothyronine, T_4) and L-triiodothyronine (T_3) (Fig. 1). Iodine is an indispensable component of the thyroid hormones, comprising 65% of T_4 's weight, and 58% of T_3 's. The thyroid hormones are the only iodine-containing compounds with established physiologic significance in vertebrates.

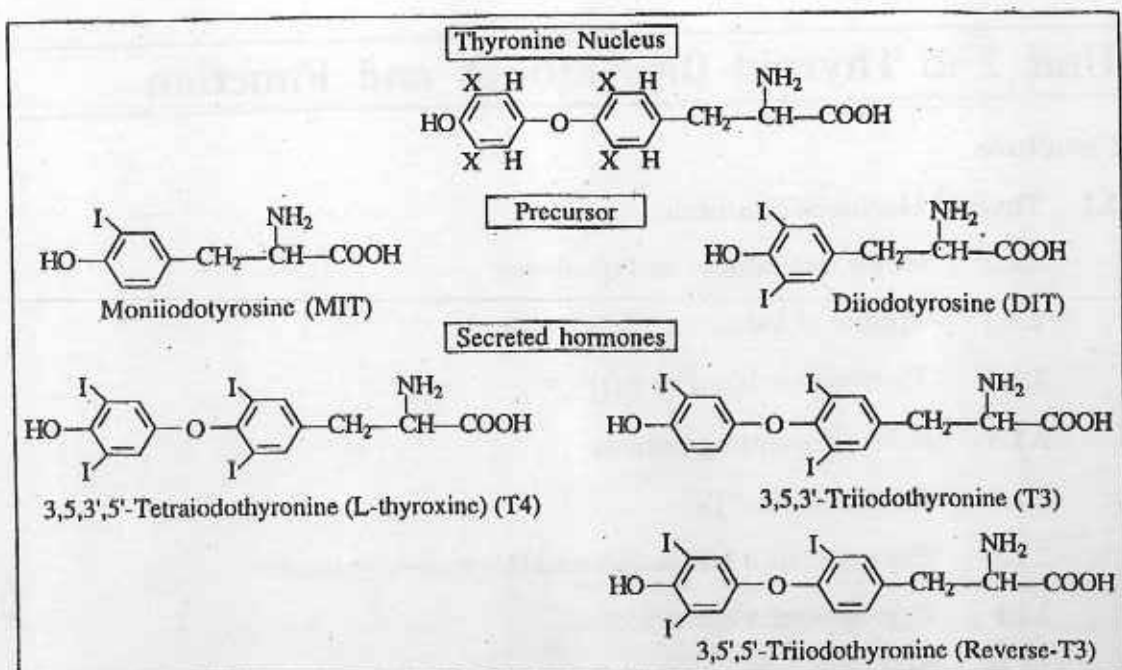


Fig. 1. Structural formula of thyroid hormones and precursor compounds.

The term "iodine" occasionally causes confusion because it may refer to the iodine atom itself but also to molecular iodine (I_2). In this chapter "iodine" refers to the element in general, and "molecular iodine" refers to I_2 . "Iodide" refers specifically to the ion I^- .

Ingested iodine is absorbed through the small intestine and transported in the plasma to the thyroid, where it is concentrated, oxidized, and then incorporated into thyroglobulin (Tg) to form MIT and DIT and later T_4 and T_3 (Fig. 2). After a variable period of storage in thyroid follicles, Tg is subjected to proteolysis and the released hormones are secreted into the circulation, where specific binding proteins carry them to target tissues.

This chapter discusses these broad steps as :

- iodine availability and absorption;
- uptake of iodide by the thyroid;
- oxidation of iodide, which involves the thyroperoxidase (TPO), H_2O_2 , and H_2O_2 generation;
- Tg, whose iodination leads to hormone formation;
- storage of thyroid hormones in a Tg-bound form;
- Tg breakdown and hormone release;
- control of synthesis and secretion by iodine supply and TSH; and
- effects of drugs and other external agents on synthesis and secretion of thyroid hormones.

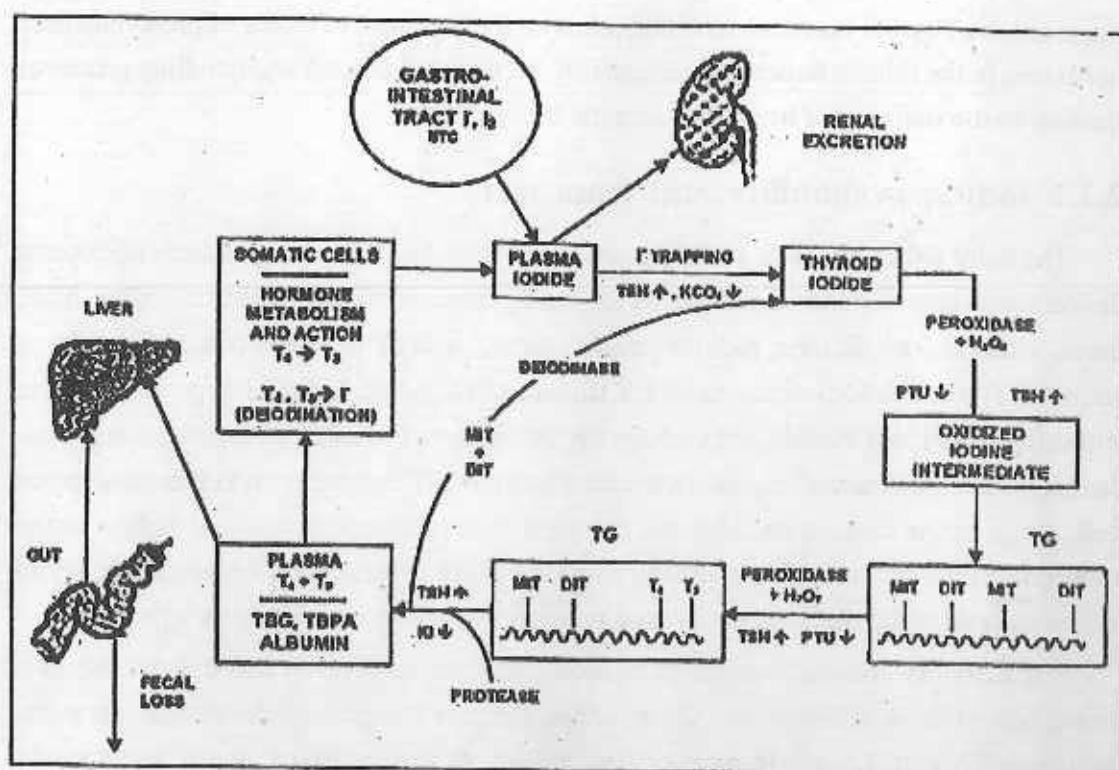


Fig. 2. The iodide cycle. Ingested iodide is trapped in the thyroid, oxidized, and bound to tyrosine to form iodotyrosines in thyroglobulin (TG); coupling of iodotyrosyl residues forms T_4 and T_3 . Hormone secreted by the gland is transported in serum. Some T_4 is deiodinated to T_3 . The hormone exerts its metabolic effect on the cell and is ultimately deiodinated; the iodide is reused or excreted by the kidney. A second cycle goes on inside the thyroid gland, with deiodination of iodotyrosines generating iodide, some of which is reused without leaving the thyroid.

The production of thyroid hormones is based on the organization of thyroid epithelial cells in functional units, the thyroid follicles. A single layer of polarized cells (Fig. 2-4A.) forms the envelope of a spherical structure with an internal compartment, the follicle lumen. Thyroid hormone synthesis is dependent on the cell polarity that conditions the targeting of specific membrane protein, either on the external side of the follicle (facing the blood capillaries) or on the internal side (at the cell-lumen boundary) and on the tightness of the follicle lumen that allows the gathering of substrates and the storage of products of

the reactions. Thyroid hormone secretion relies on the existence of stores of pre-synthesized hormones in the follicle lumen and cell polarity-dependent transport and handling processes leading to the delivery of hormones into the blood stream.

2.1.2 Iodine availability and transport

The daily iodine intake of adult humans varies from less than 10 μg in areas of extreme deficiency to several hundred milligrams for some persons receiving medicinal iodine. Milk, meat, vitamins, medicines, radiocontrast material, and skin antiseptics are important sources. Too much iodine increases the incidence of iodine-induced hyperthyroidism, autoimmune thyroid disease and perhaps thyroid cancer. Deficiency causes mental retardation, goiter, hypothyroidism, and other manifestations. The global push to eliminate iodine deficiency in the current decades has put both excess and deficiency of iodine in the spotlight. Some countries have already moved rapidly from severe iodine deficiency to iodine excess, while others are only now recognizing iodine deficiency as a problem.

Most dietary iodine is reduced to iodide before absorption throughout the gut, principally in the small intestine. Absorption is virtually complete. Iodinated amino acids, including T_4 and T_3 , are transported intact across the intestinal wall. Short-chain iodopeptides may also be absorbed without cleavage of peptide bonds. Absorbed iodide has a volume of distribution numerically equal to about 38% of body weight (in kilograms), mostly extracellular, but small amounts are found in red blood cells and bones. Milk is the principal source of virtually all the newborn's iodine, so milk substitutes need to provide adequate amounts.

2.1.3 Uptake of iodine by the thyroid

Thyroid cells extract and concentrate iodide from plasma. The normal thyroid maintains a concentration of free iodide 20 to 50 times higher than that of plasma, depending on the amount of available iodine and the activity of the gland. This concentration gradient may be more than 100:1 in the hyperactive thyroid of patients with **Graves' disease**. The thyroid can also concentrate other ions, including bromide, astatide, pertechnetate, rhenate, and chlorate, but not fluoride. Iodide transport is energy-dependent and requires O_2 . Ouabain, digitoxin, and other cardiac glycosides block iodide transport in vitro. Iodide uptake by thyroid cells is dependent on membrane ATPase.

The protein responsible for iodide transport, called sodium iodide symporter or NIS, is located at the basolateral plasma membrane of thyrocytes (Fig. 3.). NIS-mediated I^-

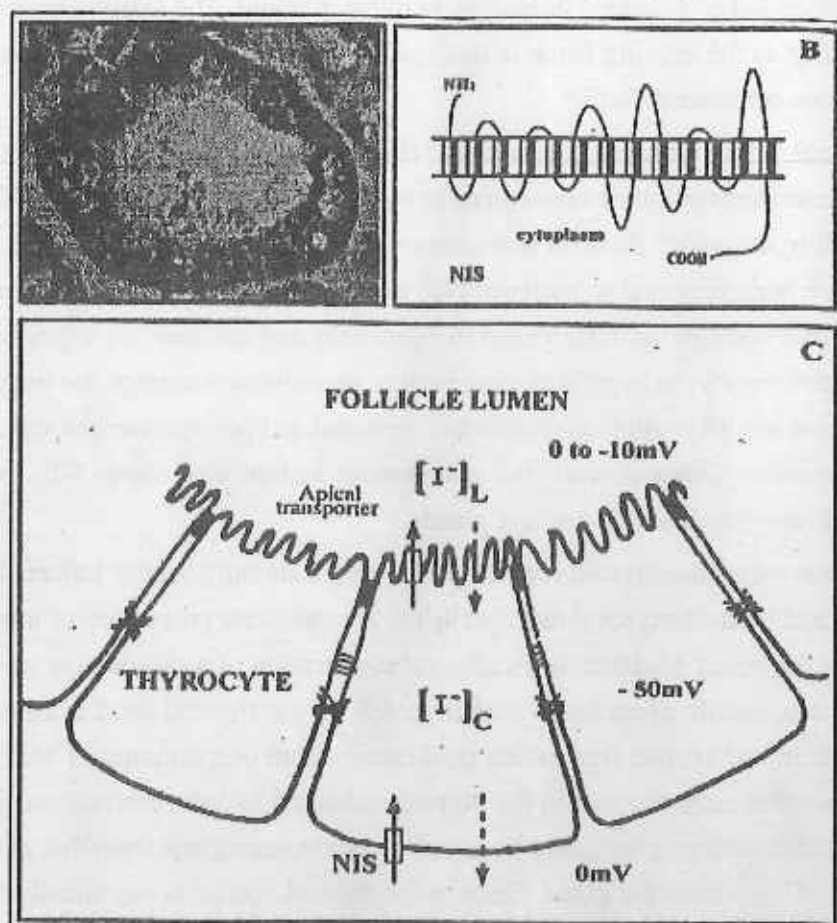


Fig. 3. NIS-mediated transport of iodide. A, immunolocalization of the human NIS protein at the basolateral plasma membrane of thyrocytes in their typical follicle organization. B, schematic representation of the membrane topology of the NIS polypeptide chain deduced from secondary structure prediction analyses. C, transport of iodide from the extracellular fluid (or plasma) to the thyroid follicle lumen. The uptake of iodide at the basolateral plasma membrane of thyrocytes must be active; it operates against an electrical gradient (0 to -50 mV) and a concentration gradient, $[I^-]_C$ being higher than extracellular $[I^-]$. The transport of iodide from the cytoplasm to the follicle lumen should be a passive process, the electrical and concentration gradients being favorable.

accumulation is a Na^+ -dependent active transport process that couples the energy released by the inward translocation of Na^+ down to its electrochemical gradient to the simultaneous inward translocation of I^- against its electrochemical gradient. The maintenance of the Na^+ gradient acting as the driving force is insured by $\text{Na}^+-\text{K}^+-\text{ATPase}$. NIS belongs to the sodium/glucose cotransport family.

Functional studies clearly show that NIS is responsible for most of the events previously described for iodide concentration by the thyroid. TSH stimulates NIS expression and iodide transport. Several mutations in the NIS gene causing defective iodide transport have been reported in humans. NIS expression is increased in Grave's disease and hyperactive nodules, and decreased in adenomas and carcinomas appearing as cold nodules at scintigraphy. In hypofunctioning benign or malignant tumors, the impairment of iodide transport would result from both transcriptional and post-transcriptional alterations of NIS expression. Other tissues that concentrate iodide also show NIS expression, including salivary glands and mammary glands.

Iodide that enters the thyroid remains in the free state only briefly before it is further metabolized and bound to tyrosyl residues in Tg. A significant proportion of intrathyroidal iodide is free for about 10-20 minutes after administration of a radioactive tracer, but in the steady state, iodide contributes less than 1% of the thyroid total iodine. A major fraction of the intrathyroidal free iodide pool comes from deiodination of MIT and DIT; this iodide is either recycled within the thyroid or leaked into the circulation. Some data suggest that iodide entering the gland by active transport segregates from that generated by deiodination of Tg within the gland. Once in the thyroid, iodide is organically bound at a rate of 50 to 100% of the pool each minute. The proportion of an iodide load that is bound varies little, despite wide shifts in daily intake. In contrast, NIS activity is sensitive to both iodine availability and TSH stimulation, and transport rather than intrathyroidal binding is the controlling factor in making iodide available for hormonogenesis.

2.1.4 Thyroperoxidase (TPO)

After concentrating iodide, the thyroid rapidly oxidizes it and binds it to tyrosyl residues in Tg, followed by coupling of iodotyrosines to form T_4 and T_3 . The process requires the presence of iodide, a peroxidase (TPO), a supply of H_2O_2 , and an iodine acceptor protein (Tg).

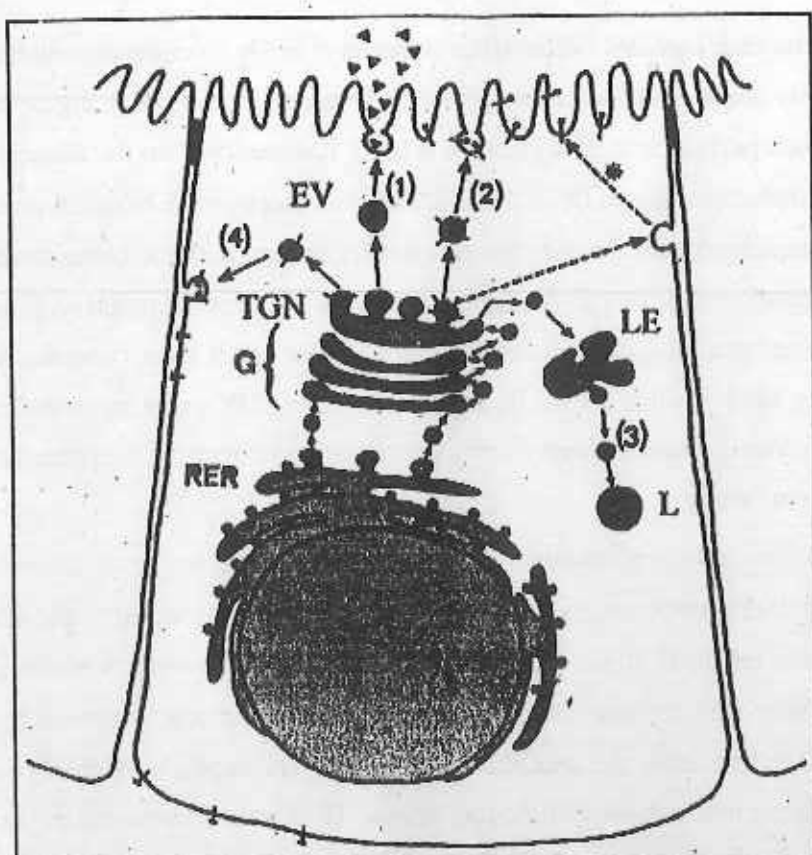


Fig. 4. A polarized thyroid epithelial cell synthesizing soluble proteins, Tg (\blacktriangle) and lysosomal enzymes (X) and membrane proteins, NIS (\perp) and TPO (\circ). The polypeptide chain(s) generated by RER membrane-bound polysomes, enter the lumen of RER for the former and remain inserted into the RER membrane for the latter. Inside the lumen of RER, newly-synthesized proteins undergo core glycosylation and by interacting with chaperones acquire their conformation. Proteins are then transported to the Golgi apparatus (G), where terminal glycosylation and other post-translational reactions take place. In the Trans-Golgi network (TGN), mature proteins undergo sorting processes and are packed into transport vesicles. The vesicles carrying soluble proteins (inside the vesicle) and membrane proteins (as integral vesicle membrane protein) deliver them at the appropriate plasma membrane domain: the apical domain (1) and (2) or the basolateral domain (4). Vesicles carrying lysosomal enzymes (3) conveyed their content to prelysosomes or late endosomes (LE) and lysosomes (L). Apical plasma membrane proteins may reach their final destination by an alternative route involving a transient transfer to and then a retrieval and transport (\hookleftarrow) from the basolateral membrane domain to the apical domain.

Thyroperoxidase oxidizes iodide in the presence of H_2O_2 . In crude thyroid homogenates, enzyme activity is associated to cell membranes. It can be solubilized using detergents such as deoxycholate or digitonin. The enzyme activity is dependent on the association with a heme, the ferriprotoporphyrin IX or a closely related porphyrin. Chemical removal of the prosthetic group inactivates the enzyme, and recombination with the heme protein restores activity. The apoprotein from human thyroid is not always fully saturated with its prosthetic group. Some congenitally goitrous children have poor peroxidase function because the apoprotein has weak binding for the heme group. Human TPO, which has 46% nucleotide and 44% amino acid sequence homology with human myeloperoxidase, clearly belongs to the same protein family.

TPO synthesized on polysomes is inserted in the membrane of the endoplasmic reticulum and undergoes core glycosylation. TPO is then transported to the Golgi where it is subjected to terminal glycosylation and packaged into transport vesicles along with Tg (Fig. 4). These vesicles fuse with the apical plasma membrane in a process stimulated by TSH. TPO delivered at the apical pole of thyrocytes exposes its catalytic site with the attached heme in the thyroid follicular lumen. TPO activity is restricted to the apical membrane, but most of the thyroid TPO is intracellular, being located in the perinuclear part of the endoplasmic reticulum. Most of this intracellular protein is incompletely or improperly folded; it contains only high mannose-type carbohydrate units, while the membrane TPO has complex carbohydrate units. Glycosylation is essential for enzymatic activity. Chronic TSH stimulation increases the amount of TPO and its targeting at the apical membrane.

2.1.5 H_2O_2 Generating system

By definition, a peroxidase requires H_2O_2 for its oxidative function. H_2O_2 is produced at the apical plasma membrane by an enzyme that requires both calcium and NADPH. There are two members of the NADPH oxidase family, viz. ThOX1 and ThOX2. The current model assigns seven transmembrane domains to ThOX1 and ThOX2 (Fig. 5B).

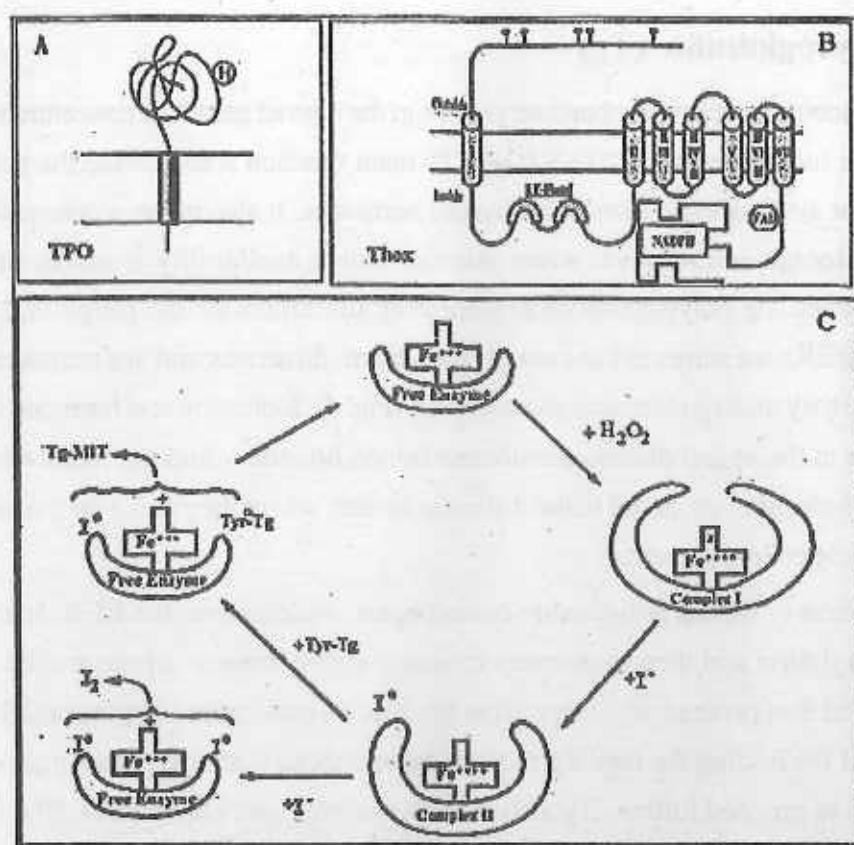


Fig. 5. Schematic representation of the membrane topology of Thyroperoxidase, TPO (A) and NADPH thyroid oxidase, ThOX (B) at the apical plasma membrane of thyrocytes. C, hypothetical reaction scheme for TPO. H₂O₂ is presumed to oxidize the free enzyme with a loss of two electrons leading to the formation of complex I. Iodide binds to complex I, is oxidized and form complex II, which then reacts with a tyrosyl residue of Tg, Tyr-Tg. The newly-formed I⁰ and Tyr⁰-Tg free radicals interact to form MIT-Tg and the enzyme returns to its free state. I₂ may be generated from two oxidized iodine atoms.

The two proteins are glycoproteins, their apparent molecular mass ranges from 170-180 kDa. Immunolabeling experiments revealed the presence of ThOX inside the cells and at the apical plasma membrane. ThOX proteins are components of the H₂O₂ generating system, but additional polypeptide chains are required to get the complete thyroid H₂O₂ generating system.

2.1.6 Thyroglobulin (Tg)

Thyroglobulin is the most abundant protein in the thyroid gland; its concentration within the follicular lumen can reach 200-300 g/L. Its main function is to provide the polypeptide backbone for synthesis and storage of thyroid hormones. It also offers a convenient depot for iodine storage and retrieval when external iodine availability is scarce or uneven. Neosynthesised Tg polypeptide chains entering the lumen of the rough endoplasmic reticulum (RER) are subjected to core glycosylation, dimerises and are transferred to the Golgi where they undergo terminal glycosylation (Fig. 4). Iodination and hormone formation of Tg occur at the apical plasma membrane-lumen boundary and the mature hormone-containing molecules are stored in the follicular lumen, where they make up the bulk of the thyroid follicle colloid content.

Maturation of the Tg polypeptide chain begins while still on the RER. It undergoes core glycosylation and then monomers fold into stable dimers. Arvan and co-workers have mapped this process and emphasize the role of molecular chaperones. The latter are essential for folding the new Tg molecules, and those that are folded improperly are not allowed to proceed further. Tg also contains sulphur and phosphorus. The former is present in the chondroitin sulfate and the complex carbohydrate units, although its form and role are not known. Several studies have reported presence of phosphate in Tg, up to 12 mol. per mol Tg. Of this, about half is in the complex carbohydrate units, the remainder is present as phosphoserine and phosphotyrosine. This may relate to protein kinase A activity.

2.1.7. Thyroglobulin Iodination and Hormone Synthesis

The step preliminary to thyroid hormone formation is the attachment of iodine to tyrosyl residues in Tg to produce MIT and DIT. This process occurs at the apical plasma membrane-follicle lumen boundary and involves H_2O_2 , iodide, TPO, and glycosylated Tg. All rendezvous occur at the apical membrane to achieve Tg iodination (Fig. 6.).

First, iodide must be oxidized to an iodinating form (iodine). One scheme proposes that oxidation produces free radicals of iodine and tyrosine, while both are bound to TPO to form MIT which then separates from the enzyme (Fig. 5C). Further reaction between

free radicals of iodine and MIT gives DIT. Experimental studies by Taurog and others suggest that the TPO reduction occurs directly in a two electron reaction.

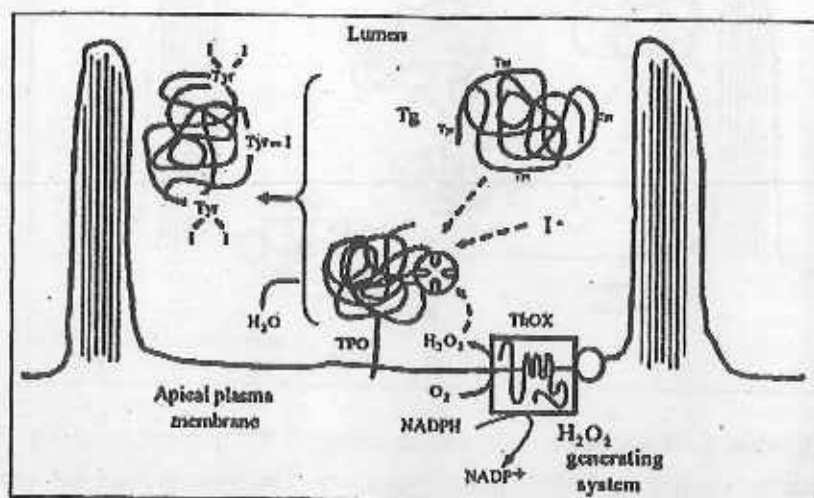


Fig. 6. Iodination of Tg at the apical plasma membrane-follicle lumen boundary. The scheme does not account for the relative size of the intervening molecules.

A second proposal, based on studies of rapid spectral absorption changes is that TPO-I^+ is the iodination intermediate and that the preferred route is oxidation of TPO by H_2O_2 followed by two electron oxidation of I^- to I^+ , which then reacts within a tyrosine.

As a third possibility, Taurog proposed a reaction between oxidized TPO and I^- to produce hypiodite (OI^-), which also involves a two electron reaction. Whatever the precise nature of the iodinating species, it is clear that iodide is oxidized by H_2O_2 and TPO, and transferred to the tyrosyl groups of Tg. All tyrosine residues of Tg are not equally accessible to iodination. The molecule has about 132 tyrosyl residues among its two identical chains; at most, only about 1/3 of the tyrosyls are iodinated. As isolated from the thyroid, Tg rarely contains more than 1% iodine or about 52 iodine atoms.

The final step in hormone synthesis is the coupling of two consenting iodotyrosyl residues to form iodothyronine (Fig. 7). Two DIT form T_4 ; one DIT and one MIT form T_3 . Coupling takes place while both acceptor and donor iodotyrosyl are in peptide linkage within the Tg molecule. The reaction is catalyzed by TPO, required H_2O_2 and is stringently

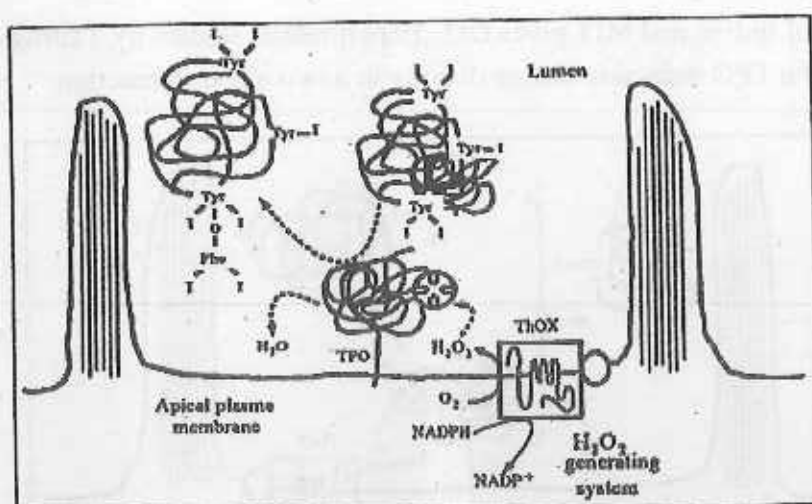


Fig. 7. Synthesis of hormone residues (coupling of iodotyrosines) in Tg at the apical plasma membrane-follicle lumen boundary. The scheme does not account for the relative size of the intervening molecules

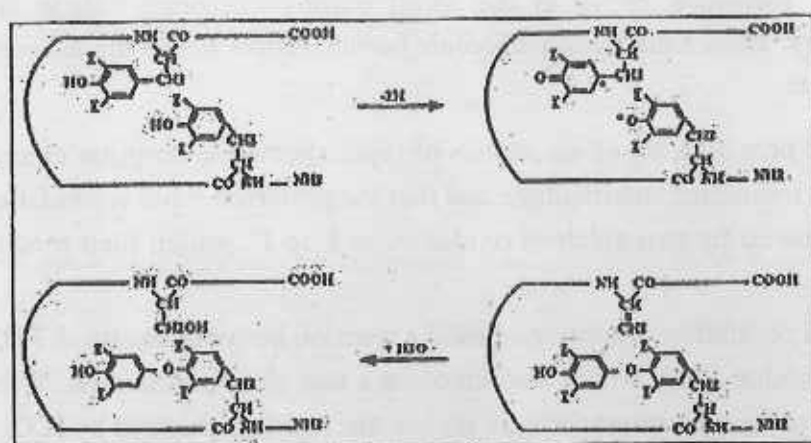


Fig. 8. Possible coupling reaction sequence. Oxidation of iodotyrosines may produce iodotyrosyl radicals. The free radicals could combine to generate the iodothyronine residue (at the tyrosine acceptor site) and a dehydroalanine residue (at the tyrosine donor site), which in the presence of H₂O₂ converts into a serine.

dependent on Tg structure. The generation of the iodothyronine residue involves the formation of an ether bond between the iodophenol part of a donor tyrosyl and the hydroxyl group of the acceptor tyrosyl (Fig 8). After the cleavage reaction that gives the

iodophenol, the alanine side chain of the donor tyrosyl remains in the Tg polypeptide chain as dehydroalanine. Observations both in vivo and in vitro show an appreciable delay in coupling after initial formation of iodotyrosines.

In addition to its role as component of the iodoamino acids, iodine is associated with cleavage of peptide bonds of Tg, at least in vitro. This has been attributed to generation of free radicals during oxidation. Exposure of Tg to reducing agents yields an N-terminal peptide of about 20-26kDa, depending on the animal species, that contains the major hormonogenic site of Tg. This peptide appears in parallel with iodination or may slightly precede it. Further addition of iodine cleaves the 26kDa further, to produce an 18kDa (in human Tg), an event that also occurs with TSH stimulation. Thus, iodination-associated cleavage appears to be part of the maturation of the Tg molecule.

The amount of iodine has important effects on thyroid hormone production. The initial reaction between TPO and H_2O_2 produces the so-called "compound I," which oxidizes iodide and iodates Tg. Next, the two reactants form compound II, which is necessary for the coupling reaction to make thyroid hormones. However, if excessive iodine is present, conversion to compound II does not take place, and hormone synthesis is impaired.

2.1.8 Thyroglobulin Endocytosis

To be useful, thyroid hormones must be released from Tg and delivered to the circulation for action at their distant target tissues. Depending on numerous factors including - the supply of iodide as substrate, the activity of enzymes catalyzing hormone formation, the concentration and physico-chemical state of Tg - the hormone content of luminal Tg molecules varies to a rather large extent. Tg molecules newly arrived in the follicle lumen with negligible hormone content would co-exist with "older" Tg exhibiting up to 6-8 hormone residues. The downstream processes responsible for the production of free thyroid hormones from these prohormonal molecules must therefore adequately manage the use of these luminal heterogeneous Tg stores to provide appropriate amounts of hormones for peripheral utilization.

The way the thyroid follicle proceeds to generate free hormones from stored hormone containing Tg molecules has been known for a long time. Tg molecules are first taken up by polarized thyrocytes and then conveyed to lysosomal compartments for proteolytic cleavage that release T_4 and T_3 from their peptide linkages. The first step represents the limiting point in the thyroid hormone secretory pathway. Over the last decade, there has

been substantial improvement in the knowledge of the cellular and molecular mechanisms governing the internalization or endocytosis and intracellular transport of the prohormone, Tg. The evolution has first been to consider that it could proceed via a mechanism different from phagocytosis, also named macropinocytosis, evidenced in rats under acute TSH stimulation. Results obtained in rats have been known for a long time extrapolated to the different animal species including human. There is now a number of experimental data indicating that in the thyroid of different species under physiological circumstances, internalization of Tg, mainly if not exclusively, occurs via vesicle-mediated endocytosis or micropinocytosis (Fig. 9), an ubiquitous cellular process accounting for macromolecule internalization by all cell types.

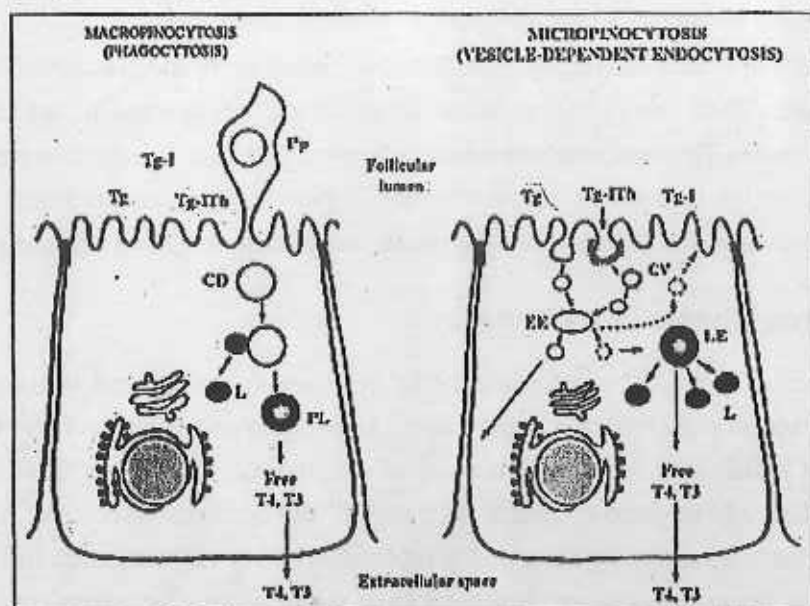


Fig 9. Schematic representation of the two modes of internalization of Tg; Micropinocytosis (on the right) and Macropinocytosis or phagocytosis (on the left). Intraluminal Tg stores potentially subjected to endocytosis are composed of recently secreted non-iodinated Tg, iodinated Tg (Tg-I) and iodinated Tg containing iodothyronine residues (Tg-Ith). Abbreviations are: CV, Coated Vesicle; EE, Early Endosome; LE, Late Endosome; L, Lysosome; Pp, Pseudopod; CD, Colloid Droplet; PL, Phagolysosome. The scheme on the right indicates the three possible routes of transport of internalized Tg molecules reaching the EE: transport to LE, recycling towards the follicle lumen and transcytosis i.e. transport towards the basolateral plasma membrane.

Under TSH stimulation, macropinocytosis would be triggered and would become operative in Tg internalization. Pseudopods representing extensions of the apical plasma membrane project into the follicle lumen and pinch off to form a resorption vacuole known as colloid droplet. The colloid droplets then deliver their content to lysosomes. Pseudopod formation is one of the earliest effects of TSH on the gland, evident within several minutes after administration. In species other than rat, TSH stimulates macropinocytosis through the activation of the cyclic AMP cascade.

2.1.9 Proteolytic Cleavage of Thyroglobulin

Internalized Tg molecules that are conveyed to lysosome compartments, are subjected to diverse hydrolytic reactions leading to the generation of free thyroid hormones and to complete degradation of the protein. Given its composition, Tg is likely the substrate for the different lysosomal enzymes. Efforts have been made to identify proteases involved in the release of hormonal residues from their peptide linkage in Tg. Endopeptidases such as cathepsin D, H and L are capable of cleaving Tg.

Initial cleavage occurs by endopeptidases and resulting products are further processed by exopeptidases. Dunn et al showed that cathepsin B has exopeptidase activity as well as an endopeptidase action. Starting from highly purified preparations of thyroid lysosomes, Rousset et al have identified intralysosomal Tg molecules with very limited structural alterations without hormone residue. After Tg digestion, T_4 and T_3 must be free from the lysosomal compartments to the cytoplasm and are transported out of the cell for circulation. It has been postulated for decades that thyroid hormones are released from thyrocytes by simple diffusion.

Among other products which are released or leaked out from the thyroid, is Tg. The secretion of Tg is clinically important. Its presence in serum can be detected by a routine assay and provides a sensitive (although not always specific) marker for increased thyroid activity. Attempts have been made to determine the biochemical characteristics of circulating Tg molecules in terms of iodine content, structural integrity and hormone content. Serum levels are elevated in patients with hyperplastic thyroid

or thyroid nodules including differentiated thyroid cancer. Tg measurement can identify congenital hyperplastic goiter, endemic goiter, and many benign multinodular goiters, but its greatest application is in the follow-up of differentiated thyroid cancer. Most papillary and follicular cancers retain some of the metabolic functions of the normal thyrocyte, including the ability to synthesize and secrete Tg. Subjects who have

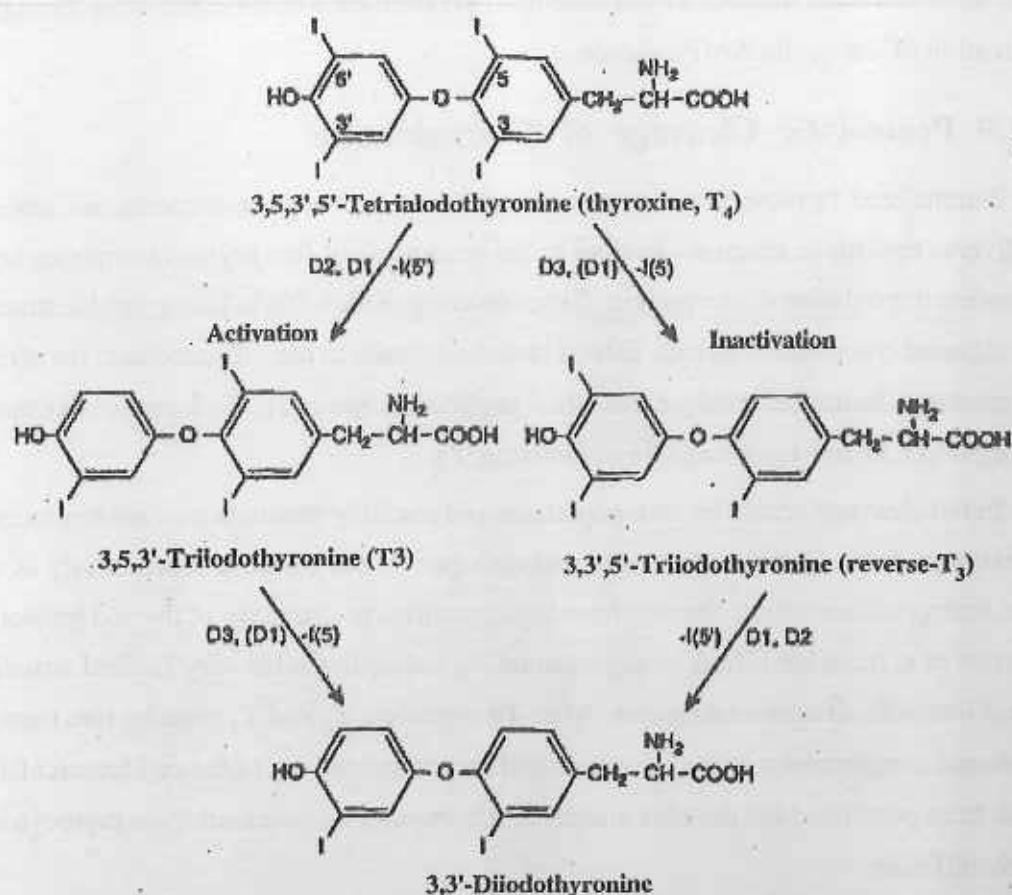


Fig. 10. Pathways for thyroid hormone activation and inactivation catalyzed by human iodothyronine selenodeiodinases. Numbers refer to the iodine positions in the iodothyronine nucleus. The iodothyronine deiodinases are abbreviated D1, D2, and D3 for types 1, 2, and 3 deiodinases, respectively. *Arrows* refer to mono-deiodination of the outer or inner ring of the iodothyronine nucleus, termed 5' or 5 by convention. The parentheses around D1 emphasize that D3, not D1, is probably the major enzyme catalyzing inner ring deiodination of T_4 and T_3 .

differentiated thyroid cancer treated by surgery and radioiodine should not have normal thyroid tissue left, and therefore, should not secrete Tg. If Tg is found in their serum, it reflects the presence of normal thyroid tissue, unlikely after its ablation, or of thyroid cancer. Tracking serum Tg levels is probably the most sensitive and practical means for the follow-up of such patients. It is more sensitive when the subject is stimulated by TSH. Until recently, this could only be done by withdrawal of thyroid hormone and consequent symptomatic hypothyroidism, but now recombinant human TSH can be administered to enhance the sensitivity of the serum Tg and thyroid scan.

2.1.10 Iodide Metabolism by the Thyroid Cell

Because the concentration of iodide in plasma is extremely low, a mechanism is required for the thyroid cell to concentrate the required amounts of this element. This process, called *iodide trapping*, is accomplished by a membrane protein, the *sodium-iodide symporter* (NIS). Human NIS is a 643 amino acid protein with 13 membrane-spanning domains.

The transport of iodide is an active process, depending on the presence of sodium gradient across the basal membrane of the thyroid cell such that downhill transport of 2 Na^+ ions results in the entry of one iodide atom against an electrochemical gradient. In addition to being expressed in the basolateral membrane of the thyroid cell, NIS has also been identified in other iodide concentrating cells, including salivary and mammary glands, choroid plexus, gastric mucosa, and in the cytotrophoblast and syncytiotrophoblast. The iodide transport system generates an iodide gradient of 20 to 40 over the cell membrane and NIS also transports TcO_4^- , ClO_4^- , and SCN^- , accounting for the utility of radioactive TcO_4^- as a thyroid scanning tool and the capacity of potassium perchlorate (KClO_4^-) to block iodide uptake. In fact, these anions have a higher affinity for NIS than does iodide itself. On the other hand, the affinity of NIS for iodide is much higher than it is for the other inorganic anions, such as bromide and chloride, accounting for the selectivity of the thyroid transport mechanism.

It has been known for decades that the iodide-concentrating mechanism is required for normal thyroid function, as its absence is associated with congenital hypothyroidism and goiter unless large quantities of inorganic iodide are provided. A number of families have

now been identified in which various mutations in the NIS gene are associated with congenital hypothyroidism and an iodide transport defect. Transcription of the NIS gene is increased by TSH. The mechanism for this has not been completely elucidated, but studies of the rat NIS promoter suggest that there is an NIS *upstream enhancer*, which confers a cyclic adenosine monophosphate (cAMP) response but also contains binding sites for the thyroid specific transcription factors PAX-8 and TTF-1, as well as a degenerate cAMP response element sequence. Importantly, several studies have documented decreases in NIS expression in human thyroid adenomas and carcinomas that contribute to the loss of iodine uptake in neoplastic thyroid cells, which thus present as "cold" nodules on radioisotopic imaging.

A second thyroid cell protein involved in iodide metabolism, *pendrin*, the product of the *PDS* gene, has now been identified by positional cloning using genomic DNA from families with the autosomal recessive disorder, *Pendred's syndrome*. This is a long-recognized inherited condition in which sensorineural hearing loss is combined with varying degrees of impaired thyroid hormone synthesis, leading to goiter. Pendrin is a transmembrane protein, a member of the sulfate transport protein family. Initially thought to be a sulfate transporter, it is now recognized to transport chloride, iodide, and bicarbonate (HCO_3^-). Pendrin is expressed in the apical border of the thyroid cell, the inner ear, and the kidney (see Fig. 10-2). Mutations in pendrin cause an inner ear malformation, although not all patients have goiter. It is postulated that pendrin is required for iodide transport across the apical membrane of the thyrocyte into the follicular lumen, where it is then oxidized and coupled to tyrosine in Tg.

The presence of thyroid dysfunction in Pendred's syndrome can be ascertained by the *perchlorate discharge test*, which illustrates the physiologic role of pendrin in thyroidal iodine metabolism. In normal individuals, more than 90% of thyroidal radioiodine is present as iodotyrosine and iodothyronine within minutes of its entry into the thyroid. It is then no longer in the intracellular iodide pool. In patients with Pendred's syndrome, or with other disorders inhibiting the iodination of tyrosine (see later topics, such as Hashimoto's thyroiditis), this process is delayed, as shown by the exit (discharge) of more than 10% of the thyroidal radioiodine within 2 hours of administration of 500 mg of KClO_4 . Perchlorate inhibits NIS function by an as yet unidentified mechanism eliminating the iodide gradient,

which is required for maintaining the 125 I-iodide in the gland. This illustrates that both iodide transport by NIS at the basal pole of the thyrocyte and its efflux across the apical membrane by pendrin are required for thyroid hormone synthesis. Deafness in patients with Pendred's syndrome is due to formation of a common cavity in the upper coils of the cochlea with dilatation of the vestibular aqueducts, not to the hypothyroidism per se.

In addition to being brought into the thyroid gland by active transport from the extracellular fluid, thyroidal iodide is generated by the deiodination of iodotyrosines liberated during the hydrolysis of Tg. A portion of this iodide is oxidized and used to iodinate tyrosine, and the remainder is lost from the gland as the *iodide leak* (see Fig. 10-2). This conservation process is interrupted when antithyroid drugs—which inhibit iodide oxidation, such as methimazole (MMI), carbimazole (CB) or propylthiouracil (PTU)—are given, thus further enhancing the effectiveness of these thyroid peroxidase inhibitors in blocking thyroid hormone synthesis.

2.1.11 Control of Hormone Synthesis

The most important controlling factors are iodine availability and TSH. Inadequate amount of iodine leads to inadequate thyroid hormone production, increased TSH secretion and thyroid stimulation, and goiter. Excess iodine acutely inhibits thyroid hormone synthesis, known as the Wolff-Chaikoff effect, that occurs apparently by inhibiting H_2O_2 generation resulting blocking Tg iodination. A proposed mechanism is that the excess iodide leads to the formation of 2-iodohexadecanal, which is endowed with an inhibitory action on H_2O_2 generation. TSH influences virtually every step in thyroid hormone synthesis and release. All these effects appear to be mediated through the cAMP cascade.

In summary, TSH stimulates the expression of NIS, TPO, Tg and generation of H_2O_2 , which in turn increase the formation of T_3 and T_4 , that alters the priority of iodination and hormonogenesis among tyrosyls and promotes the rapid internalization of Tg by thyrocytes. These several steps are interrelated and have the net effects of increasing the amount of iodine available to the cells for synthesis and releasing of a larger amount and a more effective type of thyroid hormone (T_3).

Anti-thyroid drugs are external compounds influencing thyroid hormone synthesis. The major inhibitory drugs are the thionamides: propylthiouracil and methimazole. In the thyroid,

they appear to act by competing with tyrosyl residues of Tg for oxidized iodine, at least in the rat. Iodotyrosyl coupling is also inhibited by these drugs and appears more sensitive than tyrosyl iodination.

2.2 Thyroid : Function

2.2.1 Thyroid Hormone Secretion

Secretion of thyroid hormone requires endocytosis of human thyroglobulin, its hydrolysis, and the release of thyroid hormones from the cell. Thyroglobulin can be ingested by the thyrocyte by three mechanisms.

In *macropinocytosis*, at first, pseudopods engulf clumps of thyroglobulin. In all species this process is triggered by acute activation of the cAMP/PKA cascade induced by TSH. Stimulation of macropinocytosis is preceded and accompanied by an enhancement of thyroglobulin exocytosis. In dog thyroid slices and even primary cultures, TSH and PKA activation acutely induces phagocytosis and macropinocytosis of thyroglobulin involved in stimulated thyroid hormone secretion. This process might be mediated by inactivation of the Rho family small G proteins, resulting in microfilament depolymerization and stress fiber disruption accompanied by dephosphorylation of cofilin and myosin light chains.

Subsequently in *micropinocytosis* a small amount of colloid fluid is ingested. This process does not appear to be greatly influenced by acute modulation of the regulatory cascades. It is enhanced in chronically stimulated thyroids and thyroid cells by early mobilization in the membrane and later by induction of vesicle transport proteins Rab 5 and 7. It probably accounts for most of basal secretion. Eventually receptor-mediated endocytosis is enhanced in chronically stimulated thyroid cells. The protein involved is megalin and asialoglycoprotein. This process probably accounts for the transcytosis of low hormone containing thyroglobulin. Macropinocytosis is inhibited by microfilament and microtubule poisons and by lowering of the temperature (below 23°C). Whatever is the mechanism, endocytosis is followed by lysosomal digestion with complete hydrolysis of thyroglobulin. The main iodothyronine in thyroglobulin is thyroxine. However, during its secretion a small fraction is deiodinated by type I 5 and in main type II 5-deiodinase to triiodothyronine (T_3), resulting in increasing T_3 (the active hormone) secretion.

The free thyroid hormones are released by an unknown mechanism, which may be diffusion or transport. The iodotyrosines are deiodinated by specific deiodinases and their iodides are recirculated in the thyroid iodide compartments. Under acute stimulation, a release (spillover) of amino acids and iodide from the thyroid is observed. A mechanism for lysosome retention of poorly iodinated thyroglobulin on N-acetylglucosamine receptors and recirculation to the lumen has been proposed. Under normal physiologic conditions, endocytosis is the limiting step of secretion, but after acute stimulation, hydrolysis may be the limiting step of thyroid secretion. Secretion by macropinocytosis is triggered by activation of the cAMP cascade and inhibited by Ca^{2+} . It is also inhibited in some thyroids by protein kinase C downstream from cAMP. Thus the PIP_2 cascade negatively controls macropinocytosis.

2.2.2 Cellular Action of Thyroid Hormone

The thyroid hormones (THs, thyroxine (T_4) and triiodothyronine (T_3)) have important effects on development, growth, and metabolism. Some of the most prominent effects of TH occur during fetal development and early childhood. In humans, the early developmental role of TH is illustrated by the distinctive clinical features of cretinism observed in iodine-deficient areas. In childhood, lack of TH can cause delayed growth. However, in the latter case, many of the effects of TH may be metabolic rather than developmental, as growth is restored rapidly after TH treatment. In adults, the primary effects of THs are manifested by alterations in metabolism. These effects include changes in oxygen consumption, protein, carbohydrate, lipid, and vitamin metabolism. The clinical features of hypothyroidism and hyperthyroidism emphasize the pleiotropic effects of these hormones on many different pathways and target organs.

Since the initial description of TH effects on metabolic rate more than 100 years ago, many theories have been proposed to explain its mechanism of hormone action. The proposed models include: uncoupling oxidative phosphorylation, stimulation of energy expenditure by the activation of Na^+ - K^+ ATPase activity, and direct modulation of TH transporters and enzymes in the plasma membrane and mitochondria. Recently, there has been increasing evidence for non-genomic actions; however, the major effects of TH occur via nuclear receptors that mediate changes in gene expression.

In many respects, T_4 can be regarded as a prohormone for the more potent hormone, T_3 . Most of the TH bound to receptors is in the form of T_3 , either secreted into the

circulation by the thyroid gland or derived from T_4 to T_3 conversion by 5' monodeiodinases. There are three distinct deiodinases- type I, type II, and type III. The distribution and regulation of these enzymes can have important effects on TH action. For example, Type II deiodinase has high affinity for T_4 and is found primarily in the pituitary gland, brain, and brown fat where conversion of T_4 to T_3 modulates the intracellular concentration of T_3 . Thus, tissues that contain type II deiodinase can respond differently to a given circulating concentration of T_4 (by intracellular conversion to T_3) compared to the organs that only can respond to T_3 . T_3 binds to its receptors with approximately 10-15 fold higher affinity than T_4 . Nuclear receptors are approximately 75% saturated with TH in brain and pituitary and 50% saturated with TH in liver and kidney. It is notable that the extent of TH receptor occupancy varies in different tissues, providing a mechanism for alterations in circulating TH levels to alter receptor activity. In contrast to the related steroid hormone receptors, TRs are mostly nuclear both in the absence and presence of TH. In fact, TH receptors are tightly associated with chromatin, consistent with their proposed role as DNA-binding proteins that regulate gene expression.

Unit 3 □ Anterior Pituitary Structure, Hormone and Function

Structure

3.1 The Normal Pituitary Gland

3.1.1 Development

3.2 Anterior Pituitary

3.2.1 Histology

3.2.2 Cell type

3.3 Anterior Pituitary Hormones

3.3.1 Growth Hormones

3.3.2 Prolactin

3.3.3 ACTH

3.3.4 TSH

3.3.5 FSH

3.3.6 LH

3.4 Feedback Control

3.1 The Normal Pituitary Gland

The pituitary is a bean-shaped gland located at the base of the brain in the midline. It measures 0.6 cm SI × 0.9 cm AP × 1.3 cm and an average gland weighs 0.6. Females tend to have larger glands, especially during or after pregnancy, with the weight up to 1 g. The gland lies within the bony sella turcica that surrounds it inferiorly and laterally. Superiorly it is covered by the diaphragm sella, a reflection of the dura matter. Lateral to the sella are the cavernous sinuses; anteroinferior is the sphenoid sinus; anterosuperior is the optic chiasma; superior to it is the hypothalamus. The pituitary is composed of two anatomically and functionally distinct parts: the neurohypophysis and the adenohypophysis.

3.1.1 Development

The pituitary gland is formed as a result of two separate developmental processes giving the anterior and posterior lobes.

- The posterior pituitary develops as an extension of the hypothalamus itself. The infundibulum is formed from the neuroectoderm of the floor of the third ventricle and develops to form the posterior pituitary. The median eminence is also formed from neuroectoderm.
- The anterior pituitary is derived from oral epithelium from the roof of the mouth cavity, which migrates upwards towards the neural tube. This outgrowth is known

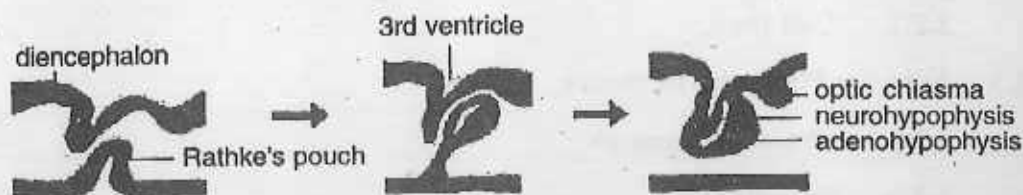


Fig. 3.1 : Development of hypophyseal-portal system

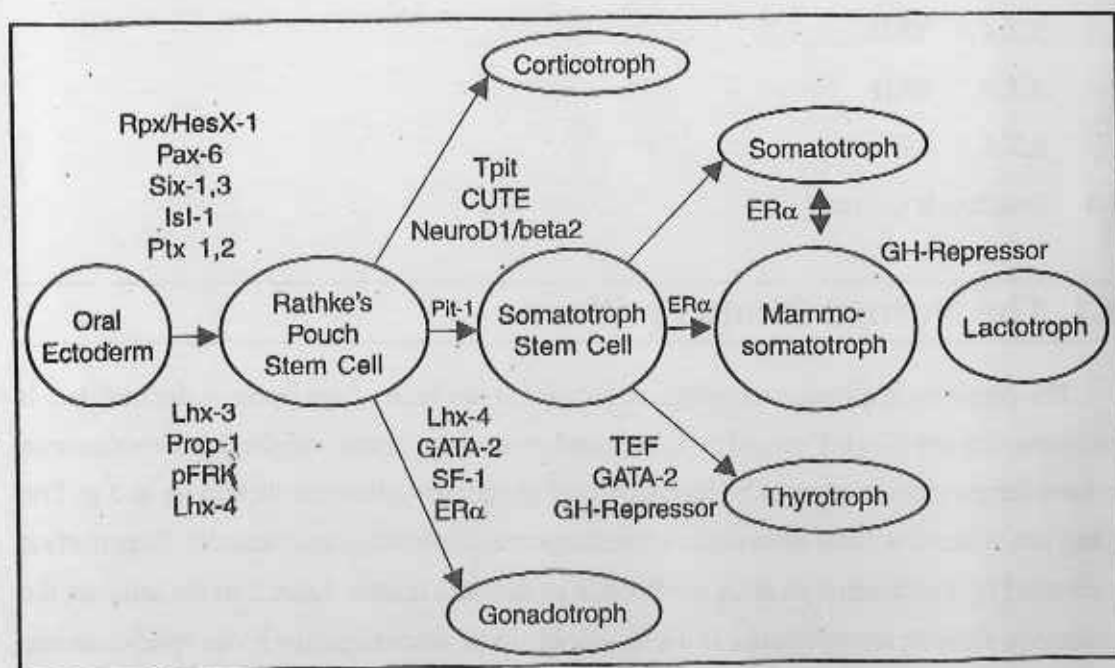


Fig. 3.2 : Pituitary development and cytodifferentiation of adenohypophysis. Transcription factors implicated in each step are identified.

as **Rathke's pouch**. It detaches itself by the 6th week of development although detachment is not always complete and may cause problems such as craniopharyngioma.

- The hypothalamo-pituitary axis is a functional unit by mid gestation.

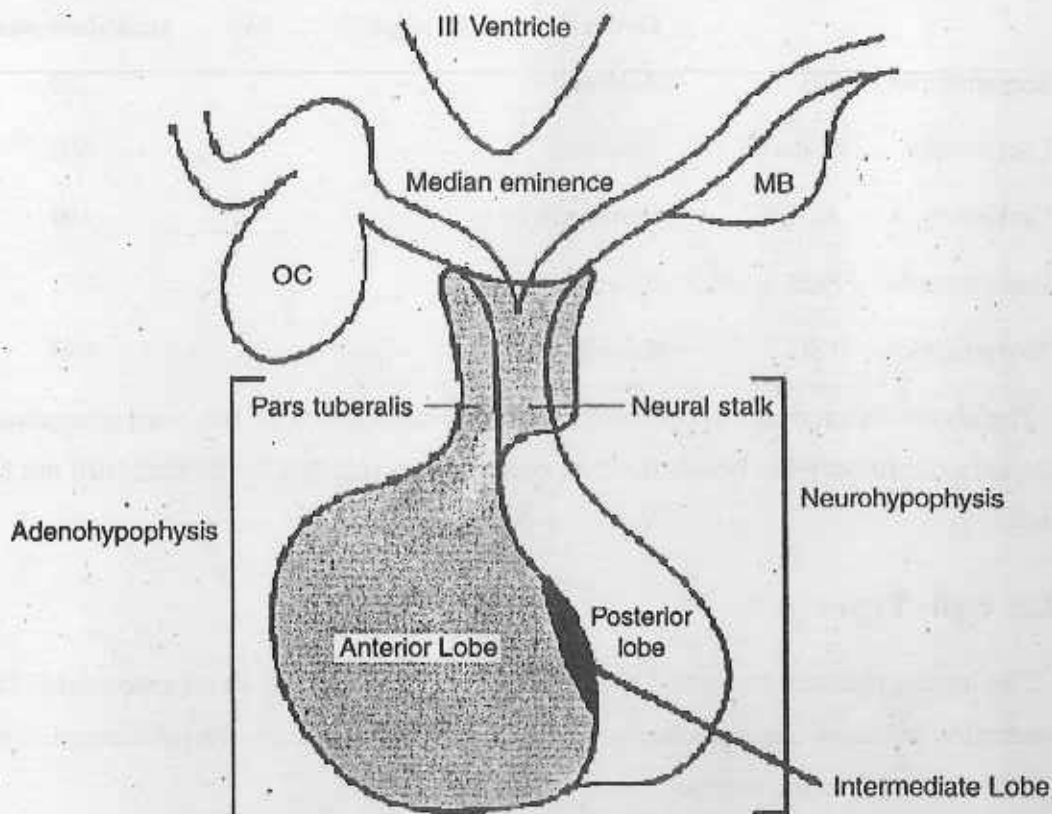


Fig. 3.3 : Anatomical organisation showing hypothalamic and hypophyseal neurovascular link for the control of hormonal secretion from hypophysis cerebri. (OC = optic chiasma; MB = mammillary body)

3.2 Anterior Pituitary

3.2.1 Histology

The cells of the anterior pituitary were originally classified using techniques for staining intracellular granules as acidophils, basophils and chromophobe cells. Immunocytochemical

and electron microscopic techniques now permit classification of cells by their specific secretory products—

CELL TYPES	HORMONE SECRETED	STAINING REACTION			GRANULAR SIZE (nm/diameter)
		General	Orange-G	PAS	
1. Somatotrophs	GH	Acidophil	+	—	350
2. Lactotrophs	Prolactin	Acidophil	+	—	600
3. Corticotrophs	ACTH	Chromophobe	—	—	100
4. Gonadotrophs	FSH + LH	Basophil	—	+	200
5. Thyrotrophs	TSH	Basophil	—	+	140

The above different cell types which secrete specific hormone has been recognised in the anterior pituitary but beside that few cells also present but their nature still not be found.

3.2.2 Cell Types :

The human pituitary contains 5 or more distinct cell types, which are responsible for the secretion of atleast 6 independent hormon. It is logical to classify the pituitary cells on the basic of the hormone secreted.

1. **Somatotrophic cell** : It is rounded or ovoid, the cytoplasm is packed with dense and round granules 350-400 nm in size. These cells account for about 4-10% of the net weight of the anterior pituitary.

2. **Lactotrophic cell** : A second but distinct staining cell randomly distributed in the anterior pituitary has been associated with prolactin secretion. Granule are frequently ovoid or elleypsoidal and approx. 600 nm on plectron microscopy. *These cells proliferate during pregnancy* as a result of elevated estrogen levels and account for the increase in gland size.

3. **Thyrotrophic cell** : These TSH—secreting cells, because of their glycoprotein product, are basophilic and also show a positive reaction with PAS stain. The thyrotroph granules are small (50-140 nm) polygonal (found in rat) with small nucleus. These cells are usually located in the anteromedial and anterolateral portions of the gland.

4. **Corticotrophic cell** : Characterisation of these cell have been difficult on morphological ground. Immanofluorescent studies with antibodies that react with corticotrophin have definitely localised the hormone within basophilic cells, but some cells also may fluorescene with antibodies against thyrotrophin. Considering the similarities in the amino acid sequences in the structure of melanocyte stimulating hormone (MSH) and ACTH, it is reported that these two hormones are secreted from the same cells.

5. **Gonadotrophic cell** : The gonadotrophins are secreted by basophilic cells which are PAS+ve. These cells are located in the lateral portion of the gland. They become hypertrophied and cause the gland to enlarge during states of primary gonadal failure. Such as Klinefelter's Syndrome and Turner's Syndrome. A provisional separation of two types of gonadotrophin cells has been made by *Barnes* :

(a) FSH gonadotrophic cells are larger, rounded whose secretory granules are spherical between 150 and 300 nm in diameter. Certain other differences in the E.R and mitochondria have been noted.

(b) LH or ICSH gonadotrophic cells are comparatively small with scant cytoplasm. The cells are rounded or polygonal and found in proximity of the sinusoidal capillaries. These cells also contain spherical secretory granules having diameter 100-300 nm which are of uniform electron dense appearance.

6. **Other cell types** : Despite immunocytochemical staining with antibodies directed against all of the known anterior pituitary hormones, some cells remain unstained.

These are chromophobes by conventional staining methods, but electron microscopy has identified secretory granules in many of them. It is not certain whether they represent undifferentiated primitive secretory cells or whether they produce an as yet unidentified hormone, such as adrenal androgen—stimulating hormone or ovarian growth factor.

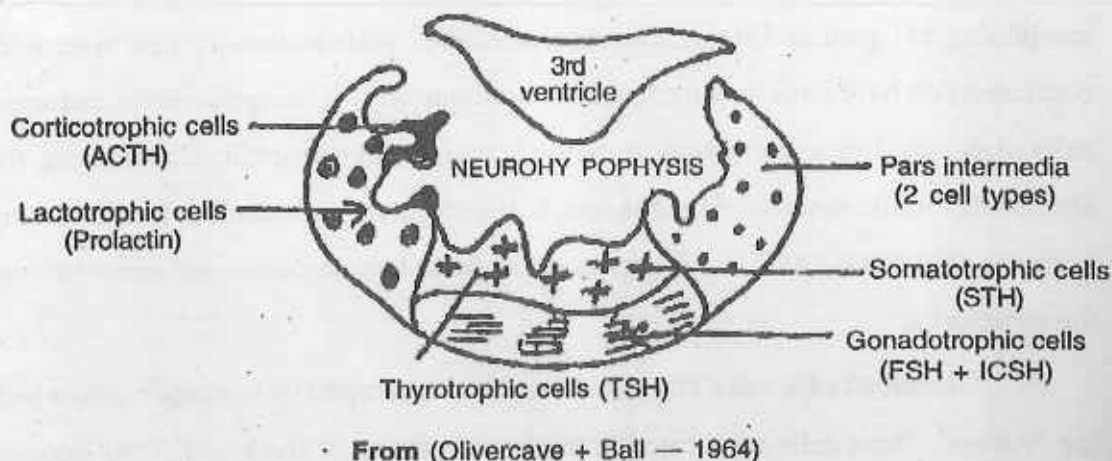


Fig. 3.4 : Diagram of a mid sagittal section of the pituitary gland of a bony fish (*Poecilia*) showing Localisation of cell types in adenohypophysis.

3.3 Anterior Pituitary Hormones

There are 6 major anterior pituitary hormones whose biosynthesis, structure, function and secretory control have been well characterized and which can be accurately measured in tissue or body fluids. These hormones—ACTH, GH, PRL, TSH, LH and FSH may be classified into 3 groups: corticotropin related peptides (ACTH, LPH, MSH and endorphins), the somatomammotropins (GH and PRL), which are also peptides; and the glycoproteins (LH, FSH and TSH).

3.3.1 Growth hormones or Somatotrophic hormone (GH or STH) :

Chemistry : The human growth hormone (HGH) is the smallest of the growth hormones that have been examined with molecular weight 21,500. It is composed of a single

chain of 188 amino acids *without carbohydrate substituents*. In man the amino acid chain probably exists with a large and small loop formed from intramolecular disulphide bonds

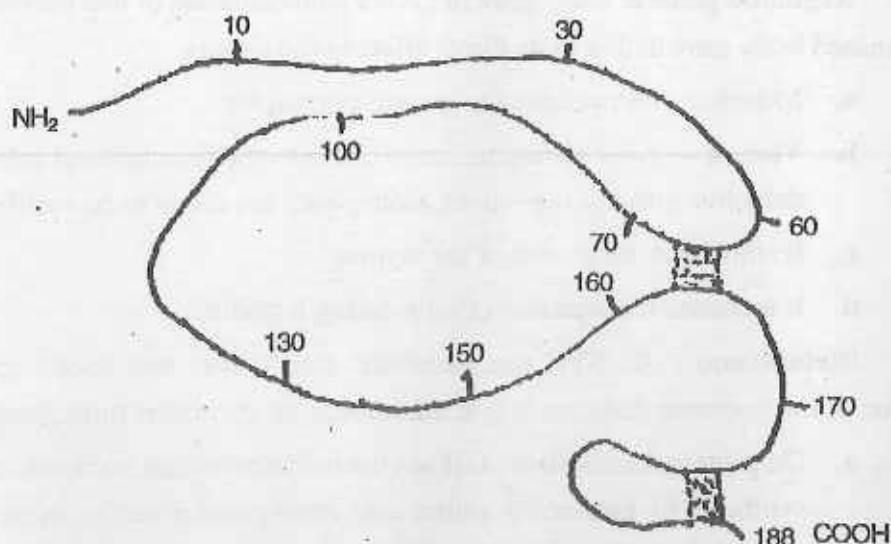


Fig. : Schematic representation of HGH.

unlike the disulphide bonds of insulin and the neurohypophysial hormones, the disulfide bonds of HGH are not essential for biologic activity.

Growth hormone from pig, whale, sheep and cow pituitary is believed to have a significantly larger molecular weight than HGH; Bovine (cattle) GH weights about 46,000 with 400 amino acids. End-group analysis of the bovine hormone has revealed one amino end-group and two carboxyl end groups which suggest that this hormone exists as a branched chain.

It has been noted that human growth hormone (HGH) exerts lactogenic effect along with the growth stimulating one.

Biological action : As its name implies, the primary function of growth hormone (somatotropin) is promotion of linear growth. Its basic metabolic effects serve to achieve this result, but most of the growth promoting effects are mediated by the somatomedins, a family of small peptides produced in the liver.

1. **Skeletal growth :** Stimulates the multiplication of the epiphyseal cartilage and this

increases the length of the cartilage bones. In adult animals with closed epiphysis growth hormone causes thickening of bone.

2. Regulates general body growth : After administration of this hormone there is an increased body growth due to its direct effect in the tissues.

- a. **Muscles** — Stimulates the growth of muscles.
- b. **Viscera** — After administration of GH in hypophysectomised animal various defective growths (eg—liver, kidney etc.) are found to be rectified.
- c. It stimulates the growth of the thymus.
- d. It increases the secretion of milk during lactation.

3. Metabolism : As STH has metabolic effect over and above growth, the secretion of the hormone does not stop at adulthood, but continues throughout the life.

- a. **On protein metabolism :** GH via the somatomedians increases the protein synthesis by enhancing amino acid uptake and directly accelerating the transcription and translation of mRNA. It decreases nitrogen excretion in the urine and the nitrogen thus retained helps in the synthesis of tissue protein. GH is a protein-anabolic hormone and prevents the catabolism of amino acids.
- b. **On fat metabolism :** GH tends to decrease protein catabolism by mobilizing fat as a more efficient fuel source. It directly causes the release of fatty acids from adipose tissue and enhances their conversion to acetyl CoA, from which energy is derived. This protein sparing effect may be the most imp. mechanism by which GH promotes growth and development.
- c. **On carbohydrate metabolism :** GH also affects carbohydrate metabolism. In excess, it decreases carbohydrate utilization and impairs glucose uptake into cells. The high blood glucose level then leads to overproduction of insulin by β -cells and finally to its exhaustion and atrophy. The GH is diabetogenic specially in man.
- d. **Ion or mineral metabolism :** GH (STH) increases intestinal absorption of calcium as well as its excretion. In addition to calcium, sodium, potassium, magnesium phosphate and chloride are also retained.

4. STH stimulates proliferations of thymic lymphocytes both in *vivo* and in *vitro*.
5. The GH also has lactogenic effect.

3.3.2 Lactogenic hormone/Prolactin :

It is secreted during pregnancy and lactation in women by acidophil pregnancy cells.

Chemistry : Prolactin (PRL) is a 198(180–205) amino acid polypeptide hormone (MW-22,000) synthesized and secreted from the lactotrophs of the anterior pituitary. Despite evolution from an ancestral hormone common to GH and human placental lactogen (hPL), PRL share only 16% of its residue with the former and 13% with hPL.) It has one free amino acid group, but on free carboxyl end-group. For this reason, Li has suggested that the peptide chain has an intrachain disulphide bridge forming a ring similar to that present in vasopressin and oxytocin. No bound carbohydrate has been found in prolactin. The nature of human prolactin remains a mystery of current pituitary endocrinology.

Biological Action :

1. Prolactin (LTH) is responsible for lactation in the post partum women, the breast having been prepared by oestrogen and progesterone. It helps initiating (lactogenesis) rather than maintaining milk secretion. Growth or somatotrophic and thyroid hormones help in the maintenance of the secretion of milk (galactopoiesis). The level of prolactin increases during the night. Oestradiol stimulates prolactin release where as L-dopa inhibits it by promoting the discharge of PIF.
2. It stimulates slightly the proliferation of the glandular elements of the mammary glands during pregnancy and thus helps to complete the development of breasts.
3. It helps in maintenance of secretory activity of corpus luteum and secretion of the hormone, Progesterone, due to combined action of LH and Prolactin.
4. Prolactin induces changes in maternal behaviour which are imp. for the helpless young. In some birds of both sexes it promotes the resting behaviour. The actual pathways by which prolactin induces these changes have not been established.

5. Under suitable experimental conditions prolactin has been shown to be calorogenic, to be diabetogenic, to promote *protein synthesis*, and to increase the rate of chondroitin sulphate formation in cartilage. An increase in the weight of the liver and several other organs has been observed in prolactin-treated pigeons.

The possible significance of these various actions of prolactin under physiologic conditions remains to be determined. As yet there is no known role of the hormone in the male sex.

3.3.3 Adrenocorticotrophic hormone (ACTH) :

Chemistry : ACTH is a 39-amino acid peptide hormone. Molecular weight about 4,500. The amino acids are numbered from the end with the free NH_2 group (the N-terminal end). The first 24 are common to ACTH from man and other mammals and biological activity is provided by the first 20. The arrangement of amino acids 25 to 33 varies in different species (found in man is shown). It has been isolated in α and β forms. Both these forms contain a large number of amino acids and have got straight chain linkage. Unlike other pituitary hormones, can withstand heating to 100°C .

Biological action :

1. The primary effect of ACTH is to stimulate the secretion of glucocorticoids, mineralocorticoids and androgenic steroids from the adrenal cortex is responsible for this biologic activity. ACTH binds to receptors on the adrenal cortex and provokes steroidogenesis through the mediation of cyclic 3', 5'-adenosine monophosphate (cyclic AMP, CAMP).

2. In addition to this, some of the effects of ACTH on the adrenal cortex are the following :

- a. Augmented oxidative phosphorylation.
- b. Increased protein synthesis.
- c. Accelerated glycolysis.
- d. Altered lipid metabolism.
- e. Ascorbic acid depletion.

3. Corticotrophic also induces changes in carbohydrate metabolism in the adrenalectomized animal.

Administration of ACTH to normal human being produces the following effect :

- a. Increased excretion of N_2 , K and P.
- b. Retention of sodium chloride and secondary retention of water.
- c. Elevation of fasting blood sugar and a diabetic glucose tolerance curve.
- d. Increase in circulating free fatty acids.
- e. Increased excretion of uric acid.
- f. Decline in circulating eosinophils and lymphocytes, and increase in neutrophils.
- g. It has a slight melanocyte-stimulating effect.

3.3.4 Thyrotropin/Thyroid Stimulating Hormone (TSH) :

Chemistry : Chemically, TSH is a basic glycoprotein with a molecular weight of about 28,000. It is composed of 2 non covalently linked subunits termed α and β . α -chain consists of 89 amino acid residues and $\alpha\beta$ -chain with 112 amino acid residues. The structure of the α -subunit of TSH resembles—FSH, LH and human chorionic gonadotropin (hcG)—but the G subunit differs in these glycoproteins and is responsible for their biologic and immunologic specificity.

Biological action : Controls the growth and activity of the thyroid gland. Primary physiologic action of TSH is probably to stimulate the release of thyroid hormone from the intrafollicular thyroglobulin. TSH is necessary for coupling of di-iodotyrosine to form thyroxine (T_4).

1. Thyrotropin can be shown to increase iodine uptake, iodine clearance from the plasma, iodotyrosine and iodothyronine formation. Thyroglobulin Proteolysis and thyroxine release from thyroid gland.

This occurs through activation of adenylate cyclase and the generation of cAMP.

2. There is an increase in respiration, nucleic acid synthesis, glucose utilization and fatty acid release.
3. TSH accelerates lipolysis by isolated rat adipose tissue in vitro.
4. TSH may exert a direct effect upon extra-ocular retrobulbar structures (lipid, muscle, connective tissue), with consequent protrusion of the eye ball (exophthalmos).

3.3.5 Follicle-Stimulating Hormone (FSH) :

FSH is a heterodimeric glycoprotein consisting of

- the same alpha chain found in TSH (and LH)
- a beta chain of 115 amino acids, which gives it its unique properties.

Synthesis and release of FSH is triggered by the *gonadotropin-releasing hormone* (GnRH) from the hypothalamus. The effect of FSH depends on one's sex.

FSH in females

In sexually-mature females, FSH (assisted by LH) acts on the follicle to stimulate it to release *estrogens*. FSH produced by recombinant DNA technology is available to promote ovulation in women planning to undergo *in vitro fertilization* (IVF) and other forms of assisted reproductive technology.

FSH in males

In sexually-mature males, FSH acts on spermatogonia to stimulate (with the aid of testosterone) the production of sperm.

3.3.6 Luteinizing Hormone (LH) :

LH is synthesized within the same pituitary cells as FSH and under the same stimulus (GnRH). It is also a heterodimeric glycoprotein consisting of

- the same 89-amino acid alpha subunit found in FSH and TSH (as well as in chorionic gonadotropin);
- a beta chain of 115 amino acids is responsible for its characteristic properties.

The effects of LH also depend on sex.

LH in females

In sexually-mature females,

- a surge of LH triggers the completion of *meiosis I* of the egg and its release (*ovulation*) in the middle of the cycle;
- LH also stimulates the empty follicle cells to develop into the *corpus luteum*, which secretes *progesterone* during the latter half of the menstrual cycle.

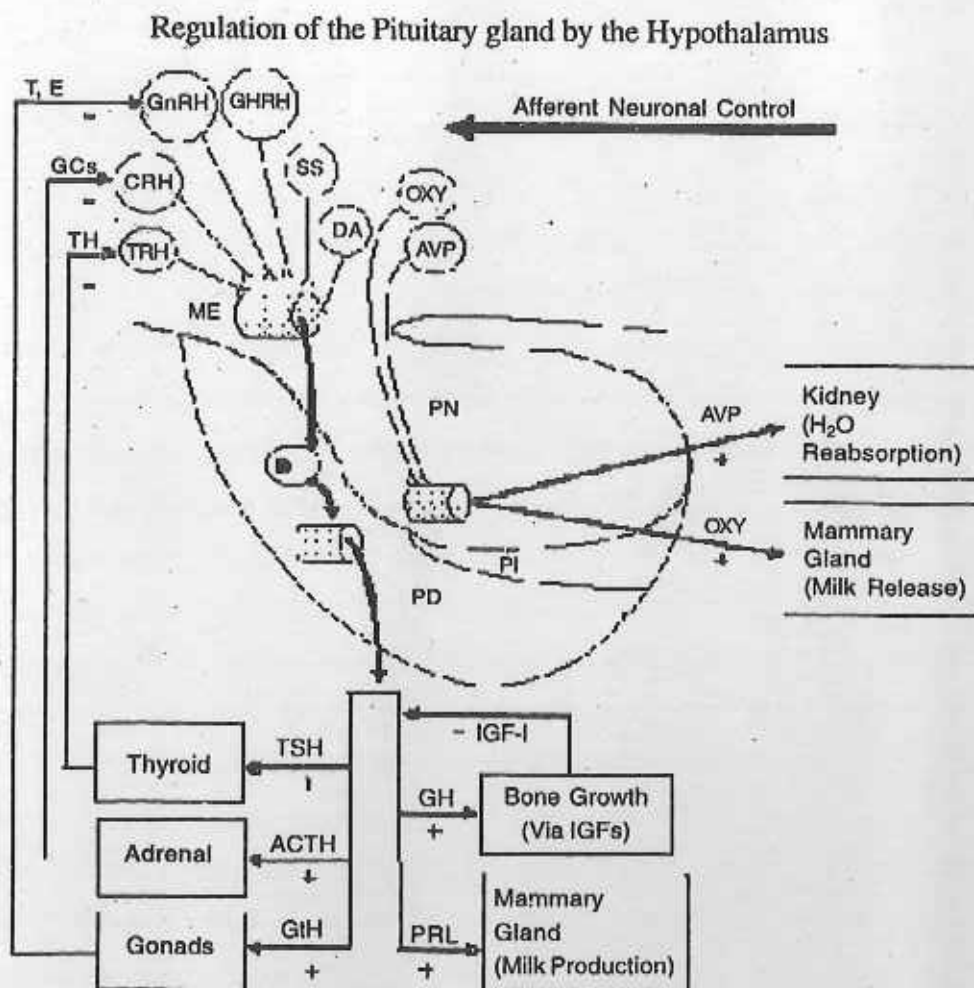
Women with a severe LH deficiency can now be treated with human LH produced by recombinant DNA technology.

LH in males

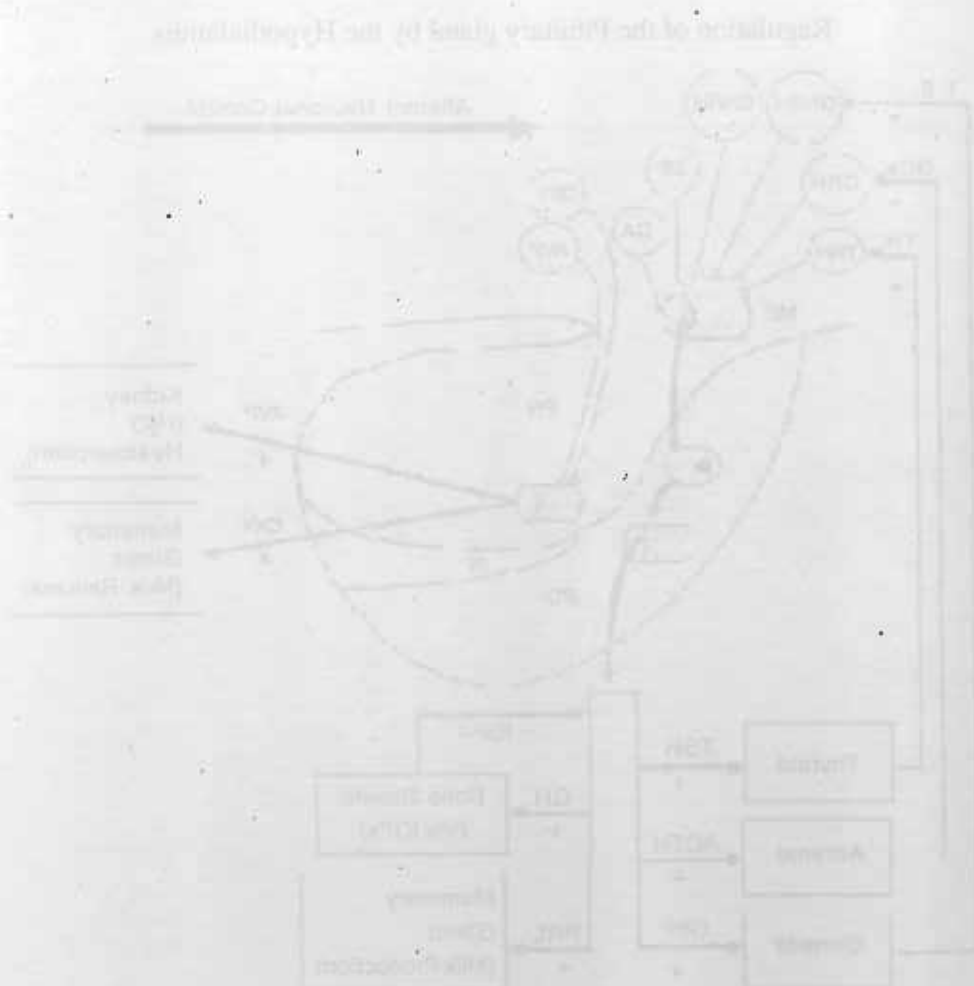
LH acts on the interstitial cells (also known as Leydig cells) of the testes stimulating them to synthesize and secrete the male sex hormone, testosterone. LH in males is also known as **interstitial cell stimulating hormone (ICSH)**.

3.4 Feedback Control

Negative feedback is an important factor in controlling the hypothalamic-pituitary-target organ axis function. Once hypothalamic hormones stimulate the release or inhibition



of the pituitary hormone, this may then act on a target gland, such as the thyroid, causing release of further hormones or causing metabolic effects. The action of hypothalamic hormones may be inhibited by long feedback loops from the target gland hormone or by short feedback loops from the pituitary hormone. There may also be direct feedback from the target gland hormone to the pituitary gland. Input is also received at the hypothalamus from higher brain centres, which can be due to internal or external influences. Positive feedback action also plays a partial in certain systems. For example, in the situation where high levels of oestradiol in the blood causes a surge in LH levels during the menstrual cycle.



Unit 4 □ Adrenal Cortical Hormone, Biosynthesis and Function

Structure

4.1 Introduction

4.2 The Adrenal Cortex

4.2.1 Glucocorticoids

4.2.1.1 Functions

4.2.1.2 Mechanism of action of glucocorticoids

4.2.2 Mineralocorticoids

4.2.2.1 Aldosterone and Mineralocorticoid Receptors

4.2.2.2 Functions of Mineralocorticoids

4.2.2.3 Physiology

4.2.2.4 Mechanism of action of mineralocorticoids

4.2.3 Androgens

4.3 Diseases

4.3.1 Excessive levels of glucocorticoids : Cushing's Syndrome

4.3.2 Hyposecretion of the adrenal cortices : Addison's Disease

4.3.3 Hyperaldosteronism

4.1 Introduction

The adrenal glands are small paired structures situated above each kidney. Both in anatomy and in function, they consist of two distinct regions :

an outer layer, the **adrenal cortex**, which surrounds the **adrenal medulla**.

4.2 The Adrenal Cortex

Using cholesterol as the starting material, the cells of the adrenal cortex secrete a variety of **steroid hormones**. **Glucocorticoids** (e.g., cortisol), **Mineralocorticoids** (e.g., aldosterone) and **Androgens** (e.g., testosterone)

Production of all these hormones are triggered by the secretion of ACTH from the anterior lobe of the pituitary.

These hormones achieve their effects by:

- travelling through the body in the blood. Because they are so hydrophobic, they must be carried bound to a serum globulin.
- entering from the blood into all cells
- binding to their **receptor** — a protein present in the cytoplasm and/or nucleus of “target” cells
- The hormone-receptor complex binds to a second to form a **dimer**.
- The dimer migrates into the nucleus (if it did not form there).
- The hormone-receptor dimer binds to specific **hormone response elements** in DNA.
- These are specific DNA sequences in the promoter of genes that will be turned on (sometimes off) by the interaction.
- Other **transcription factors** are recruited to the promoter and gene transcription begins.

4.2.1 Glucocorticoids

Glucocorticoids (GC) are a class of steroid hormones that bind to the glucocorticoid receptor (GR), which is present in almost every vertebrate animal cell. The glucocorticoids get their name from their effect of raising the level of blood sugar (glucose). One way they do this is by stimulating **gluconeogenesis** in the liver: the conversion of fat and protein into intermediate metabolites that are ultimately converted into glucose. (Fig. 1)

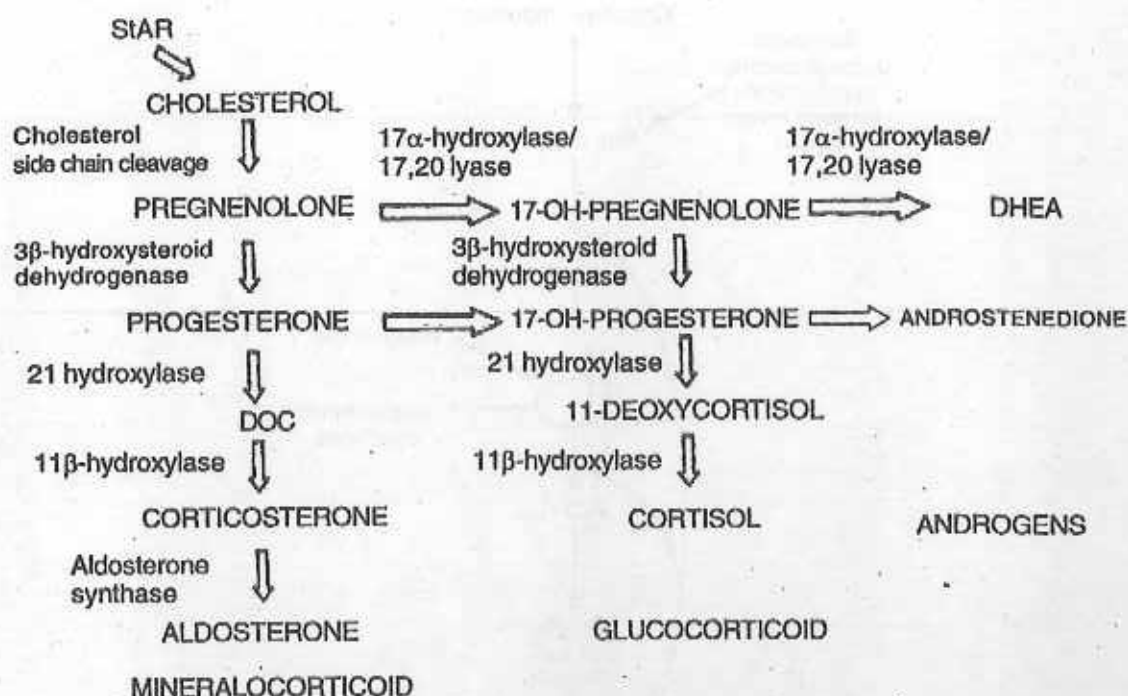


Fig. 1. Adrenal steroidogenesis. After the steroidogenic acute regulatory (StAR) protein-mediated uptake of cholesterol into mitochondria within adrenocortical cells, aldosterone, cortisol, and adrenal androgens are synthesized through the coordinated action of a series of steroidogenic enzymes in a zone-specific fashion. Androstenedione; DHEA, dehydroepiandrosterone; DOC, deoxycorticosterone.

GCs are part of the feedback mechanism in the immune system that turns immune activity (inflammation) down. They are therefore used in medicine to treat diseases that are caused by an overactive immune system, such as allergies, asthma, autoimmune diseases and sepsis. GCs have many diverse (pleiotropic) effects, including potentially harmful side effects. They also interfere with some of the abnormal mechanisms in cancer cells, so they are used in high doses to treat cancer.

GCs cause their effects by binding to the glucocorticoid receptor (GR). The activated GR complex in turn up-regulates the expression of anti-inflammatory proteins in the nucleus (a process known as transactivation) and represses the expression of pro-inflammatory proteins in the cytosol by preventing the translocation of other transcription factors from the cytosol into the nucleus (transrepression).

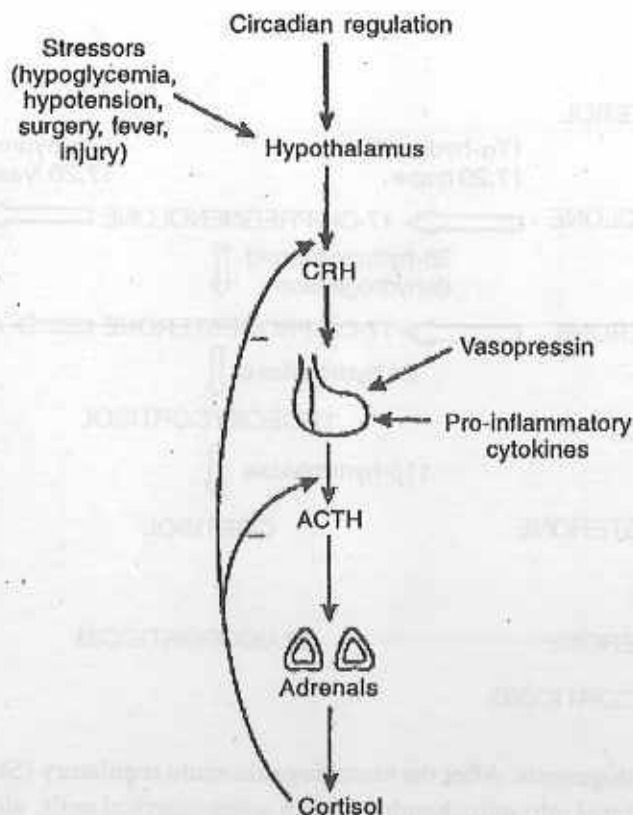


Fig. 2. Normal regulation of adrenal glucocorticoid secretion Adrenocorticotrophic hormone (ACTH) is secreted from the anterior pituitary under the influence of two principal secretagogues, corticotropin-releasing hormone (CRH) and arginine vasopressin; other factors including cytokines also play a role. CRH secretion is regulated by an inbuilt circadian rhythm and additional stressors operate through the hypothalamus. Secretion of both CRH and ACTH is inhibited by cortisol, highlighting the importance of negative feedback control.

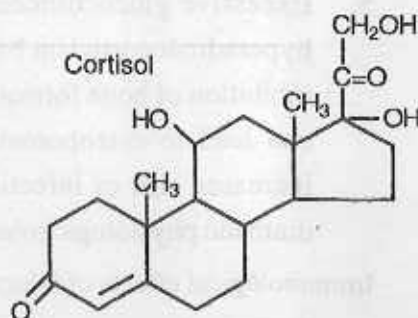
GCs are distinguished from mineralocorticoids and sex steroids by their specific receptors, target cells, and effects. Corticosteroid refers to both glucocorticoids and mineralocorticoids (as both are mimics of hormones produced by the adrenal cortex).

Cortisol (or hydrocortisone) is the most important and abundant human glucocorticoid. It is essential for life, and it regulates or supports a variety of important cardiovascular, metabolic, immunologic, and homeostatic functions. Glucocorticoid receptors are found in

the cells of almost all vertebrate tissues. Various synthetic glucocorticoids are available; these are used either as replacement therapy in glucocorticoid deficiency or to suppress the immune system.

Cortisol and the other glucocorticoids also have a potent anti-inflammatory effect on the body. They depress the immune response, especially cell-mediated immune responses.

For this reason glucocorticoids are widely used in therapy to reduce the inflammatory destruction of rheumatoid arthritis and other autoimmune diseases, to prevent the rejection of transplanted organs and to control asthma.



4.2.1.1 Functions

Glucocorticoid effects may be broadly classified into two major categories: metabolic and immunological. In addition, glucocorticoids play important roles in fetal development.

As discussed in more detail below, glucocorticoids through interaction with the glucocorticoid receptor up-regulate the expression of anti-inflammatory proteins and down-regulate the expression of pro-inflammatory proteins.

The name "glucocorticoid" derives from early observations that these hormones were involved in glucose metabolism. In the fasted state, cortisol stimulates several processes that collectively serve to increase and maintain normal concentrations of glucose in blood.

Metabolic effects of Glucocorticoids :

1. Stimulation of gluconeogenesis, particularly in the liver : This pathway results in the synthesis of glucose from non-hexose substrates such as amino acids and glycerol from triglyceride breakdown, and is particularly important in carnivores and certain herbivores. Enhancing the expression of enzymes involved in gluconeogenesis is probably the best-known metabolic function of glucocorticoids.
2. Mobilization of amino acids from extrahepatic tissues : These serve as substrates for gluconeogenesis.

3. Inhibition of glucose uptake in muscle and adipose tissue : A mechanism to conserve glucose.
4. Stimulation of fat breakdown in adipose tissue : The fatty acids released by lipolysis are used for production of energy in tissues like muscle, and the released glycerol provide another substrate for gluconeogenesis.
5. Excessive glucocorticoid levels resulting from administration as a drug or hyperadrenocorticism have effects on many systems. Some examples include inhibition of bone formation, suppression of calcium absorption (both of which can lead to osteoporosis), delayed wound healing, muscle weakness, and increased risk of infection. These observations suggest a multitude of less-dramatic physiologic roles for glucocorticoids.

Immunological effects of Glucocorticoids :

1. Immunosuppression: Glucocorticoids suppress the cell-mediated immunity. They act by inhibiting genes that code for the cytokines IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-8 and IFN- γ , the most important of which is IL-2. Smaller cytokine production reduces the T cell proliferation. Glucocorticoids do however not only reduce T cell proliferation, but also lead to another well known effect called glucocorticoid induced apoptosis. The effect is more prominent in immature T cells that still reside in the thymus, but also affect peripheral T cells. The exact mechanism underlying this glucocorticoid sensitivity still remains to be elucidated. Glucocorticoids also suppress the humoral immunity, causing B cells to express smaller amounts of IL-2 and of IL-2 receptors. This diminishes both B cell clone expansion and antibody synthesis. The diminished amounts of IL-2 also causes fewer T lymphocyte cells to be activated. Since glucocorticoid is a steroid, it regulates transcription factors.
2. Anti-inflammatory: Glucocorticoids are potent anti-inflammatories, regardless of the inflammation's cause. Glucocorticoids' primary anti-inflammatory mechanism is lipocortin-1 (annexin-1) synthesis. Lipocortin-1 both suppresses phospholipase A2, thereby blocking eicosanoid production, and inhibits various leukocyte inflammatory events (epithelial adhesion, immigration, chemotaxis, phagocytosis, respiratory burst, etc.). In other words, Glucocorticoids not only suppress immune response, but also inhibit the two main products of inflammation,

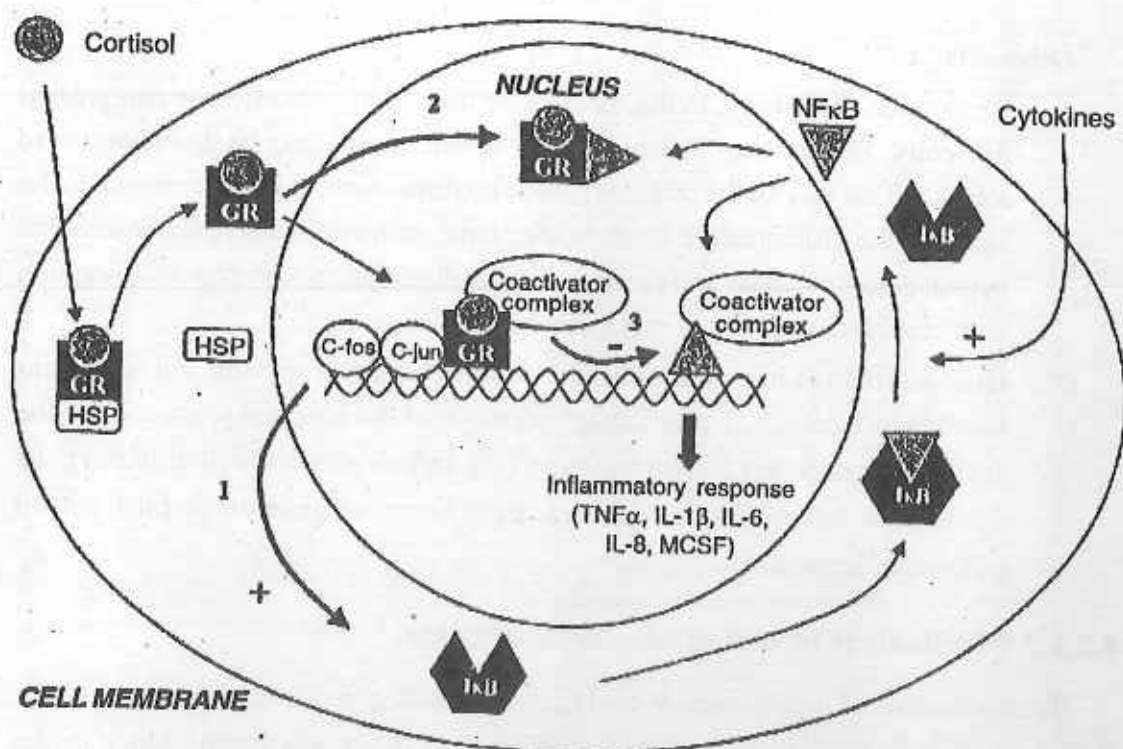


Fig. 3. The anti-inflammatory action of glucocorticoids. Cortisol binds to the cytoplasmic glucocorticoid receptor (GR). Conformational changes in the receptor-ligand complex result in dissociation from heat shock proteins (HSPs) 70 and 90 and migration to the nucleus. Binding occurs to specific DNA motifs—glucocorticoid response elements in association with the activator protein-1 (AP-1) comprising c-fos and c-jun. Glucocorticoids mediate their anti-inflammatory effects through several mechanisms: (1) The inhibitory protein I κ B, which binds and inactivates nuclear factor κ B (NF κ B), is induced. (2) The GR-cortisol complex is able to bind NF κ B and thus prevent initiation of an inflammatory process. (3) Both GR and NF κ B compete for the limited availability of coactivators that include cyclic adenosine monophosphate response element binding protein (CREB) and steroid receptor coactivator-1.

prostaglandins and leukotrienes. In addition, glucocorticoids also suppress cyclooxygenase (both COX-1 and COX-2) expression much like NSAIDs, potentiating the anti-inflammatory effect. Glucocorticoids marketed as anti-inflammatories are often topical formulations, such as nasal sprays for rhinitis or inhalers for asthma. These preparations have the advantage of only affecting the targeted area, thereby reducing side effects or potential interactions.

Other effects :

1. **Resistance:** Resistance to the therapeutic uses of glucocorticoids can present difficulty; for instance, 25% of cases of severe asthma may be unresponsive to steroids. This may be the result of genetic predisposition, ongoing exposure to the cause of the inflammation (such as allergens), immunological phenomena that bypass glucocorticoids, and pharmacokinetic disturbances (incomplete absorption or accelerated excretion or metabolism).
2. Glucocorticoids have multiple effects on fetal development. An important example is their role in promoting maturation of the lung and production of the surfactant necessary for extrauterine lung function. Mice with homozygous disruptions in the corticotropin-releasing hormone gene die at birth due to pulmonary immaturity.

4.2.1.2 Mechanism of action of glucocorticoids

Transactivation : Glucocorticoids bind to the cytosolic glucocorticoid receptor (GR). This type of receptor is activated by ligand binding. After a hormone binds to the corresponding receptor, the newly-formed receptor-ligand complex translocates itself into the cell nucleus, where it binds to glucocorticoid response elements (GRE) in the promoter region of the target genes resulting in the regulation of gene expression. This process is commonly referred to as transactivation.

Dissociation : The ordinary glucocorticoids do not distinguish among transactivation and transrepression and influence both the "wanted" immune and "unwanted" genes regulating the metabolic and cardiovascular functions. Intensive research is aimed at discovering selectively acting glucocorticoids that will be able to repress only the immune system.

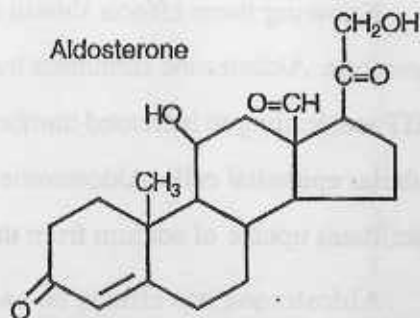
Therapeutic use : Glucocorticoids may be used in low doses in adrenal insufficiency. In much higher doses, glucocorticoids are used to suppress various allergic, inflammatory, and autoimmune disorders. They are also administered as posttransplantory immunosuppressants to prevent the acute transplant rejection and the graft-versus-host disease. Nevertheless, they do not prevent an infection and also inhibit later reparative processes.

Physiological replacement : Any glucocorticoid can be given in a dose that provides approximately the same glucocorticoid effects as normal cortisol production. This is approximately 6-12 mg/m²/day (m² refers to body surface area (BSA), and is a measure of body size; an average man is 1.7 m²).

4.2.2 Mineralocorticoids

Mineralocorticoids are acutely critical for maintenance of life. The mineralocorticoids get their name from their effect on mineral metabolism. Removal of the adrenal glands leads to death within just a few days reflecting a direct result of loss of mineralocorticoid activity. Observation of such an unfortunate subject would reveal several key derangements :

- the concentration of potassium in extracellular fluid becomes dramatically elevated
- urinary excretion of sodium is high and the concentration of sodium in extracellular fluid decreases significantly
- volume of extracellular fluid and blood decrease
- the heart begins to function poorly, cardiac output declines and shock ensues



4.2.2.1 Aldosterone and Mineralocorticoid Receptors

The most important mineralocorticoid is **aldosterone**.

Aldosterone acts on the kidney promoting the reabsorption of sodium ions (Na⁺) into the blood. Water follows the salt and this helps maintain normal blood pressure. Aldosterone also acts on sweat glands to reduce the loss of sodium in perspiration and taste cells to increase the sensitivity of the taste buds to sources of sodium. The secretion of aldosterone is stimulated by a drop in the level of sodium ions in the blood, a rise in the level of potassium ions in the blood and angiotensin II.

4.2.2.2 Functions of Mineralocorticoids

Mineralocorticoids play a critical role in regulating concentrations of minerals - particularly sodium and potassium - in extracellular fluids. As described above, loss of these hormones leads rapidly to life-threatening abnormalities in electrolyte and fluid balance. The major target of aldosterone is the distal tubule of the kidney, where it stimulates exchange of sodium and potassium. Three primary physiologic effects of aldosterone are known. Increased resorption of sodiumic sodium loss in urine is decreased under aldosterone stimulation. Increased resorption of water, with consequent expansion of extracellular fluid volume. This is an osmotic effect directly related to increased resorption of sodium. Increased renal excretion of potassium.

Knowing these effects should quickly suggest the cellular mechanism of action this hormone. Aldosterone stimulates transcription of the gene encoding the sodium-potassium ATPase, leading to increased numbers of "sodium pumps" in the basolateral membranes of tubular epithelial cells. Aldosterone also stimulates expression of a sodium channel which facilitates uptake of sodium from the tubular lumen.

Aldosterone has effects on sweat glands, salivary glands and the colon which are essentially identical to those seen in the distal tubule of the kidney. The major net effect is again to conserve body sodium by stimulating its resorption or, in the case of the colon, absorption from the intestinal lumen. Conservation of water follows conservation of sodium.

4.2.2.3 Physiology

The name mineralocorticoid derives from early observations that these hormones are involved in the retention of sodium—a mineral. The primary endogenous mineralocorticoid is aldosterone, although a number of other endogenous hormones (including progesterone and deoxycorticosterone) have mineralocorticoid function.

Aldosterone acts on the kidneys to provide active reabsorption of sodium and an associated passive reabsorption of water, as well as the active secretion of potassium in the principal cells of the cortical collecting tubule and active secretion of protons via proton ATPases in the luminal membrane of the intercalated cells of the collecting tubule. This in turn results in an increase of blood pressure and blood volume.

Control over aldosterone secretion is truly multifactorial and tied into a spider web of other factors which regulate fluid and electrolyte composition and blood pressure. If the major effects of aldosterone are considered, it is rather easy to predict factors which stimulate or suppress aldosterone secretion. (Fig. 4)

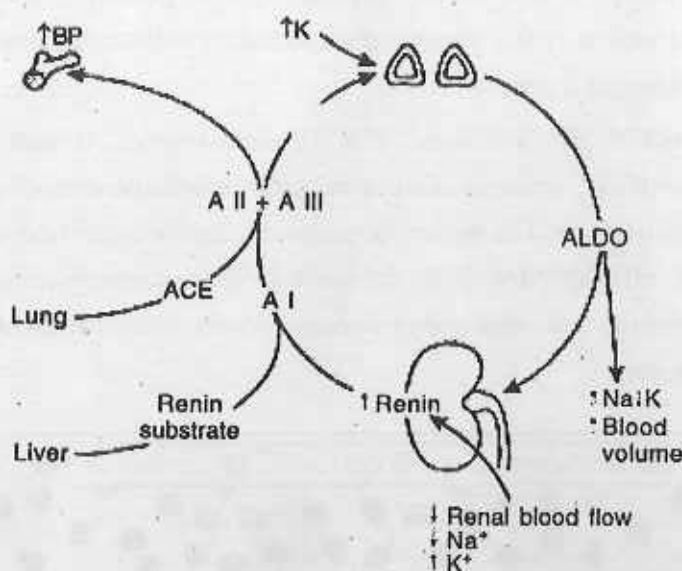


Fig. 4. The normal renin-angiotensin-aldosterone regulatory system. Renin, secreted by the kidney, cleaves angiotensin I (A I) from renin substrate (angiotensinogen), an α_2 -globulin produced by the liver. Angiotensin I is converted into biologically active angiotensin II by angiotensin-converting enzyme (ACE), mainly in the lung. Angiotensin II increases peripheral vascular resistance, and, together with angiotensin III, stimulates aldosterone (ALDO) secretion, which results in sodium retention and increased plasma volume.

The two most significant regulators of aldosterone secretion :

- Concentration of potassium ions in extracellular fluid: Small increases in blood levels of potassium strongly stimulate aldosterone secretion.

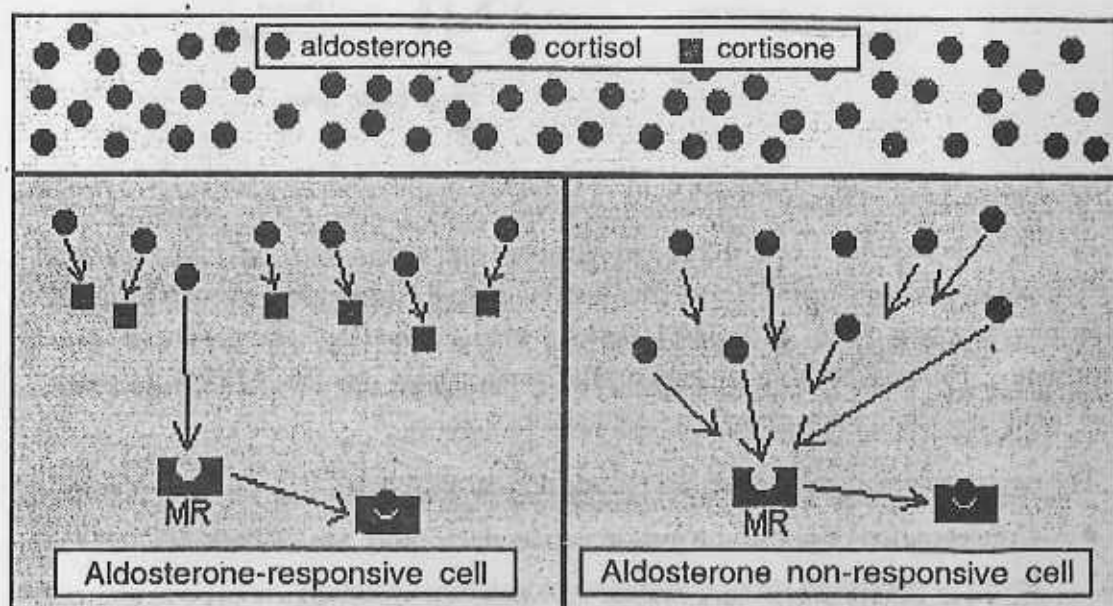
- **Angiotensin II:** Activation of the renin-angiotensin system as a result of decreased renal blood flow (usually due to decreased vascular volume) results in release of angiotensin II, which stimulates aldosterone secretion.

Other factors which stimulate aldosterone secretion include adrenocorticotrophic hormone (short-term stimulation only) and sodium deficiency. Factors which suppress aldosterone secretion include atrial natriuretic hormone, high sodium concentration and potassium deficiency.

4.2.2.4 Mechanism of action of mineralocorticoids

The effects of mineralocorticoids are mediated by slow genomic mechanisms through nuclear receptors as well as by fast nongenomic mechanisms through membrane-associated receptors and signaling cascades.

Cortisol, the major glucocorticoid in non-rodent species, is said to have “weak mineralocorticoid activity”, which is of some importance because cortisol is secreted more abundantly than aldosterone. The mineralocorticoid receptor binds both aldosterone and cortisol with equal affinity. Moreover, the same DNA sequence serves as a hormone response element for the activated (steroid-bound) forms of both mineralocorticoid and glucocorticoid receptors.



In aldosterone-responsive cells, cortisol is effectively destroyed, allowing aldosterone to bind its receptor without competition. Target cells for aldosterone express the enzyme 11-beta-hydroxysteroid dehydrogenase, which has no effect on aldosterone, but converts cortisol to cortisone, which has only a very weak affinity for the mineralocorticoid receptor. In essence, this enzyme "protects" the cell from cortisol and allows aldosterone to act appropriately. Some tissues (e.g. hippocampus) express abundant mineralocorticoid receptors but not 11-beta HSD - they therefore do not show responses to aldosterone because aldosterone is not present in quantities sufficient to compete with cortisol. 11-beta hydroxysteroid dehydrogenase type II catalyzes the deactivation of glucocorticoids to 11-dehydro metabolites.

18 hydroxy 11 deoxycorticosterone (also designated 18OH-DOC) is a steroid hormone probably used to conserve sodium and stimulate hydrogen ion (or acid) excretion. 18OH-DOC lowers urine pH but has no affect on potassium excretion. This would seem to indicate that 18OH-DOC's primary purpose is to stimulate hydrogen ion or ammonium excretion. Under low sodium intake 18 OH DOC is increased in serum. There is a marked increase in serum 18OH DOC after injection of insulin and this may be due to the hypokalemic (low serum potassium) tendency after a rise in insulin which in turn would make the serum more acidic. Since 18OH-DOC lowers urine pH (increases acidity) but has no affect on potassium excretion. This would seem to indicate that 18OH-DOC's primary purpose is to stimulate hydrogen ion or ammonium excretion. Its use by the body to conserve potassium would be indirect by virtue of hydrogen ion's interference with potassium excretion. This interference is further indicated because injecting sodium bicarbonate or even hyperventilating (breathing rapidly beyond need) can triple potassium excretion. The daily rhythm for potassium and hydrogen ion excretion show a rather close inverse relationship, which gives additional circumstantial support to the supposition that they compete at a common site. 18OH-DOC is strongly dependent on the potassium cell or plasma content, because in potassium deficient rats markedly less 18OH-DOC is converted to 18OH-corticosterone and less yet if sodium is deficient.

ACTH (a peptide hormone) has a large affect on 18OH DOC, causing 18OH DOC to go down to zero when ACTH does. This could be for the primary purpose of keeping

serum immune enzymes and cell fluids at a high pH (alkaline) during internal infection, but not doing so during the intestinal infection of diarrhea, during which disease the resulting dehydration forces ACTH to decline. It probably is important normally to keep the vacuoles where pathogens are digested at a high pH because if the pH or alkalinity is not high enough, the pathogens inside the immune cells are not digested and thus released intact. So when an intestinal disease is not calling for ACTH to decline, the indirect potassium conserving attribute of 18OH-DOC by virtue of stimulating acid excretion would be valuable, as would also increased acid excretion during internal disease be valuable.

18OH DOC may act primarily by blocking aldosterone's effect on potassium, and must have aldosterone to assist it with sodium. Nichols, et al., have been able to show that injection of 18OH-DOC, which raised blood levels of this hormone ten times, were more retentive of sodium than a similar amount of aldosterone. So there must be a synergism involved. At the same time, the ratio of sodium to potassium excretion declined very little for 18OH-DOC, while for aldosterone, the ratio fell to as little as 1/3 that of control men. This implies a considerable sparing of potassium by 18OH-DOC. Urine potassium excretion is not altered by 18OH-DOC injection.

Angiotensin II has very little effect on 18OH-DOC and is ambiguous nor does serum potassium above 4.8 mEq/litter (187 mg). This last is not surprising since 18OH-DOC should not be used by the body at high serum potassium. Under low sodium intake, 18OH-DOC rises in the serum. ACTH causes a marked increase in 18OH-DOC, probably by a generalized affect on the zona fasciculata of the adrenal cortex where 18OH-DOC is synthesized. So when it is necessary for sodium to be unloaded during the dehydration induced decline of ACTH during diarrhea in order to preserve osmotic pressure, the resulting 18OH-DOC decline would assist in this.

18OH-DOC is deeply involved in one of the three forms (at least) of hypertension (high blood pressure).

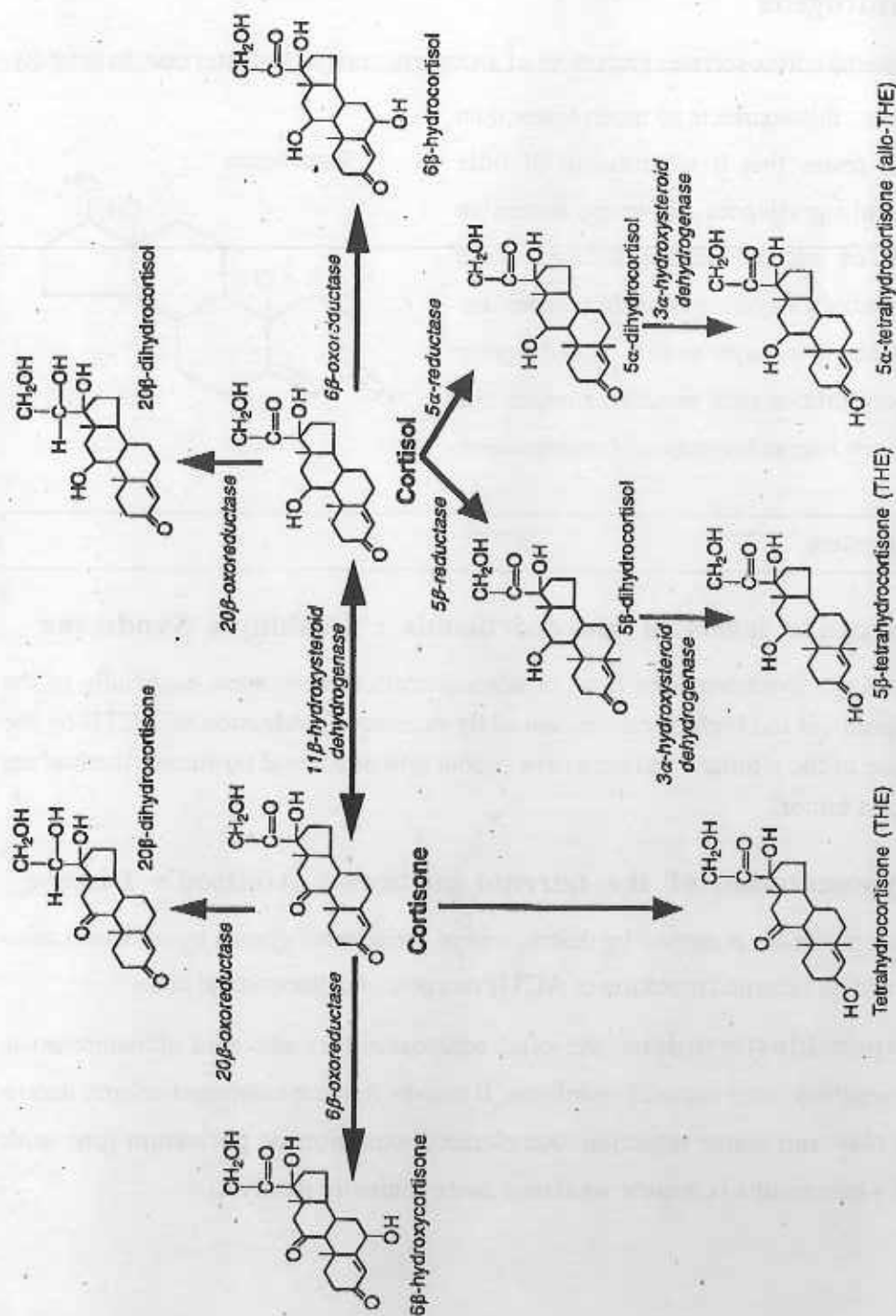


Fig. 5. The principal pathways of cortisol metabolism. Interconversion of hormonally active cortisol to inactive cortisone is catalyzed by two isozymes of 11 β -hydroxysteroid dehydrogenase (11 β -HSD), 11 β -HSD1 principally converting cortisone to cortisol and 11 β -HSD2 the reverse. Cortisol can be hydroxylated at the C6 and C20 positions. A ring reduction is undertaken by 5 α -reductase or 5 β -reductase and 3 α -hydroxysteroid dehydrogenase.

4.2.3 Androgens

The adrenal cortex secretes precursors of androgens such as **testosterone**. In sexually-mature males, this source is so much lower than that of the testes that it is probably of little physiological significance. However, excessive production of adrenal androgens can cause premature puberty in young boys. In females, the adrenal cortex is a major source of androgens. Their hypersecretion may produce a masculine pattern of body hair and cessation of menstruation.



4.3 Diseases

4.3.1 Excessive levels of glucocorticoids : Cushing's Syndrome

In Cushing's syndrome, the level of adrenal cortical hormones, especially of the glucocorticoids, is too high. It can be caused by excessive production of ACTH by the anterior lobe of the pituitary and excessive production of adrenal hormones themselves (because of a tumor).

4.3.2 Hyposecretion of the adrenal cortices : Addison's Disease

Addison's disease is caused by destruction of the adrenal glands by infection, auto immunity and an inherited mutation of ACTH receptor on adinocortical cells.

4.3.3 Hyperaldosteronism (the syndrome caused by elevated aldosterone) is generally resulted from adrenal neoplasm. It causes hypertension and edema due to excessive Na⁺ and water retention. Accelerated excretion of potassium ions with extreme K⁺ loss results in muscle weakness and eventually paralysis.

Unit 5 □ Norepinephrine and Epinephrine : Hormones of the Adrenal Medulla

Structure

5.1 Introduction

5.2 Biosynthesis

5.3 Function

5.3.1 Physiological effects

5.3.2 Mechanism of action

5.3.3 Regulation

5.1 Introduction

The adrenal medulla consists of masses of neurons that are part of the sympathetic branch of the autonomic nervous system. Instead of releasing at a synapse these neurons release their neurotransmitters called **Catecholamines** into the blood. Catecholamines are released in response to stress. They are called catecholamines because they contain a catechol group, and are derived from the amino acid tyrosine.

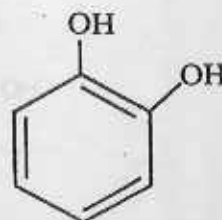


Fig. 1. Catechol group

Thus, although part of the nervous system, the adrenal medulla functions as an endocrine gland. Basically, Norepinephrine, Epinephrine and Dopamine are the principal catecholamines found in the body. Both Norepinephrine and Epinephrine are derived from the amino acid tyrosine. The hormones bind to adrenergic receptors — transmembrane proteins in the plasma membrane of many cell types. The term epinephrine is derived from the Greek roots epi- and nephros, and literally means above the kidney, in reference to the gland's anatomic location. The Latin roots ad- and renes have similar meanings, and give rise to adrenaline. The term "norepinephrine" is derived from the chemical prefix nor-, which indicates that norepinephrine is the next lower homolog of epinephrine. In particular, the two structures are identical except that epinephrine has a methyl group attached to its nitrogen, while the methyl group is replaced by a hydrogen atom in norepinephrine.

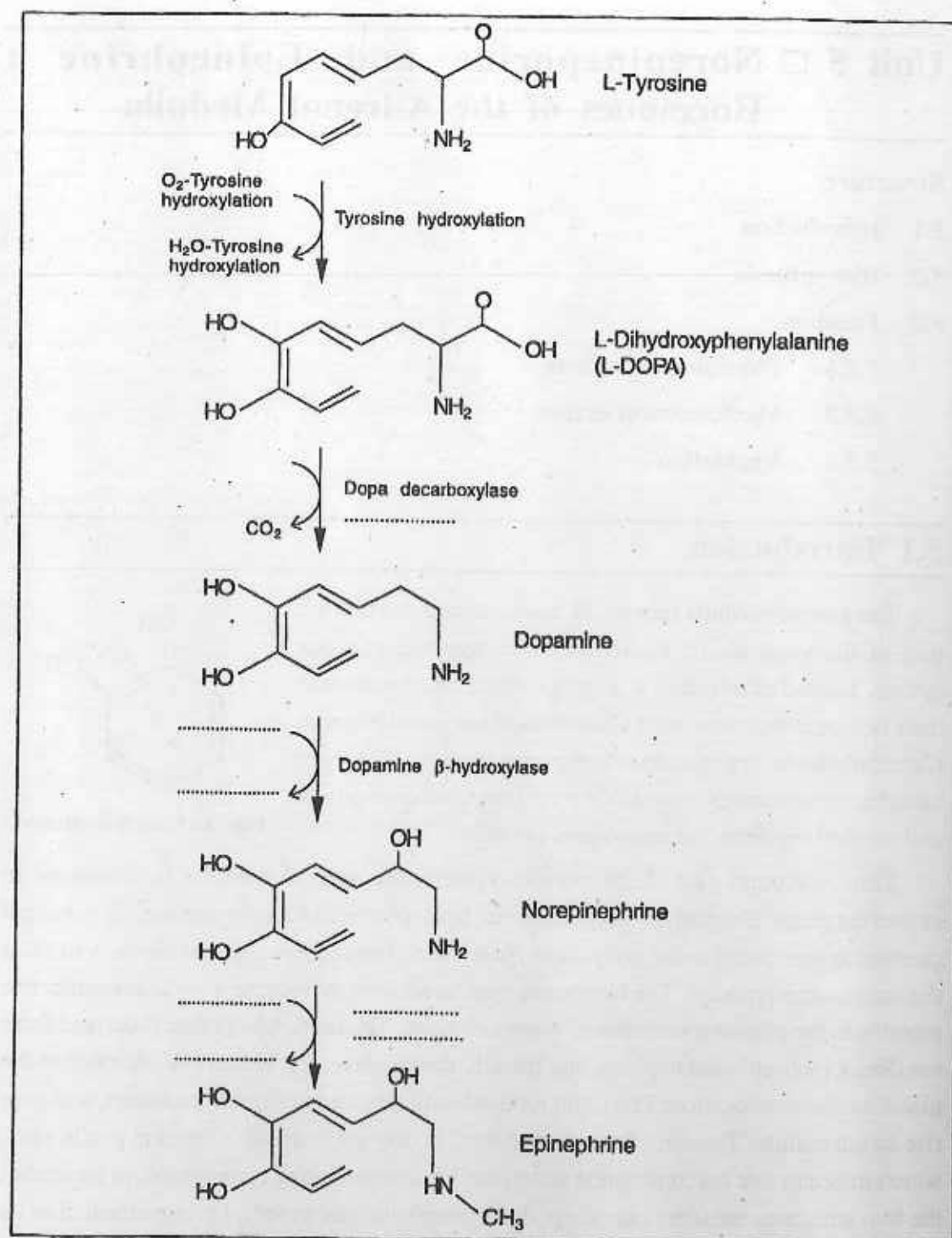


Fig. 2. Biosynthetic pathway of Catecholamines.

5.2 Biosynthesis

Norepinephrine is formed by hydroxylation and decarboxylation of tyrosine, and Epinephrine is synthesized by the methylation of norepinephrine. The synthetic pathway is shared by all catecholamines. Some of the Tyrosine is formed from Phenylalanine, but mostly is of dietary origin. Phenylalanine hydroxylase is found primarily in the liver. Tyrosine is transported into catecholamine secreting adrenal medullary cells by a concentrating mechanism. It is converted to DOPA and then to Dopamine in the cytoplasm of the cells by tyrosine hydroxylase and Dopa decarboxylase. The Dopamine then enters the granulated vesicles and is converted to Norepinephrine by Dopamine β -hydroxylase. L-Dopa is the isomer involved, but the norepinephrine is formed in the D configuration. The rate-limiting step in synthesis is the conversion of tyrosine to Dopa. Tyrosine hydroxylase, catalyzing this step is subject to feedback inhibition by dopamine and norepinephrine. The cofactor for tyrosine hydroxylase is tetrahydrobiopterin. This is converted to dihydrobiopterin, when tyrosine is converted to Dopa.

Some neurons and adrenal medullary cells contain the cytoplasmic enzyme phenylethanolamine-N-Methyltransferase (PNMT). This enzyme catalyzes the conversion of norepinephrine to epinephrine. In these cells, norepinephrine apparently leaves the vesicles, is converted to epinephrine, and then enters the storage vesicles. The catecholamines are held in the granulated vesicles by an active transport system, and the action of this transport system is inhibited by the drug Reserpine.

5.3 Function

5.3.1 Physiological effects

Both of them mimic the effects of noradrenergic nervous discharge. Along with epinephrine, norepinephrine mediates the **fight-or-flight response**, directly increasing heart rate, triggering the release of glucose, and increasing blood flow to skeletal muscle. The fight-or-flight response, also called the 'fright, fight or flight response', 'hyperarousal' or 'the acute stress response', was first described by Walter Cannon in 1915. Animals react to threats with a general discharge of the sympathetic nervous system, priming the

animal for fighting or fleeing. This response was later recognized as the first stage of a general adaptation syndrome (GAS) that regulates stress responses.

However, when norepinephrine acts as a drug it increases blood pressure by its prominent increasing effects on the vascular tone from α -adrenergic receptor activation. The resulting increase in vascular resistance triggers a compensatory reflex that overcomes its direct stimulatory effects on the heart, called the baroreceptor reflex, which results in a drop in heart rate called reflex bradycardia. Epinephrine, when in the bloodstream, it rapidly prepares the body for action in emergency situations. The hormone boosts the supply of oxygen and glucose to the brain and muscles, while suppressing other non-emergency bodily processes (digestion in particular). It increases heart rate and stroke volume, dilates the pupils, and constricts arterioles in the skin and gastrointestinal tract while dilating arterioles in skeletal muscles. It elevates the blood sugar level by increasing catabolism of glycogen to glucose in the liver, and at the same time begins the breakdown of lipids in fat cells. Like some other stress hormones, epinephrine has a suppressive effect on the immune system. All of these effects prepare the body to take immediate and vigorous action. The type of action in various cell types depends on their expression of adrenergic receptors.

Norepinephrine and epinephrine also produce a prompt rise in the metabolic rate that is independent of the liver. This calorogenic action does not occur in the absence of the thyroid and the adrenal cortex. The cause of the initial rise in metabolic rate may be due to cutaneous vasoconstriction, that decreases heat loss leading to an increase in body temperature or muscular activity, or both.

5.3.2 Mechanism of action

The effects of these two hormones are brought about by actions on α - and β -adrenergic receptors. There are two types of α receptors, α_1 and α_2 receptors, while β receptors are subdivided into β_1 , β_2 and β_3 receptors. Both these hormones increase heart rate mediated by β_1 receptors. Norepinephrine produces vasoconstriction in most organs via α_1 receptors, while Epinephrine dilates the blood vessels in skeletal muscle and liver via β_2 receptors. This usually overbalances the vasoconstriction produced by epinephrine elsewhere, and the total peripheral resistance drops. Epinephrine causes a widening of the pulse pressure, but because baroreceptor stimulation is insufficient to obscure the direct effect of the hormone on the heart, cardiac rate and output increase.

Both epinephrine and norepinephrine cause glycogenolysis either via β receptors by increasing cyclic AMP, with activation of phosphorylase, or via α receptors, by increasing intracellular Ca^{2+} . Additionally, both the catecholamines increase secretions of insulin and glucagon via β adrenergic reception mechanism and inhibit their secretion via α adrenergic mechanisms.

5.3.3 Regulation

Neural control :

The physiologic stimuli affect medullary secretion through the nervous system at basal states, the secretion of these hormones is low, and their secretion is further reduced during sleep. Increased adrenal medullary secretion is part of the diffuse sympathetic discharge provoked in emergency. The small granulated vesicles in post ganglionic noradrenergic neurons contain ATP and norepinephrine, and the large granulated vesicles contain neuropeptide Y. There is evidence that low frequency stimulation promotes release of ATP and high frequency stimulation causes release of neuropeptide Y.

The sympathetic nervous system, which acts via splanchnic nerves to the adrenal medulla, stimulates the release of epinephrine. Acetylcholine released by preganglionic sympathetic fibers of these nerves acts on nicotinic acetylcholine receptors and causes cell depolarization and an influx of calcium. Calcium triggers the exocytosis of chromaffin granules and thus the release of epinephrine (and norepinephrine) into the bloodstream. Epinephrine (as with norepinephrine) does exert negative feedback to down-regulate its own synthesis at the presynaptic α_2 adrenergic receptor.

The calorogenic action of catecholamines in animals exposed to cold is important. With such exposure, animals with experimental denervation of the adrenal glands shiver sooner and more vigorously than normal controls. Again, hypoglycemia is a potent stimulus to catecholamine secretion, which enhances the glycogenolysis.

Unit 6 □ Biosynthesis of Sex Steroids

Structure

- 6.1 Hormones of the Ovary**
- 6.2 Metabolism of Steroid Hormones**
- 6.3 Oestrogen**
- 6.4 Progesterone**
- 6.5 Control of Ovarian Functions**
- 6.6 Androgen**
- 6.7 Control of Testicular Function**

6.1 Hormones of the Ovary

The mature ovary actively synthesizes and secretes a variety of hormones. Among these are the steroids, which include estrogens, progesterone, androgens and their precursors. In addition to these substances the ovary also produces relaxin, prostaglandins and other substances that act locally to regulate its function.

The Steroid Hormones :

The ovary is normally the major source of estrogen. The ovary also produces and secretes large amounts of progesterone during the luteal phase of the cycle. It is also the source of small amounts of testosterone and other androgens that serve not only as precursors to estrogen synthesis but also are released into the circulation to act on peripheral tissues.

Biosynthesis of Steroid Hormones :

The steroid hormones are synthesized from cholesterol, which is present in the gland both free and esterified to fatty acids (cholesterol esters). Cholesterol derived either from

circulating lipoproteins or from cholesterol esters in the gland is converted to pregnenolone by removal of a 6-carbon fragment, isocaproic acid. The reaction of or group of reactions is the rate-limiting step in the biosynthetic process and is controlled by luteinizing hormone (LH) from the anterior pituitary.

Pregnenolone formed by this reaction may be converted either to progesterone or to 17 α -hydroxy-pregnenolone. The conversion to progesterone requires the action of 3 β -hydroxysteroid dehydrogenase and $\Delta^{5,4}$ -ketosteroid isomerase, which shifts from the Δ^5 to the Δ^4 position. Progesterone is secreted by the corpus luteum in large amounts following ovulation. However, it also serves as a precursor for androgen and estrogen, which converts it to 17 α -hydroxyprogesterone in the ER. Following 17 α -hydroxylation, the 2-carbon (20-21) side chain may be cleaved by the C17, 20-lyase enzyme to form androgens.

17 α -Hydroxypregnenolone is converted by the lyase enzyme to dehydroepiandrosterone (DHEA). This compound can then be converted to androstenedione by the 2 successive action of enzymes Δ^5 , 3 β -hydroxysteroid dehydrogenase and Δ^5 , 3-ketosteroid isomerase respectively. Androstenedione is the major androgen secreted by the ovary, but small amounts of DHEA and testosterone are also released.

Androstenedione is converted to oestrogen by aromatisation. Aromatisation of androgens to oestrogens occur greatly in the microsome of the cell by a group of enzymes known as the aromatase complex or system and also requires NADAH + molecular O₂. Estradiol, the major oestrogen produced by the ovary, is synthesized by 3 steps hydroxylation of the methyl group of carbone 19, oxidation of this group and hydroxylation at the 2 α position. A 17-hydrogenes enzyme can lead to an interconversion of androstenedione and testosterone, and the interconversion of oestrone and oestradiol.

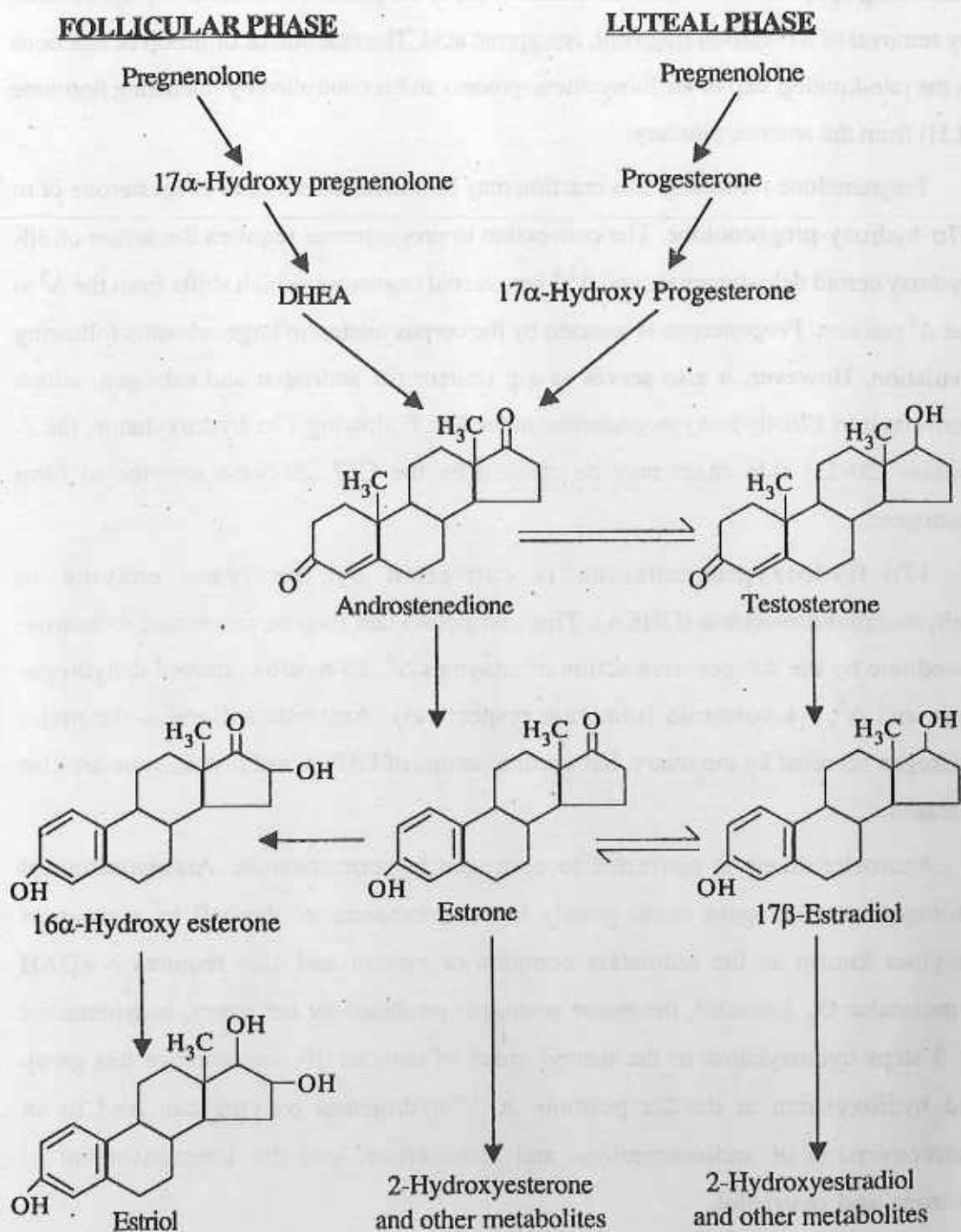


Fig. Biosynthesis and metabolism of estrogens (Basic & clinical pharmacology, lange 1982).

6.2 Metabolism of Sex Steroid Hormones

(1) **Estrogens** : Circulating estradiol is rapidly converted in the liver to estrone by 17 β -hydroxy steroid dehydrogenase. Some of the estrone re-enters the circulation,

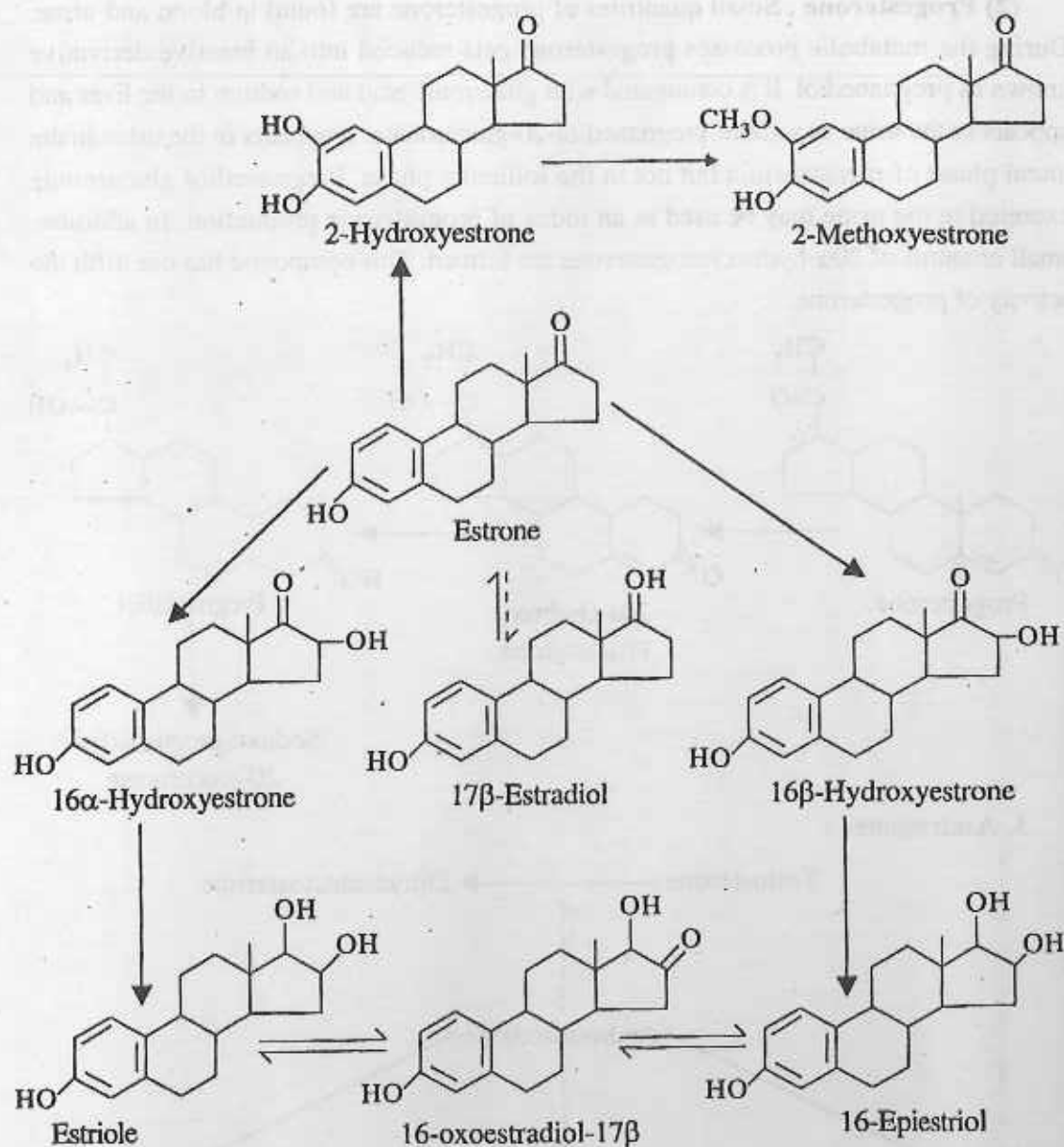
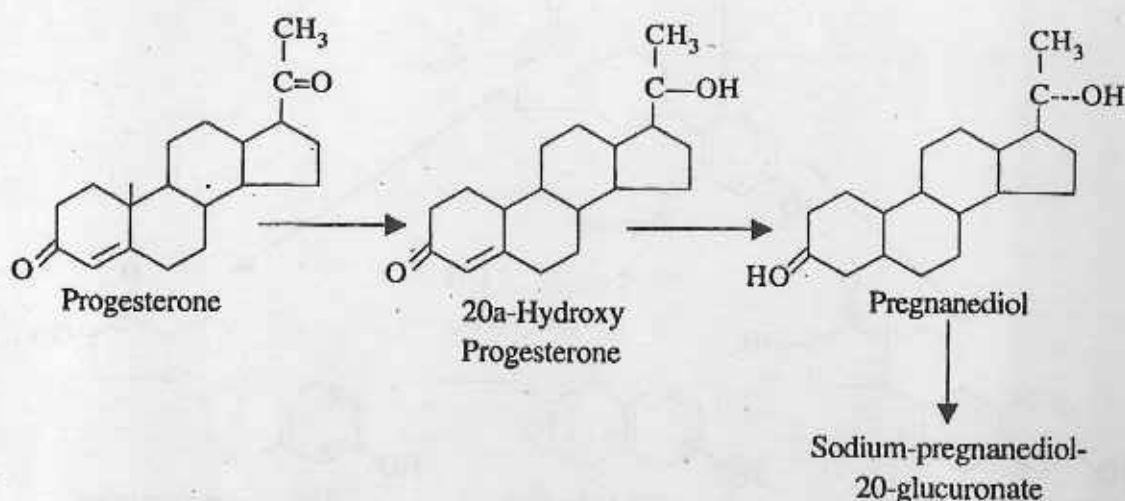


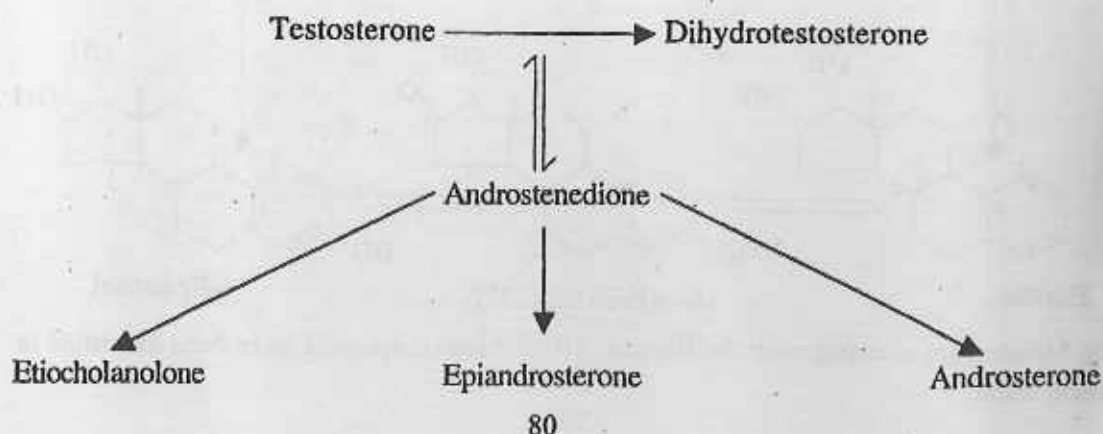
Fig. Metabolism of estrogen in the Human. All of these compounds have been identified in human urine.

however, most of it is further metabolized to 16α -hydroxyestrone (which is then converted to estriol) or to 2-hydroxy-estrone. Much of the estrone is conjugated to form estrone sulfate. Estriol is converted largely to form estriol 3-sulfate-16-glucuronide before excretion by the kidney.

(2) **Progesterone** : Small quantities of progesterone are found in blood and urine. During the metabolic processes progesterone gets reduced into an inactive derivative known as pregnanediol. It is conjugated with glucuronic acid and sodium in the liver and appears in the urine as sodium-pregnanediol-20-glucuronate. It appears in the urine in the luteal phase of menstruation but not in the follicular phase. Pregnanediol glucuronide excreted in the urine may be used as an index of progesterone production. In addition, small amounts of 20α -hydroxyprogesterone are formed. This compound has one-fifth the activity of progesterone.

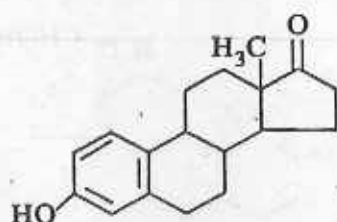


3. Androgens :

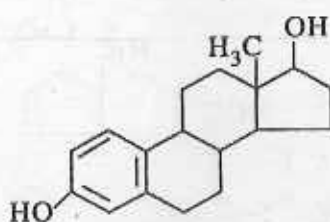


6.3 Oestrogen

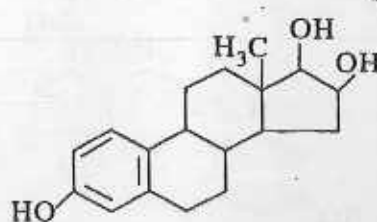
Oestrogen are compounds which can produce oestrus in ovariectomised animals. They are all sterol derivatives. They are less effective by mouth. Their structures are as follows :



Oestrone



17β-oestradiol



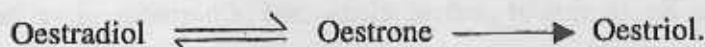
Oestriol

Oestradiol (with—OH at the 17C position)—it is the hormone secreted by the ovary.

Oestrone (with =O at the 17C position) is the possible circulating hormone.

Oestriol (with—OH at the 17C position and an additional ---OH at the 16C position) — It is found in adult female urine and increased during pregnancy, is also to liberated from the placenta.

There is close relationship between oestradiol, oestrone and oestriol in the body such as—



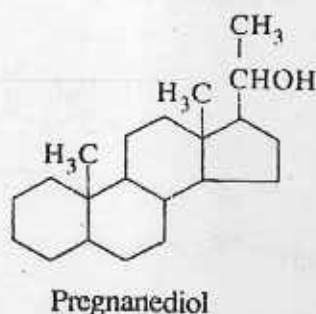
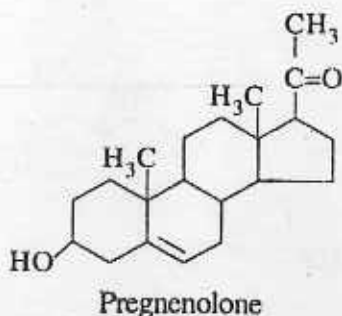
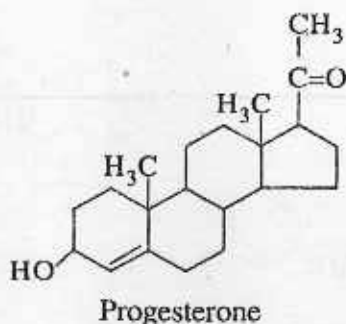
● **Sources :** Ovary is the chief source of oestrogen.

1. From the Graafian follicles—The liquor folliculi and the follicular epithelium are rich in oestrogens.
2. From the ovarian interstitial cells.
3. The oestrogen secreted during the luteal phase of the cycle is formed by the theca lutein cells of the corpus luteum.

In addition, the oestrogen also is secreted from adrenal cortex, testes and placenta.

6.4 Progesterone

Progesterone is the active principle of corpus luteum. It is a sterol derivative with a side chain at the 17C position. It is found in two crystalline forms, eg- α and β .



- Sources : (i) Corpus between
- (ii) Placenta
- (iii) Adrenal cortex.

6.5 Control of Ovarian Functions

1. The Hypothalamic—Hypophysial—Ovarian axis

After hypophysectomy the ovaries are atrophied and follicles do not develop beyond the antrum stage. Regulation of gamete release and of hormone secretion by the ovary is mediated by the pituitary gonadotropins. These protein hormones are synthesized and released by the pituitary under hypothalamic regulation.

(a) Effect of pituitary gonadotrophins :

FSH controls (a) maturation of the Graafian follicles and (b) Secretion of oestrogens. luteinizing hormone (LH) causes ovulation of the follicle that has been ripened by FSH, formation, growth and maintenance of corpus luteum and secretion of progesterone.

It seems probable that pure FSH does not cause estrogen secretion but that small amounts of LH are necessary for oestrogen production.

The structural and functional maintenance of the corpus luteum by a luteotropin (probably prolactin) is clearly established only in the rat. In larger mammals including the human, the corpus luteum probably has a predestined life and an intrinsic secretory activity that are initiated by LH at the time of ovulation.

(b) Effect of Hypothalamic centre :

The synthesis and release of gonadotropins by the pituitary is regulated by centers in the hypothalamus that mediated their effects by neurohumoral substances which are transported to the anterior lobe through the portal vessels. These vessels originate in the median eminence of the hypothalamus and terminate in the anterior pituitary. Direct nervous control of the anterior pituitary appears to be of negligible importance, because lesion of the hypothalamus causes abolition of gonadotrophic hormone secretion and atrophy of the ovary along with changes in the reproductive organs and stoppage of sexual cycle.

In the lower species that have been extensively investigated, different are as of the hypothalamus appears to regulate release of different gonadotropins, but other centers inhibit the release of gonadotropins. The human child becomes sexually nature precociously because of the presence of lesions in the posterior hypothalamus that normally inhibits untimely release of gonadotropins.

(c) Effect of ovarian steroids :

Ovarian steroids exert a regulating influence on gonadotropin secretion, mediated probably through hypothalamic centers.

1. Negative feed-back : Under normal conditions, ovarian steroids limit or reduce the secretions of pituitary gonadotropins. Serum concentrations of both FSH + LH are increased markedly following ovariectomy or in postmenopausal women, whereas administration of estrogen (or estrogen and progesterone) lowers serum gonadotropins levels. Throughout the normal menstrual cycle, the negative feed back effects of ovarian steroids predominate.

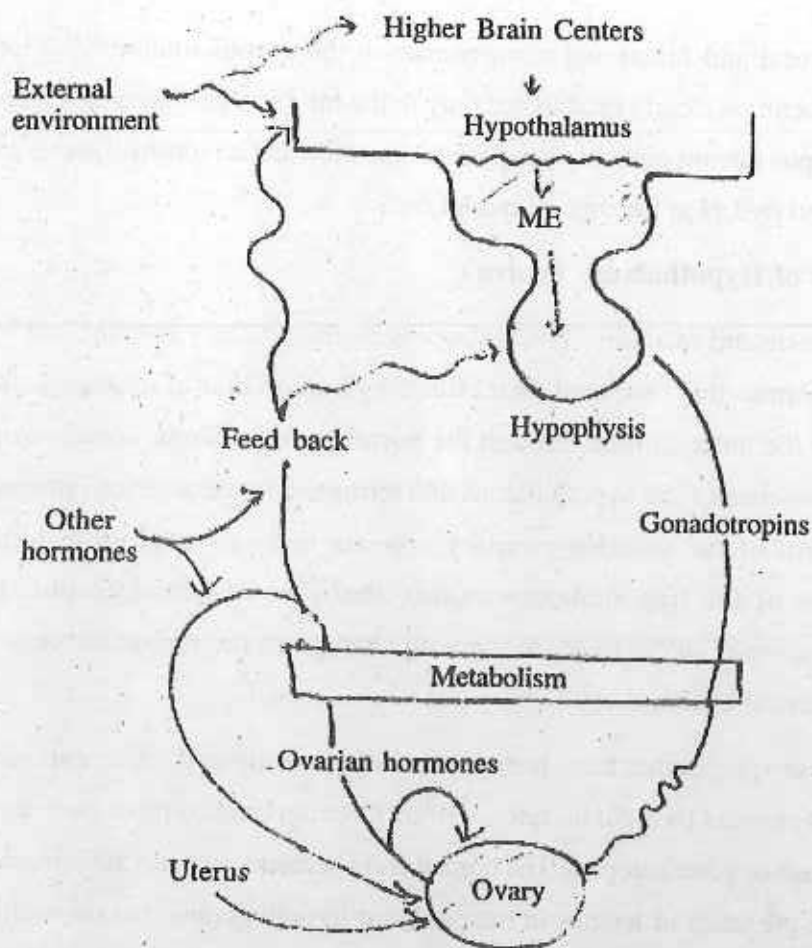


Fig. Hypothalamic-hypophysial-ovarian circuit. Schematic representation with some of the variables that may modify function. The undulations in the arrows indicate rhythmicity.

2. Positive feed-back : Estradiol and progesterone under certain conditions, can induce the release of LH and FSH. During the menstrual cycle, rising concentration of estradiol in the latter part of the follicular phase initiate the preovulatory surge of LH via this mechanism. This increase in LH secretion in turn stimulates a small but significant increase in the secretion of progesterone which in turn with estradiol initiates the mid cycle surge of FSH.

It is probable that the negative and positive feedback actions of ovarian sex steroids result from both (1) a direct effect of the steroids on the pituitary gonadotropes that alters their sensitivity to GnRH and (2) Modulation of the frequency and magnitude of the pulses of hypothalamic GnRH.

Uterus : It is possible that uterine endometrium synthesizes a specific luteolytic factor named as luteolysin, which acting on the ovary, causes involution of corpus luteum. The uterine effect is not mediated through pituitary, it is a direct one.

3. Pineal gland : It is postulated that melatonin or some other active principle present in the pineal gland has antigonadal activity. The action may occur directly or through anterior pituitary and control nervous system.

4. In addition, there are some other endocrine glands such as adrenal cortex, thyroid, and thymus, and physical factors such as diet, vitamins and temperature may influence ovarian function.

6.6 Androgen

Androgens are substances having masculinising properties. Both in the testis and adrenal of acids, the androgens can be synthesized either from cholesterol or directly from acetyl CoA.

Chemistry and varieties :

Androgens are C-19 sterol compounds. They have 2 varieties (a) natural (b) synthetic. The chief natural androgen is called Testosterone. Methyl testosterone and testosterone propionate are important synthesis androgens, which are effective by mouth and are easily absorbed and unaffected by liver. Natural androgens are mostly inactivated by liver. Hence not much effective by mouth. *Activity increases if combined with fatty acids, such as propionic acid.* The chief degradation products of androgens are the 17-ketosteroids (17-Ks), androsterone and dehydroepiandrosterone (DHEA).

Testosterone, Δ^4 -androstenedione and dehydroepiandrosterone are the main circulatory androgens of testicular origin. Testosterone is more potent than the others. In contrast the adrenal cortex secretes DHEA and Δ^4 -androstenedione as its major androgens.

In 1965, it was shown that androgen stimulation of accessory sexual glands is not due to testosterone but *due to the reduction of testosterone dehydrotestosterone (DHT) 5 γ 5 α reductase*. DHT is the principal intracellular androgen that occurs mainly in the liver. DHT is bound by specific nuclear and cytoplasmic protein. The accessory sexual glands are sites of specific retention and accumulation of DHT complexes. The DHT receptor complex binds to DNA giving rise to stimulation of RNA synthesis.

Biosynthesis of androgens :

Interstitial cells of Leydig are the target cells that are stimulated by *gonadotrophins* for an increased synthesis of androgens. The chief products which are secreted into the spermatogenic venous blood of adult testes are testosterone and smaller quantities of Δ^4 -androstenedione and DHEA. Tissues other than Leydig cells also have the ability to transform steroid precursors to testosterone. These include the seminiferous tubules, liver, adrenal cortex, prostate gland and skeletal muscle.

The immediate precursor of the gonadal steroid as with the adrenal steroid is cholesterol. The initial alteration of the cholesterol molecule involves cleavage at the side chain to yield Δ^5 pregnenolone. The conversion of pregnenolone to estrone requires the action of 5 enzymes (i) 3β -hydroxysteroid dehydrogenase (ii) Δ^5 , Δ^4 -isomerase (iii) 17-hydroxylase (iv) 17, 20-desmolase (v) 17-ketoreductase.

Pregnenolone seems to be the common substrate for all of the normal steroids. Conversion of pregnenolone requires 3β -hydroxysteroid dehydrogenase which oxidises the hydroxyl group at position 3 and an isomerase which changes the Δ^5 double bond to Δ^4 , to yielding progesterone. The progesterone can serve as a precursor for androgens in both the ovaries and testis.

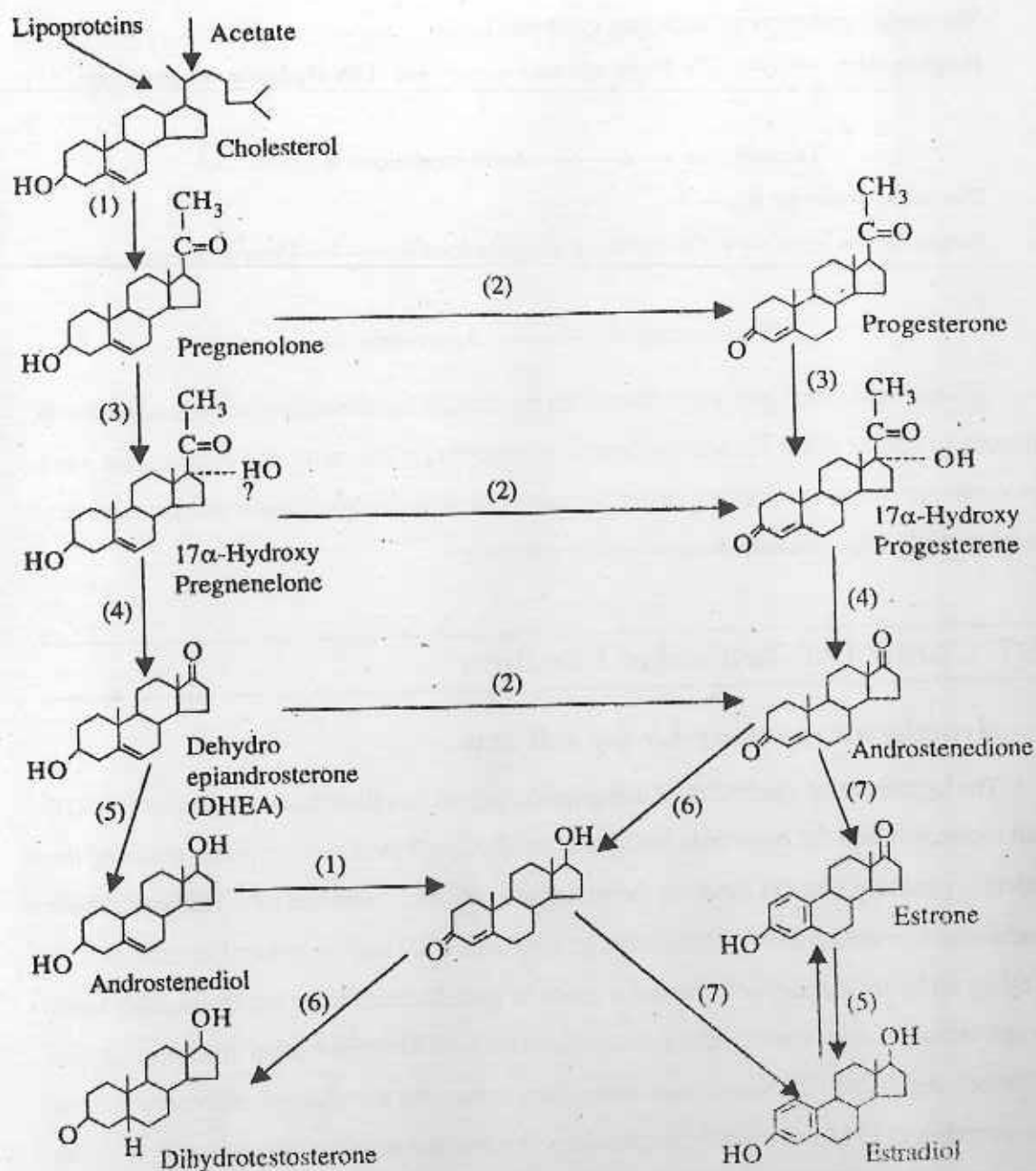
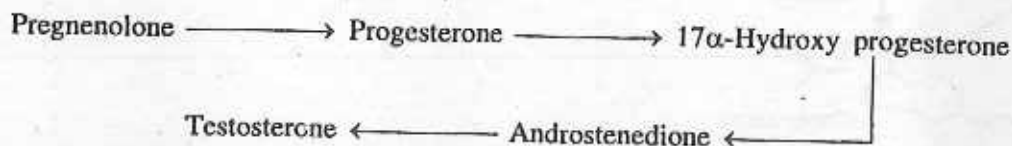
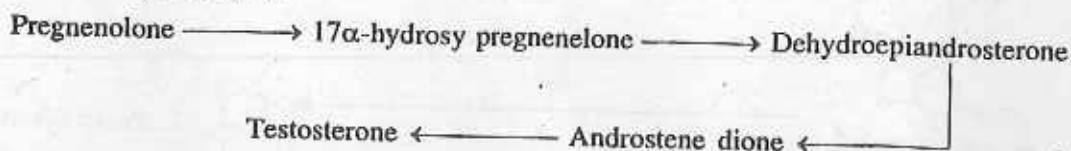


Fig. Pathways for testicular androgen and estrogen biosynthesis. Heavy arrows indicate major pathways circled number represent enzymes as follows : (1) = 20,22-desmolase (2) = 3 β -hydroxysteroid dehydrogenase and Δ^5 , Δ^4 -ketosteroid isomerase (3) = 17-hydroxylase (4) = 17, 20-demolase (5) = 17-ketoreductase (6) = 5 α -reductase (7) = aromatase

The major pathways of androgen synthesis is :—



The other pathway is :—



Several additional pathways have been postulated but the ability of human endocrin tissues to utilize them for steroid hormone production has not been proved one such possible pathways involves the direct formation of dehydroepiandrosterone from cholesterol without a C₂₁ intermediate.

6.7 Control of Testicular Function

Hypothalamic-pituitary-Leydig cell axis :

The hypothalamus synthesizes a decapeptide, gonadotropin-releasing hormone (GnRH) and secretes it into the hypothalamo hypothyseal portal blood system. After reaching the anterior pituitary, GnRH binds to the gonadotropes and stimulates the release of both luteinizing hormone (LH/ICSH) and, to a lesser extent, FSH into the general circulation. LH is taken up by the Leydig cells, where it binds to specific membrane receptors. This leads to activation of adenylate cyclase and generation of cAMP and other messengers that ultimately results into the secretion of androgens. In turn, the elevation of androgens inhibits the secretion of LH from the anterior pituitary through the negative feedback action on the pituitary and an inhibitory effect at the hypothalamic level. The inhibitory effect of androgens on the hypothalamus is mediated principally by estradiol, which is formed locally in the hypothalamus from androgens.

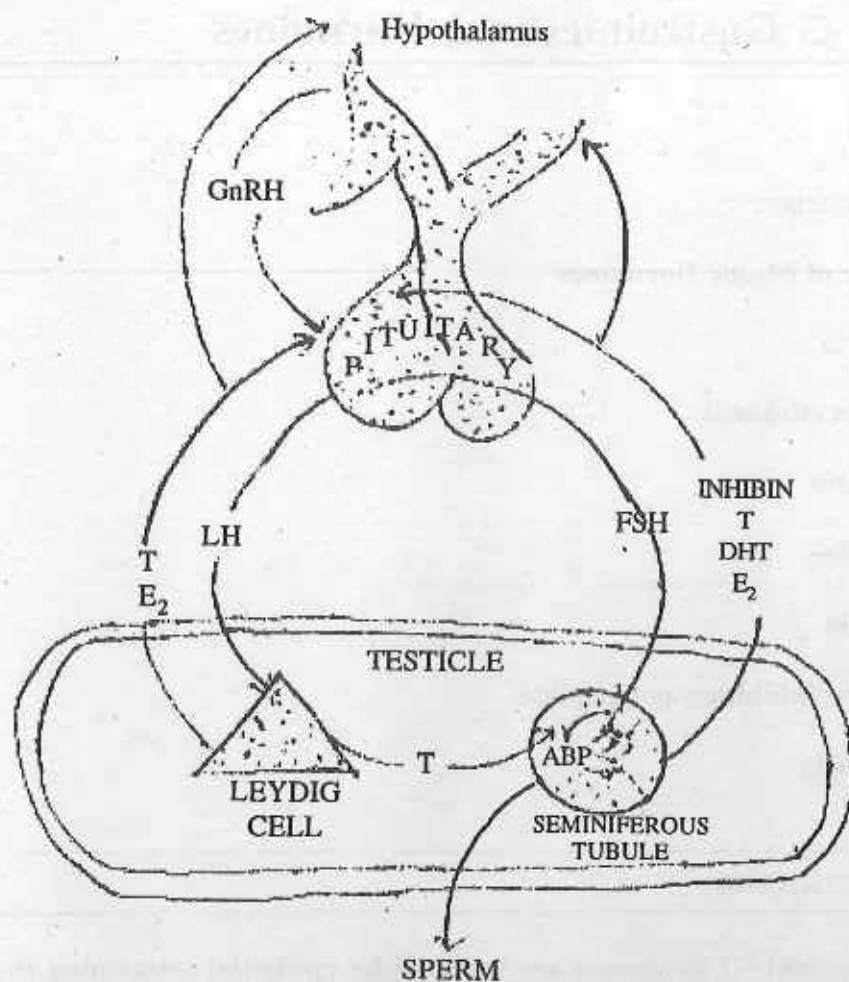


Fig. Hypothalamic-pituitary-testicular axis.

GnRH gonadotropin-releasing hormone

LH luteinizing hormone

FSH Follicle-stimulating hormone

T Testosterone

DHT dihydrotestosterone

ABP androgen binding protein

E₂ Estradiol

+ +ve influence

- -ve influence

Unit 7 □ Gastrointestinal Hormones

Structure

- 7.1 Introduction**
- 7.2 Table of Major Hormones**
- 7.3 Gastrin**
- 7.4 Cholecystokinin**
- 7.5 Secretin**
- 7.6 Ghrelin**
- 7.7 Motilin**
- 7.8 Gastric inhibitory polypeptide**
- 7.9 Summary**

7.1 Introduction

The classical GI hormones are secreted by epithelial cells lining the lumen of the stomach and small intestine. These hormone-secreting cells - endocrinocytes - are interspersed among a much larger number of epithelial cells that secrete their products (acid, mucus, etc.) into the lumen or take up nutrients from the lumen. GI hormones are secreted into blood, and hence circulate systemically, where they affect function of other parts of the digestive tube, liver, pancreas, brain and a variety of other targets.

The following table summarizes the effects and stimuli for release of the major gastrointestinal hormones, each of which is discussed in more detail in subsequent pages :

7.2 Table of Major Hormones

Hormone	Major Activities	Stimuli for Release
Gastrin	Stimulates gastric acid secretion and proliferation of gastric epithelium	Presence of peptides and amino acids in gastric lumen
Cholecystokinin	Stimulates secretion of pancreatic enzymes, and contraction and emptying of the gall bladder	Presence of fatty acids and amino acids in the small intestine
Secretin	Stimulates secretion of water and bicarbonate from the pancreas and bile ducts	Acidic pH in the lumen of the small intestine
Ghrelin	Appears to be a strong stimulant for appetite and feeding; also a potent stimulator of growth hormone secretion	Not clear, but secretion peaks prior to feeding and diminishes with gastric filling
Motilin	Apparently involved in stimulating housekeeping patterns of motility in the stomach and small intestine	Not clear, but secretion is associated with fasting
Gastric inhibitory polypeptide	Inhibits gastric secretion and motility, and potentiates release of insulin from beta cells in response to elevated blood glucose concentration	Presence of fat and glucose in the small intestine

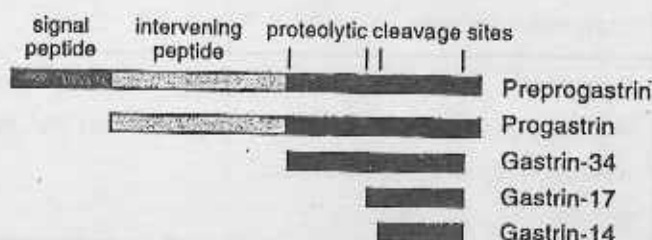
There are a *bunch* of hormones, neuropeptides and neurotransmitters that affect gastrointestinal function. Interestingly, a number of the classical GI hormones are also synthesized in the brain, and sometimes referred to as "brain-gut peptides". The significance of this pattern of expression is not clear.

7.3 Gastrin

Gastrin is a major physiological regulator of gastric acid secretion. It also has an important trophic or growth-promoting influence on the gastric mucosa. Gastrin is synthesized in G cells, which are located in gastric pits, primarily in the antrum region of the stomach and binds with the receptors, found predominantly on parietal and enterochromaffin-like cells.

Structure of Gastrin and the Gastrin Receptor

Gastrin is a linear peptide that is synthesized as a preprohormone and is post-translationally cleaved to form a family of peptides with identical carboxytermini. The predominant circulating form is gastrin-34 ("big gastrin"), but full biologic activity is present in the smallest peptide (gastrin-14 or minigastrin). Further, full bioactivity is preserved in the five C-terminal amino acids of gastrin, which is known as pentagastrin. The five C-terminal amino acids of gastrin and cholecystokinin are identical, which explains their overlapping biological effects.



The gastrin receptor is also one of the receptors that bind cholecystokinin, and is known as the CCK-B receptor. It is a member of the G protein-coupled receptor family. Binding of gastrin stimulates an increase in intracellular Ca^{++} , activation of protein kinase C, and production of inositol phosphate.

Control and Physiologic Effects of Gastrin

The primary stimulus for secretion of gastrin is the presence of certain foodstuffs, especially peptides, certain amino acids and calcium, in the gastric lumen. Also, as yet unidentified compounds in coffee, wine and beer are potent stimulants for gastrin secretion. Secretion of this hormone is inhibited when the luminal pH of the stomach becomes very low (less than 3 approximately).

Gastrin appears to have at least two major effects on gastrointestinal function :

- **Stimulation of gastric acid secretion:** Gastrin receptors are found on parietal cells, and binding of gastrin, along with histamine and acetylcholine, leads to fully-stimulated acid secretion by those cells. Canine parietal cells have roughly 44,000 gastrin receptors each, and in that species, it has been demonstrated that immunoneutralization of gastrin blocks secretion of acid in response to intragastric administration of peptides. Enterochromaffin-like (ECL) cells also bear gastrin receptors, and recent evidence indicates that this cell may be the most important target of gastrin with regard to regulating acid secretion. Stimulation of ECL cells by gastrin leads to histamine release, and histamine binding to H₂ receptors on parietal cells is necessary for full-blown acid secretion.
- **Promotion of gastric mucosal growth:** Gastrin clearly has the ability to stimulate many aspects of mucosal development and growth in the stomach. Treatment with gastrin stimulates DNA, RNA and protein synthesis in gastric mucosa and increases the number of parietal cells. Another observation supporting this function is that humans with hypergastrinemia (abnormally high blood levels of gastrin) consistently show gastric mucosal hypertrophy.

In addition to parietal and ECL cell targets, gastrin also stimulates pancreatic acinar cells via binding to cholecystikinin receptors, and gastrin receptors have been demonstrated on certain populations of gastric smooth muscle cells, supporting pharmacologic studies that demonstrate a role for gastrin in regulating gastric motility.

Disease States

Excessive secretion of gastrin, or **hypergastrinemia**, is a well-recognized cause of a severe disease known as Zollinger-Ellison syndrome, which is seen at low frequency in man and dogs. The hallmark of this disease is gastric and duodenal ulceration due to excessive and unregulated secretion of gastric acid. Most commonly, hypergastrinemia is the result of gastrin-secreting tumors (gastrinomas), which develop in the pancreas or duodenum.

7.4 Cholecystikinin

Cholecystikinin plays a key role in facilitating digestion within the small intestine. It is secreted from mucosal epithelial cells in the first segment of the small

intestine (duodenum), and stimulates delivery into the small intestine of digestive enzymes from the pancreas and bile from the gallbladder. Cholecystokinin is also produced by neurons in the enteric nervous system, and is widely and abundantly distributed in the brain.

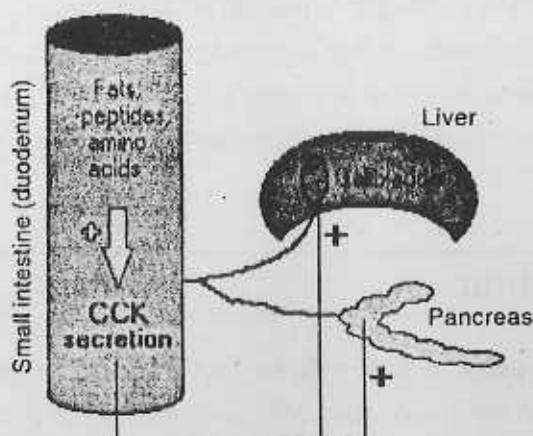
Structure of Cholecystokinin and Its Receptors

As mentioned previously, cholecystokinin and gastrin are highly similar peptides. Like gastrin, cholecystokinin is a linear peptide that is synthesized as a preprohormone, then proteolytically cleaved to generate a family of peptides having the same carboxy ends. Full biologic activity is retained in CCK-8 (8 amino acids), but peptides of 33, 38 and 59 amino acids are also produced. In all of these CCK peptides, the tyrosine seven residues from the end is sulfated, which is necessary for activity.

Two receptors that bind cholecystokinin have been identified. The CCK_A receptor is found abundantly on pancreatic acinar cells. The CCK_B receptor, which also functions as the gastrin receptor, is the predominant form in brain and stomach. Both receptors are having seven transmembrane domains typical of G protein-coupled receptors.

Control and Physiologic Effects of Cholecystokinin

Foodstuffs flowing into the small intestine consist mostly of large macromolecules (proteins, polysaccharides and triglyceride) that must be digested into small molecules (amino acids, monosaccharides, fatty acids) in order to be absorbed. Digestive enzymes from the pancreas and bile salts from the liver (which are stored in the gallbladder) are critical for such digestion. Cholecystokinin is the principle stimulus for delivery of pancreatic enzymes and bile into the small intestine.



The most potent stimuli for secretion of cholecystokinin are the presence of partially-digested fats and proteins in the lumen of the duodenum (a particularly potent stimulus is pictured above). An elevation in blood concentration of cholecystokinin has two major effects that facilitate digestion :

- **Release of digestive enzymes from the pancreas** into the duodenum. Older literature refers to cholecystokinin as *pancreozymin*, a term coined to describe this effect.
- **Contraction of the gallbladder to deliver bile** into the duodenum. The name cholecystokinin (to "move the gallbladder") was given to describe this effect. Cholecystokinin is also known to stimulate secretion of bile salts into the biliary system.

Pancreatic enzymes and bile flow through ducts into the duodenum, leading to digestion and absorption of the molecules that stimulate cholecystokinin secretion. Thus, when absorption is completed, cholecystokinin secretion ceases.

Injection of cholecystokinin into the ventricles of the brain induces satiety (lack of hunger) in laboratory animals. In view of its pattern of secretion relative to feeding, it would make physiologic sense that this hormone might participate in control of food intake. However, recent experiments suggest that cholecystokinin is at best a minor player in regulation of food intake.

In addition to its synthesis in small intestinal epithelial cells, cholecystokinin has been clearly demonstrated in neurons within the wall of the intestine and in many areas of the brain. It seems, in fact, to be the most abundant neuropeptide in the central nervous system. Secretion of cholecystokinin from neurons appears to modulate the activity of other hormones and neuropeptides, but it seems safe to say the understanding its role in function of the brain is rudimentary at best.

Disease States

Diseases resulting from excessive or deficient secretion of cholecystokinin are rare. Cholecystokinin deficiency has been described in humans as part of autoimmune polyglandular syndrome, and manifests as a malabsorption syndrome clinically similar to pancreatic exocrine insufficiency. Additionally, there is mounting evidence that aberrations in expression of cholecystokinin or its receptor within the human brain may cause certain types of anxiety

and schizophrenia. Clearly, a much better understanding of the role of cholecystokinin in brain function is required.

7.5 Secretin

The small intestine is periodically assaulted by a flood of acid from the stomach, and it is important to put out that fire in a hurry to avoid acid burns. *Secretin functions as a type of fireman; it is released in response to acid in the small intestine, and stimulates the pancreas and bile ducts to release a flood of bicarbonate base, which neutralizes the acid.* Secretin also has some historical interest, as it was discovered as the first hormone.

Structure of Secretin and Its Receptors

Secretin is synthesized as a preprohormone, then proteolytically processed to yield a single 27-amino acid peptide by removal of the signal peptide plus amino and carboxy-terminal extensions. The sequence of the mature peptide is related to that of glucagon, vasoactive intestinal peptide and gastric inhibitory peptide.

The secretin receptor has seven membrane-spanning domains, characteristics of a G protein-coupled receptor.

Control and Physiologic Effects of Secretin

Secretin is secreted in response to one known stimulus : acidification of the duodenum, which occurs most commonly when liquified ingested food from the stomach are released into the small intestine.

The principal target for secretin is the pancreas, which responds by secreting a bicarbonate-rich fluid, which flows into the first part of the intestine through the pancreatic duct. Bicarbonate ion is a base and serves to neutralize the acid, thus preventing acid burns and establishing a pH conducive to the action of other digestive enzymes. A similar, but quantitatively less important response to secretin is elicited by bile duct cells, resulting in additional bicarbonate being dumped into the small gut.

As acid is neutralized by bicarbonate, the intestinal pH rises toward neutrality, and secretion of secretin is turned off.

Disease States

Diseases associated with excessive or deficient secretion of secretin are not recognized.

7.6 Ghrelin

Structure of Ghrelin and Its Receptor

Ghrelin is synthesized as a preprohormone, then proteolytically processed to yield a 28-amino acid peptide. An interesting and unique modification is imposed on the hormone during synthesis in the form of an n-octanoic acid bound to one of its amino acids; this modification is necessary for biologic activity.

Synthesis of ghrelin occurs predominantly in epithelial cells lining the fundus of the stomach, with smaller amounts produced in the placenta, kidney, pituitary and hypothalamus.

The ghrelin receptor was known well before ghrelin was discovered. Cells within the anterior pituitary bear a receptor that, when activated, potently stimulates secretion of growth hormone and that receptor was named as the **growth hormone secretagogue receptor (GHS-R)**. The natural ligand for the GHS-R was announced in 1999 as ghrelin, and ghrelin was named for its ability to provoke growth hormone secretion (the suffix ghre means "grow").

Ghrelin receptors are present on the cells in the pituitary that secrete growth hormone, and also have been identified in the hypothalamus, heart and adipose tissue.

Control and Physiologic Effects of Ghrelin

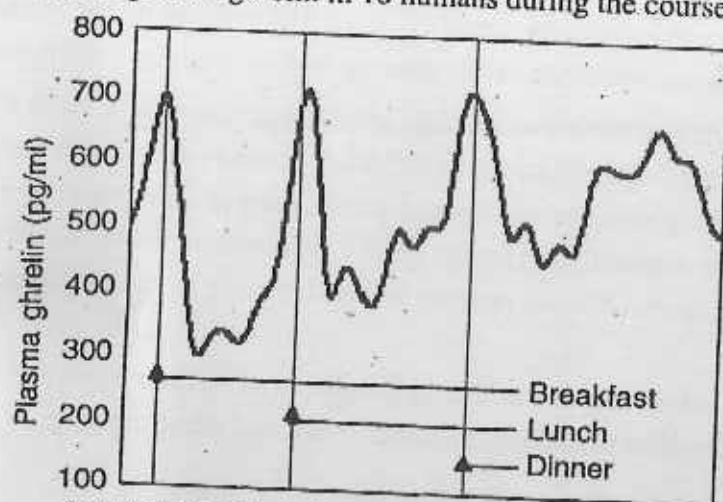
At least two major biologic activities have been ascribed to ghrelin :

- **Stimulation of growth hormone secretion :** Ghrelin, as the ligand for the growth hormone secretagogue receptor, potently stimulates secretion of growth hormone. The ghrelin signal is integrated with that of growth hormone releasing hormone and somatostatin to control the timing and magnitude of growth hormone secretion.
- **Regulation of energy balance :** In both rodents and humans, **ghrelin functions to increase hunger** though its action on hypothalamic feeding centers. This makes sense relative to increasing plasma ghrelin concentrations observed during fasting (see below). Additionally, humans injected with ghrelin reported sensations

of intense hunger. Ghrelin also appears to **suppress fat utilization in adipose tissue**, which is somewhat paradoxical considering that growth hormone has the opposite effect. Ghrelin seems to be one of several hormonal signals that communicates the state of energy balance in the body to the brain.

Other effects of ghrelin include stimulating gastric emptying activity having a variety of positive effects on cardiovascular function (e.g. increased cardiac output). It is not totally clear whether the cardiovascular effects are a direct effect of ghrelin or represent an indirect effect of ghrelin's ability to stimulate growth hormone secretion.

Blood concentrations of ghrelin are lowest shortly after consumption of a meal, then rise during the fast just prior to the next meal. The figure to the right shows this pattern based on assays of plasma ghrelin in 10 humans during the course of a day.



Adapted from Cumming et al. Diabetes 50:1714, 2001.

Given the effects of ghrelin on energy metabolism and hunger, it is a prominent target for development of anti-obesity treatments. It has been reported that immunization of rats against ghrelin resulted in decreased weight gain and adiposity relative to control rats, even though both the groups consumed equivalent amount of food. This intriguing experiment suggests the possibility of a vaccine against obesity.

Disease States

Ghrelin concentrations in blood are reduced in obese humans compared to lean control subjects, but whether this is the cause or effect is not defined. Patients with anorexia nervosa have higher than normal plasma ghrelin levels, which is decreased if weight gain occurs.

Prader-Willi syndrome is another disorder relevant to ghrelin science. Affected patients develop extreme obesity associated with uncontrolled appetite. The plasma ghrelin levels are exceptionally high in comparison to obese patients due to other causes. Prader-Willi syndrome is clearly a complex disease with many defects; it may be that excessive ghrelin production contributes to the appetite and obesity components.

7.7 Motilin

Motilin is a 22 amino acid peptide secreted by endocrinocytes in the mucosa of the proximal small intestine. Based on amino acid sequence, motilin is unrelated to other hormones.

Motilin participates in controlling the pattern of smooth muscle contractions in the upper gastrointestinal tract. There are two basic states of motility of the stomach and small intestine: the fed state, when foodstuffs are present, and the interdigestive state between meals. Motilin is secreted into the circulation during the fasted state at intervals of roughly 100 minutes. These bursts of motilin secretion are temporally related to the onset of "housekeeping contractions", which sweep the stomach and small intestine clear of undigested material (also called the migrating motor complex).

Control of motilin secretion is largely unknown, although some studies suggest that alkaline pH in the duodenum stimulates its release.

An interesting aspect of the motilin activity is that erythromycin and related antibiotics act as nonpeptide motilin agonists, and are sometimes used for their ability to stimulate gastrointestinal motility. Administration of low dose of erythromycin induces migrating motor complex, which provides additional support for the conclusion that motilin secretion triggers this pattern of GI motility, rather than results from it.

7.9 Summary

A large number of peptides are synthesized and secreted by endocrine cells of the pancreas and gastrointestinal tract. Many of these peptides circulate as hormones, but

they also function as paracrine modulators or neurotransmitters not only in the gut but in the central and peripheral nervous systems. Although some biologic actions for many of these peptides have been delineated, it seems likely that new peptides, receptors, and novel biologic functions will continue to be discovered, which may provide new opportunities for understanding the pathophysiology, diagnosis, and treatment of endocrine disease.

Unit 8 □ Biomembrane

Structure

- 8.1 Introduction
- 8.2 Structural organization
- 8.3 Function
- 8.4 Summary

8.1 Introduction

Membranes are crucial to the life of the cell. The cell has internal milieu which is different from its external environment. This difference is maintained throughout the life of the cell by thin surface membrane, cell or plasma membrane, which controls the entrance and exit of molecules and ions. Inside the eukaryotic cells the membranes of the endoplasmic reticulum (ER), Golgi bodies, mitochondria and other membrane bound organelles maintain the characteristic differences between the content of each organelle and the cytosol. The function of the membrane in regulating this exchange between cell and external medium as well as between the organelles and cytoplasm is called **permeability**. Although all biomembranes have the same basic phospholipid bilayer structure and certain common function, each type of cellular membrane also has certain distinctive activities determined largely by the unique set of protein associated with that membrane. There are two basic categories of proteins: integral proteins, all or part of which penetrate or span the phospholipid bilayer and peripheral proteins, which do not interact with the hydrophobic core of the bilayer. In this section basic principal that governs the organization of the phospholipids and integral proteins in all biological membranes has been discussed.

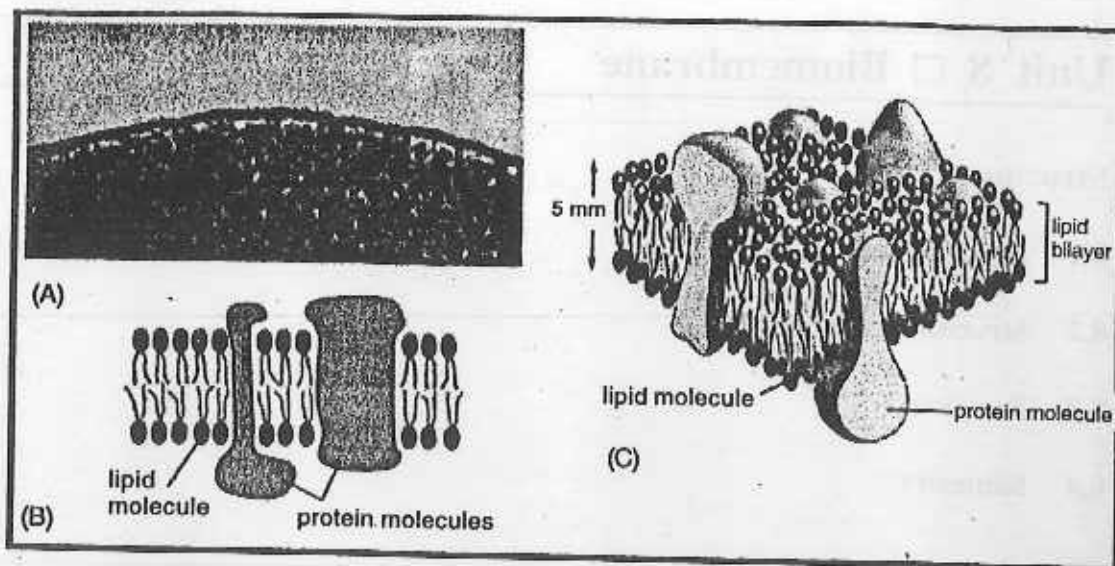


Fig. 1.

All biomembranes have a common general structure: each is a very thin film of lipid and protein molecules, held together mainly by noncovalent interaction. Cell membranes are dynamic, fluid structure and most of their molecules are able to move about in the plane of the membrane. Lipid molecules are arranged as a continuous sheet of double layer above 5nm thick. This lipid bilayer provides the basic fluid structure of the membrane and serves as relatively impermeable barrier to the passage of most water soluble molecules. Protein molecules that span the lipid bilayer mediate nearly all other functions of the membrane, transporting specific molecules across it.

8.2 Structural organization

In plasma membrane of human RBC, protein represents approximately 52% of its mass, lipids 40% and carbohydrate 8%. Oligosaccharides are bound to lipids and proteins as glycolipids and glycoproteins respectively.

Lipid bilayer :

All lipid molecules in cell membrane are amphipathic (or amphiphilic), because they have a hydrophilic (water-loving) or polar end and a hydrophobic (water-fearing) or non-polar end. The most abundant lipid components are phospholipids. These have a polar

head group and two hydrophobic hydrocarbon tails. Tails are usually fatty acids and they can differ in length. In phosphoglycerides, a major class of phospholipids, fatty acyl side chains are esterified to two of the three hydroxyl group is glycerol, and the third hydroxyl group is esterified to phosphate. The phosphate group is also esterified to a hydroxyl group of another hydrophilic compound, such as choline in phosphatidyl-choline. Instead of choline, alcohol such as ethanolamine, serine and the sugar derivatives inositol are linked to the phosphate group in other phosphoglycerides.

It is the shape and amphipathic nature of the lipid molecules that cause them to form bilayers spontaneously in aqueous environments. Hydrophilic molecules dissolve readily in water because they contain charged or uncharged groups that can form either favorable electrostatic interactions or hydrogen bonds with water molecules. Lipid molecules spontaneously aggregate to bury their hydrophobic tails in the interior and expose their hydrophilic heads to water. They can do this in either of the two ways : they can form spherical micelles with the tail inwards or can form bimolecular sheets or bilayers with hydrophobic tails sandwiched between the hydrophilic head groups (Fig. 10.4). A lipid bilayer has other characteristics besides its self sealing property that make it an ideal structure for cell membrane. Most important is its fluidity, which is crucial to many membrane functions.

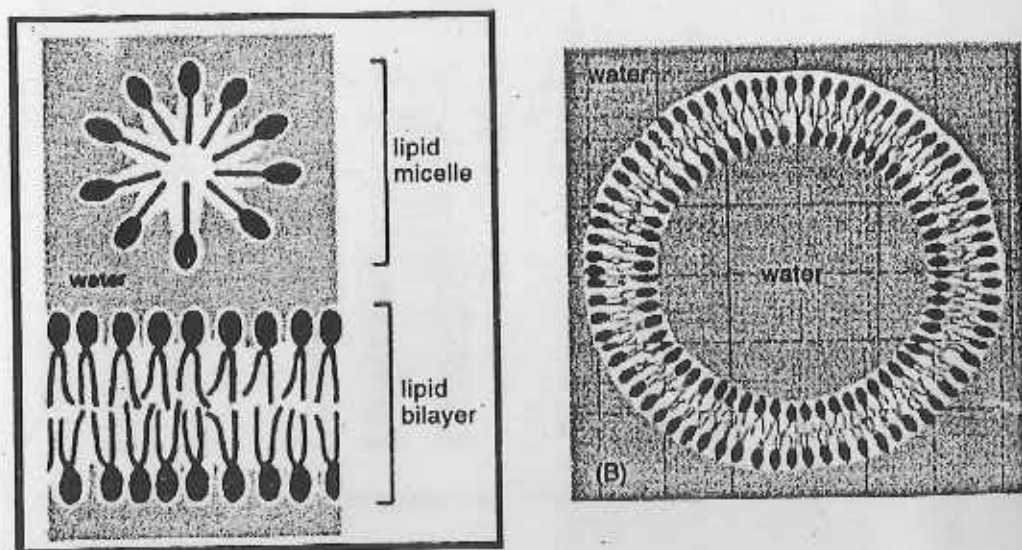


Fig. 2.

Sphingomyelin and phospholipids that lack glycerol backbone, is found mainly in plasma membrane. It contains sphingosine, an amino alcohol with long unsaturated hydrocarbon chains. Cholesterol and its derivatives constitute another important class of membrane lipid. Although cholesterol is almost entirely hydrocarbon in composition, it is amphipathic because its hydroxyl group can interact with water. Cholesterol is specially abundant in plasma membrane of mammalian cells, but is absent in most prokaryotic cells. Carbohydrate is found in many membranes, covalently bound either to proteins as constituents of glycoprotein or to lipids as glycolipids. (fig. 3). Bound carbohydrate increases the hydrophilic character of lipids and proteins and help to stabilize the conformation of many proteins. The simple glycolipid and glycosylcerbrosides contain a single glucose unit attached to serimides.

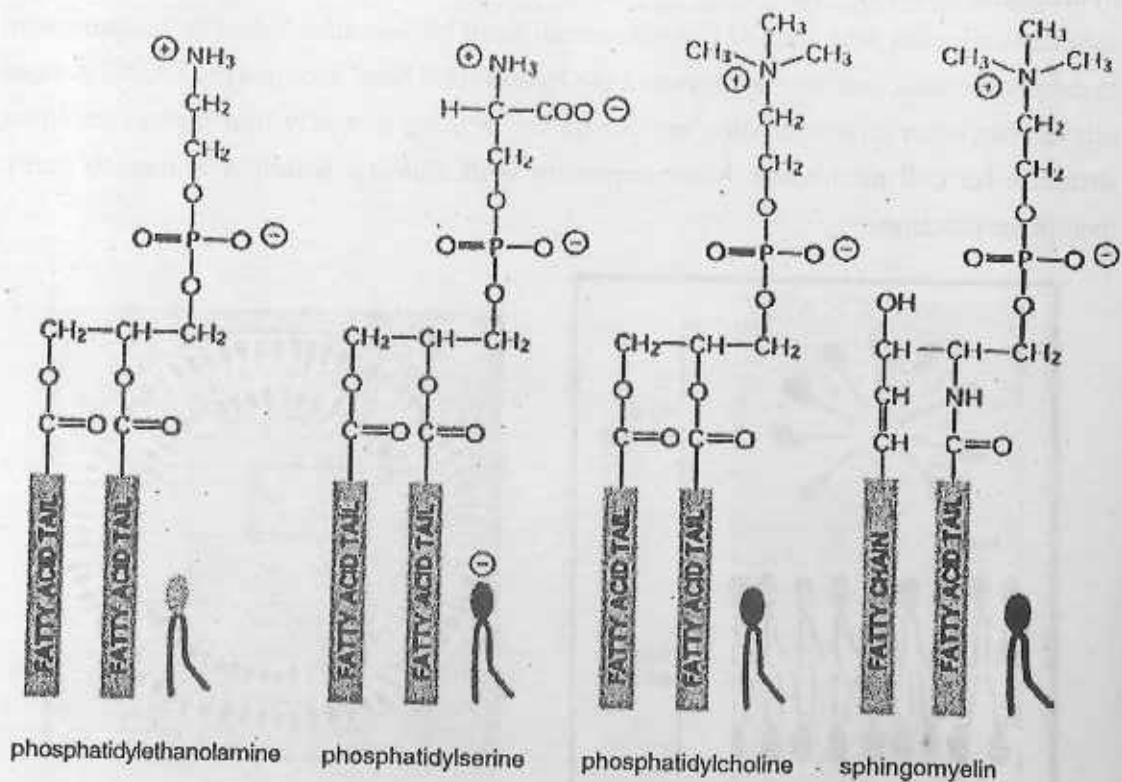


Fig. 3.

Membrane proteins

While lipids are fundamental structural elements of membrane, proteins are responsible for carrying out specific membrane functions. Most of the plasma membrane consists of approximately 50% lipid and 50% protein by weight, with carbohydrate as glycolipids or glycoprotein, constituting 5 to 10% of the membrane mass. Since proteins are much larger than lipids, there is always many more lipid molecules than protein molecules present in the membrane. About 50 lipid molecules are present for each protein molecule. In 1972 Jonathan Singer and Gorth Nicolson proposed the fluid mosaic model of membrane structure which is now accepted as basic paradigm for organization of all the biological cell membrane.

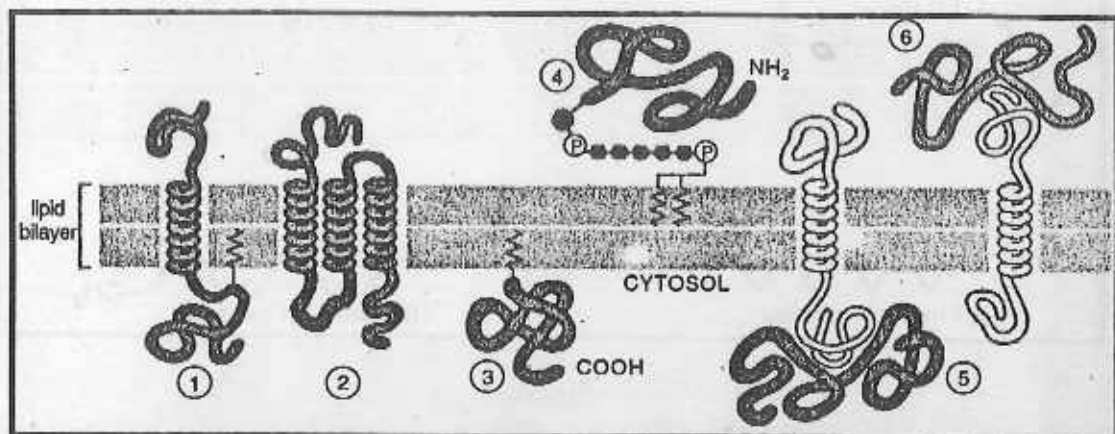


Fig. 4.

In this model, membranes are viewed as a two-dimensional fluid structures in which proteins are inserted into lipid-layers. Singer and Nicolson distinguished two classes membrane proteins, peripheral and integral. Peripheral membrane proteins are defined as proteins that dissociate from the membrane following treatment with polar reagents such as solution of extreme pH or high salt concentrations. These proteins are not inserted into hydrophobic interior of the lipid bilayer. Instead they are indirectly associated with membrane through protein-protein interactions. These interactions frequently involve ionic bond. Integral membrane proteins can be released only by treatment in the phospholipids

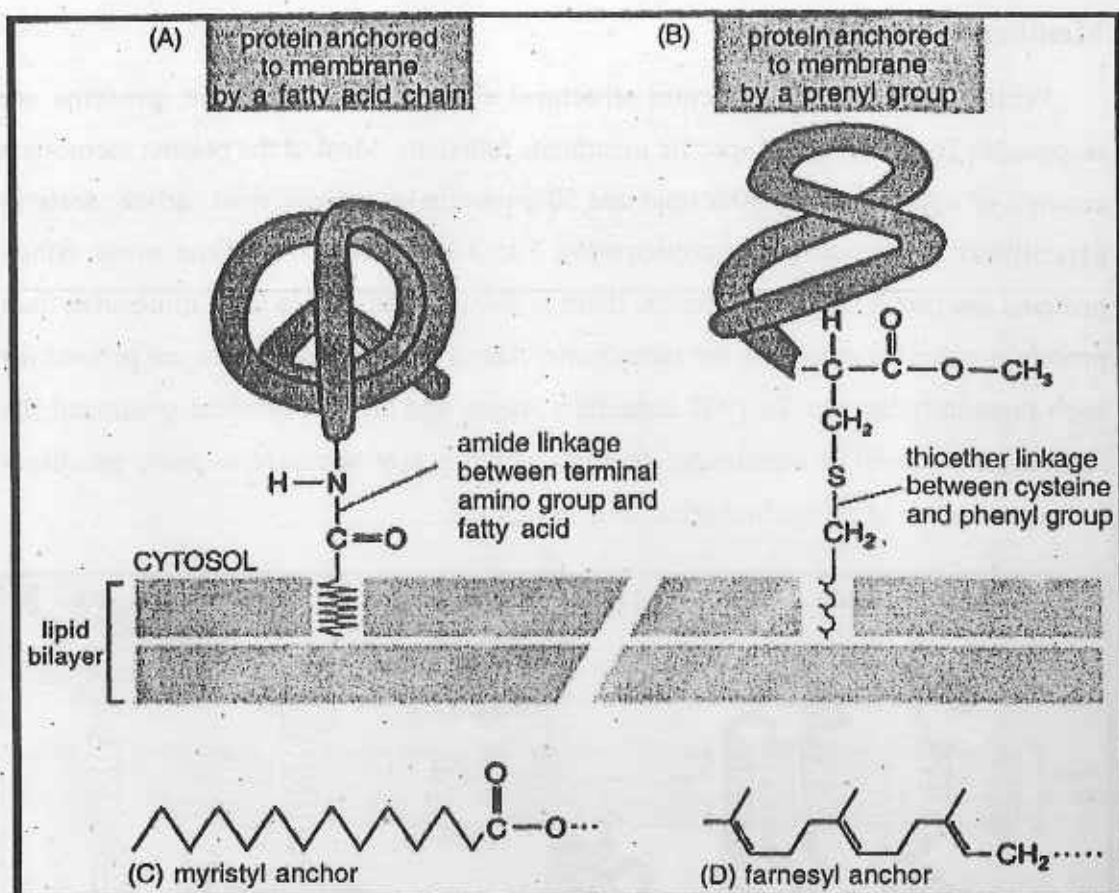


Fig. 5.

bilayer. Portions of these membrane proteins are inserted into the lipid bilayers. Most commonly used reagents for solubilization of integral membrane proteins are detergents, which are small amphipathic molecules containing both hydrophobic and hydrophilic groups. Many integral proteins are transmembrane proteins, which span the lipid bilayers with portions exposed on both sides of the membrane. They are also amphipathic and their hydrophilic regions pass through the membrane and interact with hydrophobic tails of the lipid molecules in the interior of the bilayer lipid. Their hydrophobic regions are exposed to water on either side of the membrane. Other membrane proteins are located entirely in the cytosolic monolayer of the lipid bilayer either by an amphipathic helix exposed to either surface of the proteins or by one or more covalently attached lipid chain, which can be fatty

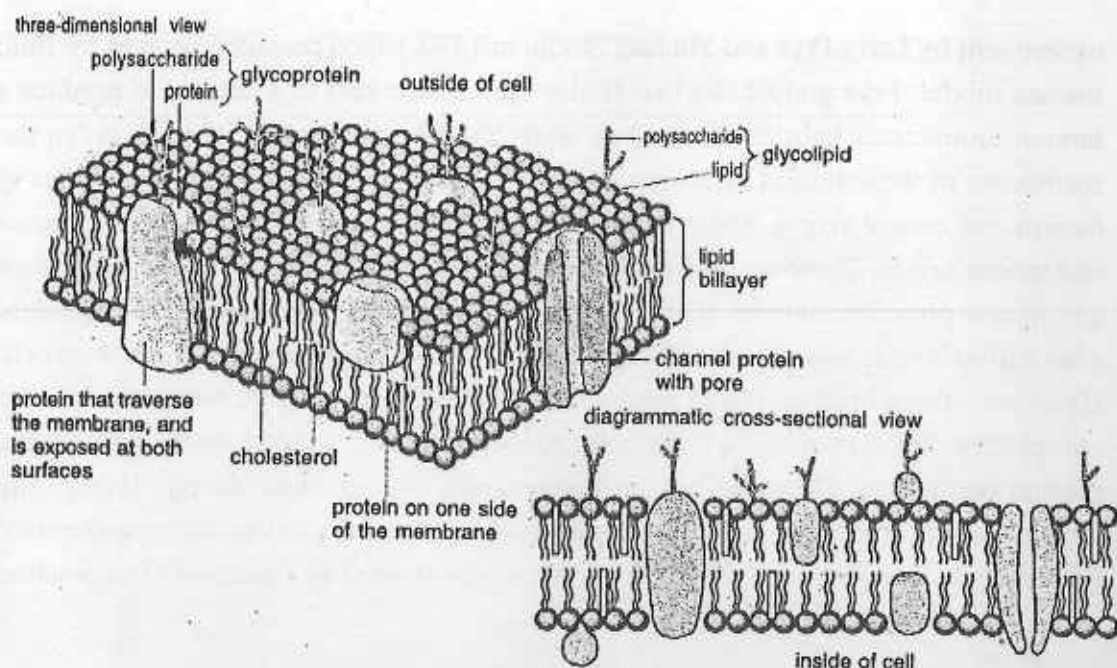


Fig. 6.

acid chains or phenyl groups. Other membrane proteins are entirely exposed at the external cell surface, being attached to the lipid bilayer only by covalent linkage to phosphatidylinositol in outer lipid monolayer.

The lipid-linked proteins are made as soluble proteins in the cytosol and are subsequently directed to the membrane by the covalent attachment of the lipid. Some proteins are made as single transmembrane proteins in the endoplasmic reticulum, while in the ER the transmembrane segments of the protein are cleaved off and a glycoposphatidylinositol anchor is added, leaving the protein bound to the noncytosolic surface of the membrane solely by their anchor.

Mobility of membrane proteins :

Membrane proteins and phospholipids are unable to move back and forth between the inner and outer leaflets of the membrane at an appreciable rate. However, because they are inserted to a fluid lipid bilayer, both proteins and lipid are able to diffuse laterally through the membrane. This lateral movement was first shown directly in an

experiment by Larry Frye and Michael Edidin in 1970, which provided support for fluid mosaic model. Frye and Edidin fuse human and mouse cell in a culture to produce a human-mouse cell hybrids. Then they analyzed the distribution of proteins in the membrane of these hybrid cells *using antibodies sufficiently to recognize proteins of human and mouse origin*. These antibodies specifically recognize proteins of human and mouse origin. These antibodies were labeled with fluorescent dyes. So the human and mouse proteins could be distinguished by fluorescence microscope. Immediately after fusion human and mouse cells are localized to different halves of the hybrid cell. However, after a brief period of incubation at 37°C, human and mouse proteins were completely mixed over the cell surface, indicating that they move freely through the plasma membrane. However, not all proteins are able to move freely through the membrane. In some cases, mobility are restricted by their association with cytoskeleton. For example, function band 3 RBC membrane is immobilized as a result of its association with ankyron spectrin.

Many membrane proteins are glycosylated

The great majority of transmembrane proteins in animal cells are glycosylated. As in glycolipids, the sugar residues are added in the lumen of ER and Golgi apparatus. For this reason, the disaccharide chains are always present in noncytosolic side of the plasma membrane.

8.3 Function

In all cells plasma membrane has several essential functions. These include transporting nutrients and metabolic waste out of the cells, preventing unwanted materials extracellular milieu into the from entering the cell into the thusly preventing loss of needed metabolites and maintaining the proper ionic composition, pH (7.2), and osmotic pressure of the cytosol. To carry out these functions, the plasma membrane contains specific transporter proteins that permit the passage for entry of certain small molecules. Several of these proteins use the energy released by ATP hydrolysis to pump ions and other molecules out of the cells against their concentration gradient. Small charged molecules such as ATP and amino acids can diffuse freely within the cytosol but are restricted in their ability to leave or enter across the plasma membrane.

In addition to their universal function, the plasma membrane has other crucial roles in multicellular organism. Few of the cells in multicellular plants and animals exist as isolated entities, rather groups of cells with related specialization combine to form tissues. Specilized area of the plasma membrane contains proteins and glycolipids that form specific contact and junction between the cells to strengthen tissues and allow the exchange of metabolites between the cells. Other proteins in the plasma membrane act as anchoring proteins for many of the cytoskeletal fibers that present in the cytosol, imparting shape and strength of the cell. In addition, enzymes bound on the plasma membrane catalyzes reactions that would occur with difficulty in environment. Plasma membrane of many types of cell also contains receptor proteins that bind specific signaling molecules, leading to various cellular responses.

8.4 Summary

The phospholipid bilayer forms the basic structure of all biomembranes, which also contain proteins, glycoproteins, cholesterol, and other sterols, and glycolipids. The presence of specific sets of membrane proteins permit each type of membrane to carry out distinctive functions. In a phospholipid bilayer, the long fatty acyl side chains in each leaflet are oriented towards one another, forming a hydrophobic core; the polar head groups line both surface. All the cellular membranes have closed compartments, and have a cytosolic and an exoplasmic components. The asymmetry of biological membranes is reflected in the specific orientation of each type of integral and peripheral membrane protein with respect to the cytosolic and exoplasmic faces. The presence of glycolipids exclusively in the exoplasmic leaflets also contribute to membrane asymmetry. Most integral proteins and lipids are laterally mobile in biomembranes. According to the fluid mosaic model, the membrane is viewed as a two-dimensional mosaic of phospholipids and protein molecules.

Unit 9 □ Basic Mechanism of Cell Signaling Pathway

Structure

9.1 Basic mechanism of cell signaling

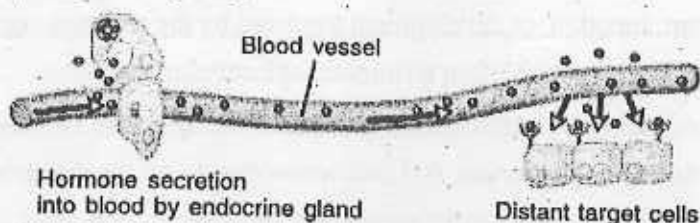
9.1 Basic mechanism of cell signaling

No cell lives in isolation. In all multicellular organisms, survival depends on elaborate intracellular communication network that coordinate growth, differentiation and metabolism of the multitude of cells in diverse tissues and organs. These communication mechanisms depend heavily on extracellular signaling molecules, which are produced by the cells to signal to their neighboring cells or further away from those cells. They also depend on elaborate system of proteins that each cell contains to enable to respond to a particular subset of these signals in a cell-specific pathway. These proteins include cell surface receptor proteins, which bind the signaling molecules and a variety of intracellular signaling proteins that distribute the signal to appropriate part of the cell. Among the intracellular signaling proteins are kinases, phosphatases, GTP-binding proteins etc. At the end of each intracellular signaling pathway are target proteins, which are altered when the pathway is active and change the behavior of the cell. These target proteins can be gene regulated proteins, ion channels, components of a metabolic pathway, part of cytoskeleton etc.

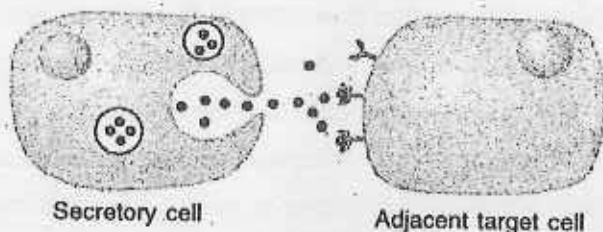
Mechanism enabling one cell to influence the behavior of the cells certainly exists in unicellular organism, long before multicellular organism appears in the earth. Yeast cells normally live independently. They can communicate and influence one another's behavior in preparation on mating. In such organism when a haploid individual is ready to mate it secretes a peptide mating factor that sends signals to the cells of the opposite sex to mate.

Communication by extracellular signaling usually involves six steps : i) synthesis and ii) release of signaling molecules by the cell, iii) transport of the signaling molecules to the

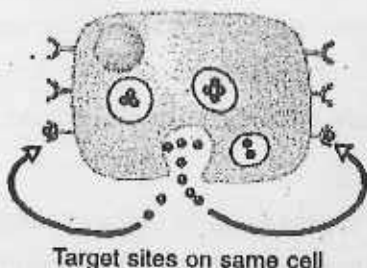
(a) Endocrine signaling



(b) Paracrine signaling



(c) Autocrine signaling



Key:

- Extracellular signal
- Y Receptor
- † Membrane-attached signal

(d) Signaling by plasma membrane-attached proteins

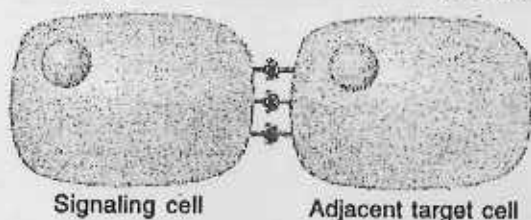


Fig. 1. General schemes of intercellular signaling in animals. (a–c) Cell-to-cell signaling by extracellular chemicals occurs over distances from a few micrometers in autocrine and paracrine signaling to several meters in endocrine signaling. (d) Proteins attached to the plasma membrane of one cell can interact directly with receptors on an adjacent cell.

target cell, iv) detection of signals by a specific receptors of the target cell, v) a change in cellular metabolism, function, or development triggered by the receptor-signal complex, and vi) removal of the signal which often terminates the cellular response.

In animals, signaling by extracellular secreted molecules can be classified into three types namely, **autocrine**, **paracrine**, and **endocrine**, based on the distance over which the signals acts. In addition certain membrane-bound proteins on one cell can directly signal an adjacent cell, which is known as **contact-dependent signaling**.

In autocrine signaling cells respond to substances that they themselves release (Fig. 1c). Many growth factors act in this fashion, and cultured cell often secrete growth factors that stimulate their own growth and proliferation. This type of signaling is particularly common in tumor cells, many of which overproduce and release growth factors that stimulate inappropriate uncontrolled growth. In paracrine signaling, the signaling molecules secreted by a cell affect only the target cells present in close proximity to it (Fig. 1b). The conduction of an electric impulse from one nerve cell to another, or from nerve cell to muscle cell occurs via paracrine signaling mediated by neurotransmitters. In endocrine signaling, the signaling molecules, called hormones, which are synthesised at one site and act on the distantly located target cells (Fig. 1a). In animals, a hormone usually is carried by the blood from its site of synthesis to the target tissue.

Some compounds can act in two or three types of cell-to-cell signaling. Certain small amino acid derivatives, such as epinephrine functions both as neurotransmitter (paracrine) and as systemic hormone. Some protein hormones such as epidermal growth factor are synthesized as the exoplasmic part of the plasma membrane protein.

Unit 10 □ Cell Surface Receptors, Second Messenger System, MAP kinase pathway

Structure

10.1 Introduction

10.2 Types of receptors

10.3 G-protein-coupled receptors and their effectors

10.4 Receptor tyrosine kinases

10.5 MAP Kinase Pathways

10.6 Summary

10.1 Introduction

All water soluble signal molecules including neurotransmitters and all signal proteins bind to specific receptor protein of the plasma membrane of the target cells and influence the target cell activity. They convert an extracellular ligand-binding events into intracellular signals that alter the behavior of the target cell. Binding of ligand to some of these receptors induces second-messenger formation, whereas ligand binding to others do not. Most cell surface receptor belongs to one of the four classes, defined by the transduction mechanism which are described below.

10.2 Types of receptors

- a) **G-protein-coupled receptors** : Ligand binding activates a GTP-binding protein (G-protein), which in turn activates or inhibits an enzyme that generates a second messenger or modulate an ion channel, causing a change in membrane potential. All G-protein-coupled receptors belong to a large family of homologous seven-transmembrane domain.

CELL-SURFACE RECEPTORS

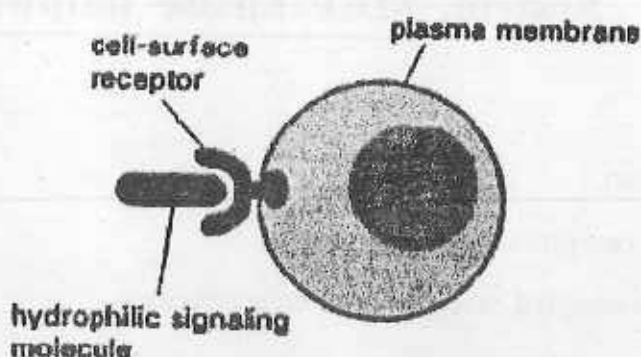
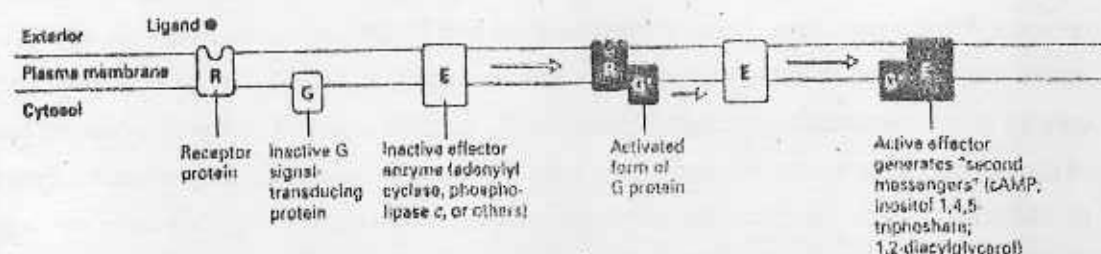


Fig. 1.

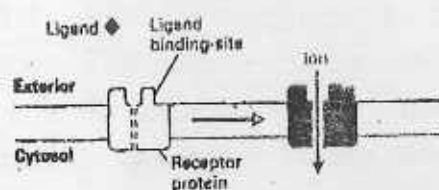
- b) **Ion-channel receptors** : They are also known as transmitter-gated ion channel or ionotropic receptors. Ligand binding changes the conformation of the receptors so that specific ions flow through it. The resultant ion movement alters the electric potential across the membrane. This type of receptors are involved in rapid synaptic signaling between electrically excitable cells and is mediated by a small number of neurotransmitters that transiently open or close an ion channel. The ion-channel-linked receptors belong to large family of homologous, multipass transmembrane protein.
- c) **Tyrosine kinase-linked receptor** : These receptors lack intrinsic catalytic activity, but ligand binding stimulates formation of a dimeric receptor, which then interacts with and activates one or more cytosolic protein-tyrosine kinases. The receptors for many cytokines, the interferons, and human growth factors are of these types. These tyrosine-kinase receptors are sometimes referred to as cytokine-receptor superfamily.
- d) **Receptor with intrinsic tyrosine-kinase activity** : When activated these receptors can function directly as enzymes. They can be formed by a single-pass transmembrane proteins that have their ligand binding site outside the cell and their catalytic or enzyme-binding site inside the cell. Some activated receptors catalyze conversion of GTP or GMP, other act as protein phosphatases, removing phosphate group from phosphotyrosine residue in the substrate proteins, thereby

modifying their activity. The receptors for insulin and many growth factors are ligand-triggered protein kinases. In most cases the ligand binds as a dimer, leading to dimerization of the receptors and activation of its kinase activity. These receptors often referred to as receptor serine/threonine kinase or receptor tyrosine kinases.

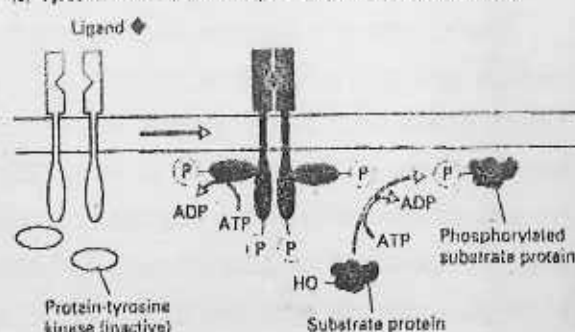
(a) G protein-coupled receptors (epinephrine, glucagon, serotonin)



(b) Ion-channel receptors (acetylcholine)



(c) Tyrosine kinase-linked receptors (erythropoietin, interferon)



(d) Receptors with intrinsic enzymatic activity

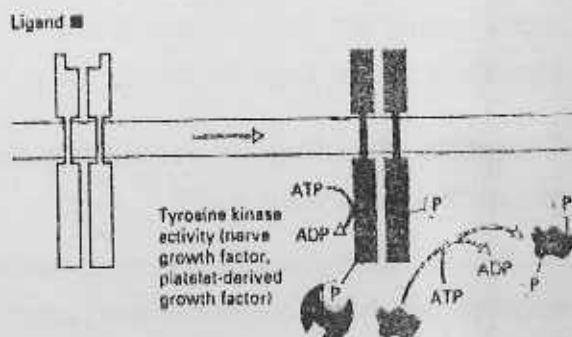
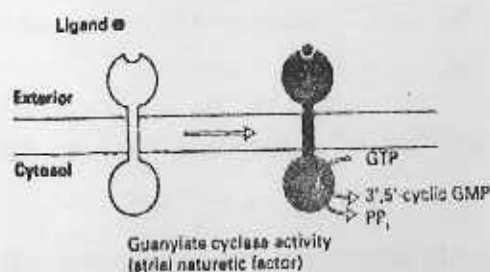


Fig. 2.

10.3 G-protein-coupled receptors and their effectors

G-protein coupled receptors (GPCRs) are the largest family of cell-surface receptors and are found in all eukaryotes. G-protein-coupled receptors mediate the response to an enormous diversity of signal molecules. These signaling molecules that activate them are as varied in structure as they are in function and include protein and small peptides, as well as derivatives of amino acids and fatty acids. Same ligand can activate many different receptor family members. Despite the chemical and functional diversity of the signaling molecules that bind to them, all G-protein-coupled receptors have a similar structure. They contain seven membrane-spanning regions with C-terminal segment on the cytoplasmic face of the plasma membrane. These receptors are also sometimes called serpentine receptors. In addition to their characteristic orientation in the plasma membrane, they have the same functional relationship to the G proteins which they use to signal the cell interior having an extracellular ligand.

The G proteins that transduce signals from extracellular ligands is a trimeric GTP binding proteins having three subunits- α , β and γ . In the unstimulated state, the α subunit has GDP bound and the G protein is inactive. When stimulated by activated receptor, α subunit releases its bound GDP, allowing GTP to bind its place. This exchange causes the trimer to dissociate into two activated components- an α subunit and a $\beta\gamma$ complex. The targets of the dissociated components of the G proteins are either enzymes or ion channels in the plasma membrane, and they relay the signal onwards. The α subunit is a GTPase, and once it is bound to GTP to GDP, it reassociates with $\beta\gamma$ complex to reform an inactive G-protein, reversing the activation process. The activated state of G-protein is short-lived. Alpha subunit of G-proteins may be G-stimulatory (G_s) or G-inhibitory (G_i) or may be G_q depending upon its targets in the plasma membrane.

G-protein signaling by regulating the activity of adenylate cyclase and production of cyclic AMP

In many types of cell, for example, binding of different hormones to their respective receptors induces the activation of adenylate cyclase through G-protein activation. Activated adenylate cyclase then converts membrane bound ATP to cyclic AMP (cAMP). Cyclic AMP was first identified as small intracellular mediator in the 1950s. The normal

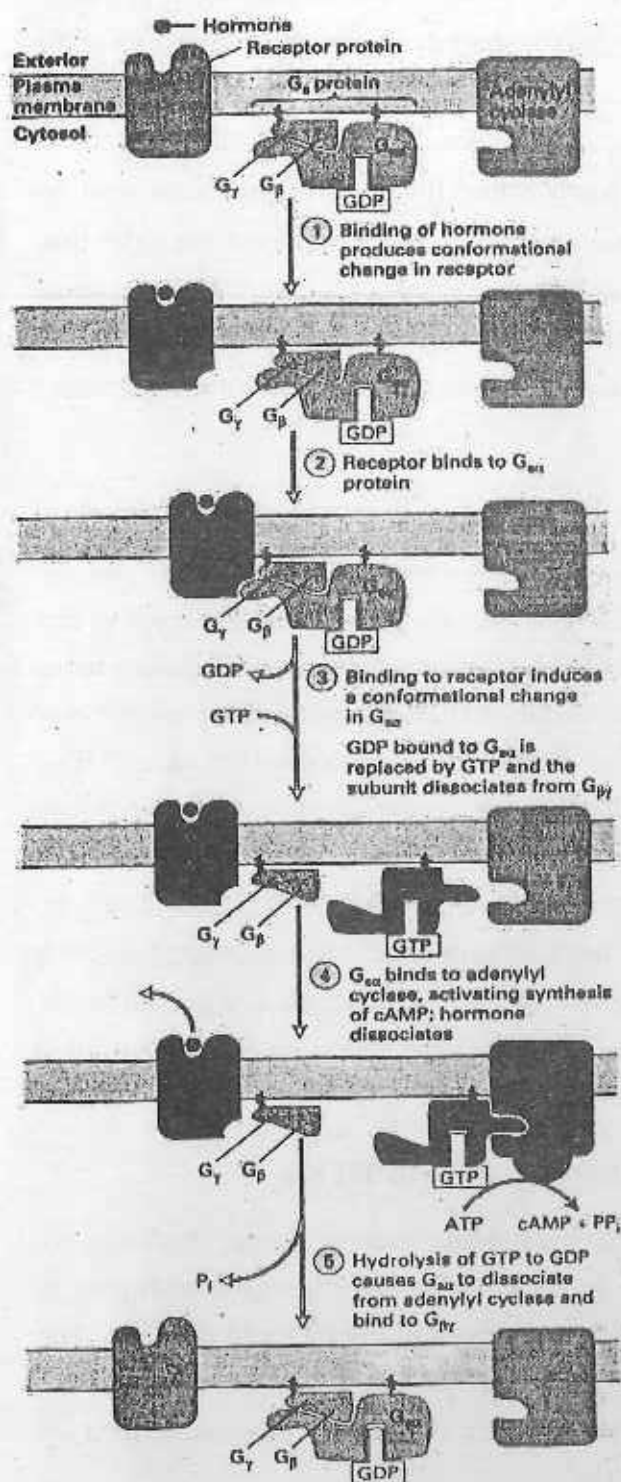


Fig. 3. Activation of adenylyl cyclase following binding of an appropriate hormone (e.g., epinephrine, glucagon) to a G_s protein-coupled receptor. Following ligand binding to the receptor, the G_s protein relays the hormone signal to the effector protein, in this case adenylyl cyclase. G_s cycles between an inactive form with bound GDP and an active form with bound GTP. Dissociation of the active form yields the $G_{s\alpha}$ GTP complex, which directly activates adenylyl cyclase. Activation is short-lived because GTP is rapidly hydrolyzed (step 5). This terminates the hormone signal and leads to reassembly of the inactive G_s GDP form, returning the system to the resting state. Binding of another hormone molecule causes repetition of the cycle. Both the G_γ and $G_{s\alpha}$ subunits are linked to the membrane by covalent attachment to lipids. Binding of the activated receptor to $G_{s\alpha}$ promotes dissociation of GDP and its replacement with GTP.

concentration of cAMP inside the cell is about 10^{-7} M, but an extracellular signal can cause cAMP levels to change more than twenty fold in seconds. Such a rapid synthesis of the molecule is balanced by its rapid breakdown or removal. In fact, cAMP is continuously destroyed by one or more cAMP phosphodiesterase that hydrolyzes cAMP to adenosine 5'-monophosphate (5'-monophosphate). Many extracellular signal molecules work by increasing cAMP and they do so by increasing the activity of adenylate cyclase rather than decreasing the activity of phosphodiesterase. All receptors that act via cAMP are coupled to stimulatory G protein. Another G protein, called inhibitory G protein inhibits adenylate cyclase but it mainly acts by directly regulating the ion channels rather than decreasing cAMP content.

10.4 Receptor tyrosine kinases

Receptor tyrosine kinase (RTKs) are second major types of cell surface receptors and ligand for RTKs are soluble or membrane-bound peptide/protein hormones including nerve growth factor (NGF), platelet-derived growth factor (PDGF), fibroblast growth factor (FGF), epidermal growth factor (EGF), insulin and insulin-like growth factor (IGFs). Binding of ligand to this type of receptor stimulates receptor's intrinsic protein-tyrosine kinase activity, which subsequently stimulates a signal transduction cascade leading to changes in cellular physiology and/or pattern of gene expression. Some RTKs have been identified in studies in human cancers associated with mutant forms of growth factor receptors, which send a proliferative signal to cells even in the absence of growth factor. One such mutant receptor, encoded at new locus, contributes to the uncontrolled proliferation of certain human breast cancers.

Ligand binding leads to autophosphorylation of RTKs

All RTKs comprises an extracellular ligand binding domain, a single hydrophobic transmembrane domain and a cytosolic domain that includes a region with protein tyrosine kinase activity. Binding of ligand causes most of the RTKs to dimerise. The protein kinase of each receptor monomer then phosphorylates a distinct set of tyrosine residues in the cytosolic domain of its dimer partner, a process termed as

autophosphorylation (Fig. 4). Autophosphorylation occurs in two stages. First, tyrosine residues in the phosphorylation tip near the catalytic site are phosphorylated. This leads to a conformational change that facilitates binding of ATP in some receptors (e.g., insulin receptors) and binding of protein substrates in other receptors (e.g., FGF receptors). The receptor kinase activity then phosphorylates other sites in the cytosolic domain; the resulting phosphotyrosines serve as docking sites for other proteins involved in RTK-mediated signal transduction. Phosphotyrosine residues in several RTKs interact with adapter proteins containing SH2 PTB domains. These proteins couple the activated receptors with the other component of the signal transduction pathway but have no intrinsic signaling properties.

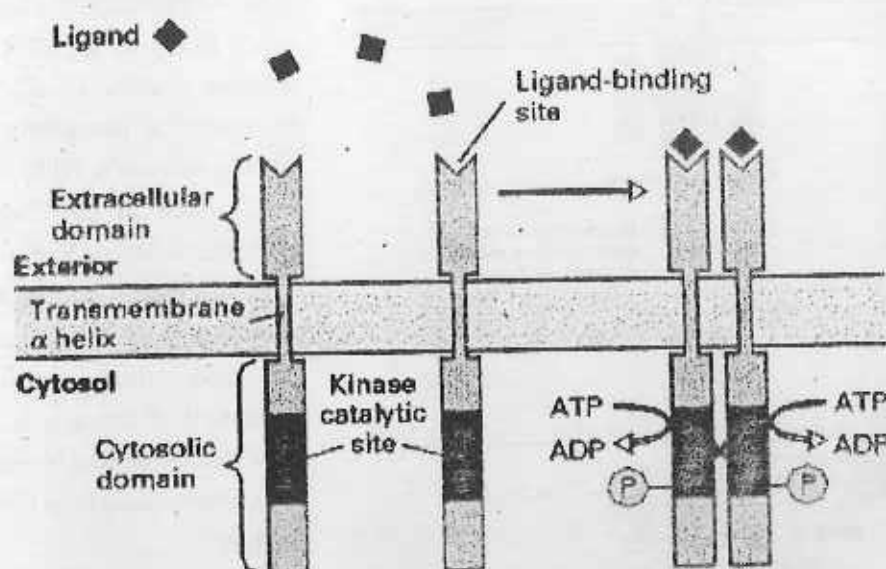


Fig. 4. General structure and activation of receptor tyrosine kinases (RTKs). The ligands for some RTKs, such as the receptor for EGF depicted here, are monomeric; ligand binding induces a conformational change in receptor monomers that promotes their dimerization. The ligands for other RTKs are dimeric; their binding brings two receptor monomers together directly. In either case, the kinase activity of each subunit of the dimeric receptor initially phosphorylates tyrosine residues near the catalytic site in the other subunit. Subsequently, tyrosine residues in other parts of the cytosolic domain are autophosphorylated.

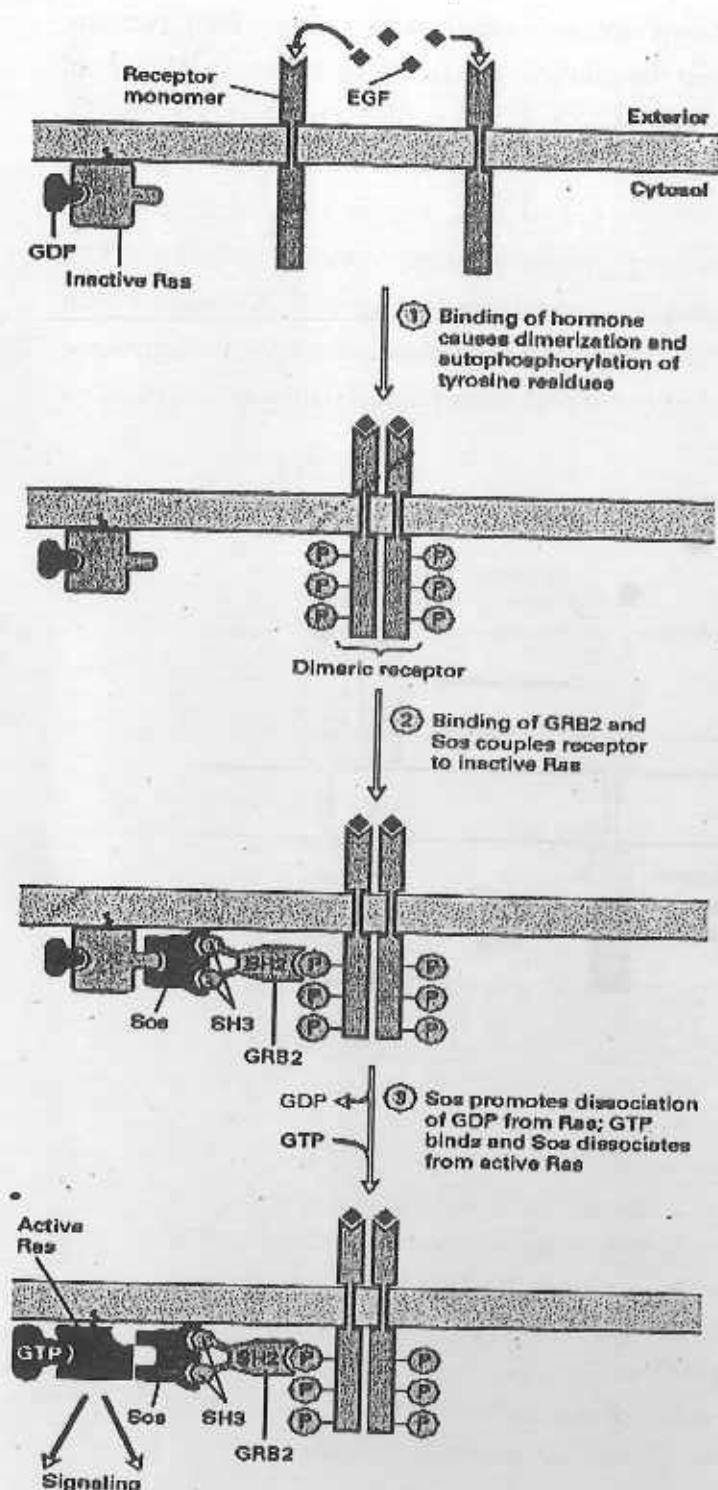


Fig. 5. Activation of Ras following binding of a hormone (e.g., EGF) to an RTK. The adapter protein GRB2 binds to a specific phosphotyrosine on the activated RTK and to Sos, which in turn interacts with the inactive Ras · GDP. The guanine nucleotide-exchange factor (GEF) activity of Sos then promotes formation of the active Ras · GTP. Note that Ras is tethered to the membrane by a farnesyl anchor.

Activation of Ras

Ras is a GTP-binding switch protein that alternates between an active on state with bound GTP and an inactive off state with bound GDP. Activation of Ras is triggered by ligand binding to RTKs. An adaptor protein and a guanosine nucleotide exchange factor (GEF) link most activated RTKs to Ras. GEF which binds to the Ras-GDP complex, causing dissociation of bound GDP yielding Ras-GTP form. Because GTP is present in cells at a higher concentration than GDP, GTP binds spontaneously to "empty" Ras molecules, with release of GEF. GTPase-activating proteins (GAPs) increase the rate of hydrolysis of bound GTP by Ras, thereby inactivating Ras (Fig. 5).

Ras belong to large Ras superfamily of monomeric GTPases. The family also contains two other subfamilies: the Rho family, involved in relaying signals from cell-surface receptors to the actin cytoskeleton and elsewhere, and the rab family is involved in regulating the traffic of intracellular transport vesicles.

An adaptor protein and GEF link most activated RTKs to Ras

The first indication that Ras functions downstream a RTKs in a common signaling pathway came from experiments in which cultured fibroblast cells were induced to proliferate by treatment with a mixture of platelet-derived growth factor (PDGF) and epidermal growth factor (EGF). Microinjection of anti-Ras antibodies into these cells blocked cell proliferation. Conversely, injection of a constitutively active mutant Ras protein (i.e., Ras^D), which hydrolyzes GTP very inefficiently and thus persists in the active state, caused the cells to proliferate in the absence of the growth factors. These findings are consistent with studies showing that addition of fibroblast growth factor (FGF) to fibroblasts leads to a rapid increase in the proportion of Ras present in the GTP-bound active form.

But how does binding of a growth factor (e.g., EGF) to the RTK (e.g., the EGF receptor) leads to activation of Ras? Two cytosolic proteins—GRB2 and Sos—provide the key links. An *SH2 domain* in GRB2 binds to a specific phosphotyrosine residue in the activated receptor. GRB2 also contains two *SH3 domains*, which bind and activate Sos. GRB2 thus functions as an adapter protein for the EGF receptor. Sos functions as a

guanine nucleotide-exchange protein (GEF), which helps to convert inactive GDP-bound Ras to the active GTP-bound form.

Genetic analysis of mutants blocked at particular stages of differentiation have provided considerable insight into RTK signaling pathways. Most of these genetic studies were done in the worm *C. elegans* and in the fly *Drosophila*. Mutants in these species in which development of specific cells is blocked is particularly useful in elucidating the pathway from an RTK to Ras.

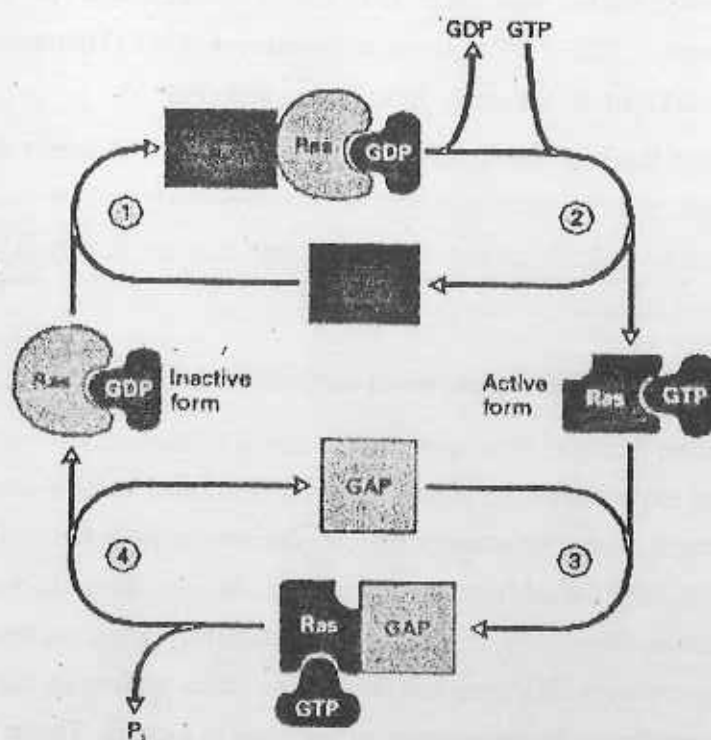


Fig. 6. Cycling of the Ras protein between the inactive form with bound GDP and the active form with bound GTP occurs in four steps. By mechanisms discussed later, binding of certain growth factors to their receptors induces formation of the active Ras · GTP complex. Step 1 : Guanine nucleotide-exchange factor (GEF) facilitates dissociation of GDP from Ras. Step 2 : GTP then binds spontaneously, and GEF dissociates yielding the active Ras · GTP form. Steps 3 and 4 : Hydrolysis of the bound GTP to regenerate the inactive Ras · GDP form is accelerated hundredfold by GTPase-activating protein (GAP). Unlike G_{α} , cycling of Ras thus requires two proteins, GEF and GAP; otherwise, G_{α} and Ras exhibit many common features.

SH2 Domain in GRB2 Adapter Protein Binds to a Specific Phosphotyrosine in an Activated RTK

To identify proteins that associate with phosphotyrosine residues in the cytosolic domain of activated EGF receptors, scientists used an expression cloning strategy. cDNAs synthesized from mRNAs isolated from human brain-stem tissue were inserted into a *ygt11* expression vector, which then was plated on a lawn of *E. coli* cells. When the resulting cDNA library was screened using a fragment of phosphorylated human EGF receptor as the probe, two cDNA clones were identified. One encoded a subunit of PI-3 kinase that contains an SH2 domain and the other encoded GRB2, a homolog of the SH2-containing adapter protein identified in the *Drosophila* Sev pathway. Thus GRB2 and its *Drosophila* homolog are adapter proteins that function downstream from RTKs but upstream of Ras in both the flies and mammalian cells.

GRB2 and similar adapter proteins bind to different phosphotyrosine residues on RTKs via the conserved SH2 domain. This domain derived its full name, the *Src* homology 2 domain, from its homology with a region in the prototypical cytosolic tyrosine kinase encoded by *src*. The three-dimensional structures of SH2 domains in different proteins are very similar. Each binds to a distinct sequence of amino acids surrounding a phosphotyrosine residue. The unique amino acid sequence of each SH2 domain determines the specific phosphotyrosine residues it binds. The SH2 domain of the *Src* tyrosine kinase, for example, binds strongly to any peptide containing the critical core sequence of phosphotyrosine–glutamic acid–glutamic acid–isoleucine. These four amino acids make intimate contact with the peptide-binding site in the *Src* SH2 domain. Binding resembles the insertion of a two-pronged “plug”—the phosphotyrosine and isoleucine residues of the peptide—into a two-pronged “socket” in the SH2 domain. The two glutamic acids fit singly into the surface of the SH2 domain between the phosphotyrosine socket and the hydrophobic socket that accepts the isoleucine residue. Variations in the nature of the hydrophobic socket in different SH2 domains allow them to bind to phosphotyrosines adjacent to different sequences, accounting for differences in their binding specificity.

Activated RTKs also can recruit signaling molecules through a different domain called the phosphotyrosine binding (PTB) domain. While SH2-binding specificity is largely

determined by residues C-terminal to the phosphotyrosine, PTB-binding specificity is determined by specific residues five to eight residues N-terminal to the phosphotyrosine residue.

Sos, a Guanine Nucleotide-Exchange Factor, Binds to the SH3 Domains in GRB2

In addition to one SH2 domain, which binds to phosphotyrosine residues in RTKs, GRB2 contains two SH3 domains, which bind to Sos, a guanine nucleotide-exchange factor. SH3 domains, which contain ≈ 55 –70 residues, are present in a large number of proteins involved in intracellular signaling. Although the three-dimensional structures of various SH3 domains are similar, their specific amino acid sequences differ. SH3 domains selectively bind to proline-rich sequences in Sos and other proteins; different SH3 domains bind to different proline-rich sequences.

Proline residues play two roles in the interaction between an SH3 domain in an adapter protein (e.g., GRB2) and a proline-rich sequence in another protein (e.g., Sos). First, the proline-rich sequence assumes an extended conformation that permits extensive contacts with the SH3 domain, thereby facilitating interaction. Second, a subset of these prolines fit into binding "pockets" on the surface of the SH3 domain. Several nonproline residues also interact with the SH3 domain and are responsible for determining the binding specificity. Hence the binding of peptides to SH2 and SH3 domains follows a similar strategy: certain residues provide the overall structural motif necessary for binding, and neighboring residues confer specificity to the binding.

Following hormone-induced activation of an RTK (e.g., the EGF receptor), a complex containing the activated RTK, GRB2, and Sos is formed on the cytosolic face of the plasma membrane. Formation of this complex depends on the dual binding ability of GRB2. Receptor activation thus leads to relocation of Sos from the cytosol to the membrane, bringing Sos near to its substrate, membrane-bound Ras-GDP. Biochemical and genetic studies indicate that the C-terminus of Sos inhibits its nucleotide exchange activity and that GRB2 binding relieves this inhibition. Binding of Sos to Ras-GDP leads to changes in the conformation of two regions of Ras, switch I and switch II, thereby

opening the binding pocket for GDP so it can diffuse out. Because GTP is present in cells at a concentration 10 times higher than GDP, GTP binding occurs preferentially, leading to activation of Ras. The activation of Ras and G_{sa} thus occurs by similar mechanisms: a conformational change induced by binding of a protein—Sos and an activated GPCR, respectively—that opens the protein structure. So bound GDP is released to be replaced by GTP. As we discuss in the next section, binding of GTP to Ras, in turn, induces a specific conformation of switch I and II that allow Ras-GTP to activate downstream effector molecules.

Several other proteins, including GAP, bind to specific phosphotyrosines in activated RTKs. This binding localizes GAP close to Ras-GTP, so it can promote the cycling of Ras; exactly how GAP interacts with Ras and perhaps other components of the RTK-Ras pathway is unclear.

10.5 MAP Kinase Pathways

All Ras-linked RTKs in mammalian cells appear to utilize a highly conserved signal-transduction pathway in which the signal induced by ligand binding is carried via GRB2 and Sos to Ras, leading to its activation. Activated Ras then induces a kinase cascade that culminates in activation of MAP kinase. This serine/threonine kinase, which can translocate into the nucleus, phosphorylates many different proteins including transcription factors that regulate expression of important cell-cycle and differentiation of specific proteins. In this section, we first examine the components of the kinase cascade downstream from Ras in RTK-Ras signaling pathways in mammalian cells. Then we discuss the linkage of other signaling pathways to similar kinase cascades and recent studies indicating that both yeasts and cells of higher eukaryotes contain multiple MAP kinases.

Activation of MAP kinase in two different cells can lead to similar or different cellular responses, and activation in the same cell occurs by stimulation of different RTKs. The mechanisms controlling the response specificity of MAP kinases are poorly understood and are not considered in this chapter.

Signal Transduction from Activated Ras to a Cascade of Protein Kinases

A remarkable convergence of biochemical and genetic studies in yeast, *C. elegans*, *Drosophila*, and mammals has revealed a highly conserved cascade of protein kinases that operate in sequential fashion downstream from activated Ras as follows :

1. Activated Ras binds to the N-terminal domain of Raf, a serine/threonine kinase.
2. Raf binds to and phosphorylates MEK, a dual-specificity protein kinase that phosphorylates both tyrosine and serine residues.
3. MEK phosphorylates and activates MAP kinase, another serine/threonine kinase.
4. MAP kinase phosphorylates many different proteins, including nuclear transcription factors, that mediate cellular responses.

Several types of experiments have demonstrated that Raf, MEK, and MAP kinase lie downstream of Ras and their sequential order in the pathway. For example, constitutively active mutant Raf proteins induce quiescent cultured cells to proliferate in the absence of hormone stimulation. These mutant Raf proteins, which initially were identified in tumor cells, are encoded by oncogenes and stimulate uncontrolled cell proliferation. Conversely, cultured mammalian cells that express a mutant, defective Raf protein cannot be stimulated to proliferate uncontrollably by a mutant, constitutively active Ras^D protein. This finding establishes a link between the Raf and Ras proteins. In vitro binding studies have shown that purified Ras-GTP protein binds directly to Raf. An interaction between the mammalian Ras and Raf proteins also has been demonstrated in the yeast two-hybrid system, a genetic system in yeast used to select cDNAs encoding proteins that bind to target, or "bait" proteins. The binding of Ras and Raf to each other does *not* induce the Raf kinase activity.

The location of MAP kinase downstream of Ras was evidenced by the finding that in quiescent cultured cells expressing a constitutively active Ras^D, activated MAP kinase is generated in the absence of hormone stimulation. More importantly, in *Drosophila* mutants that lack a functional Ras or Raf but express a constitutively active MAP kinase specifically

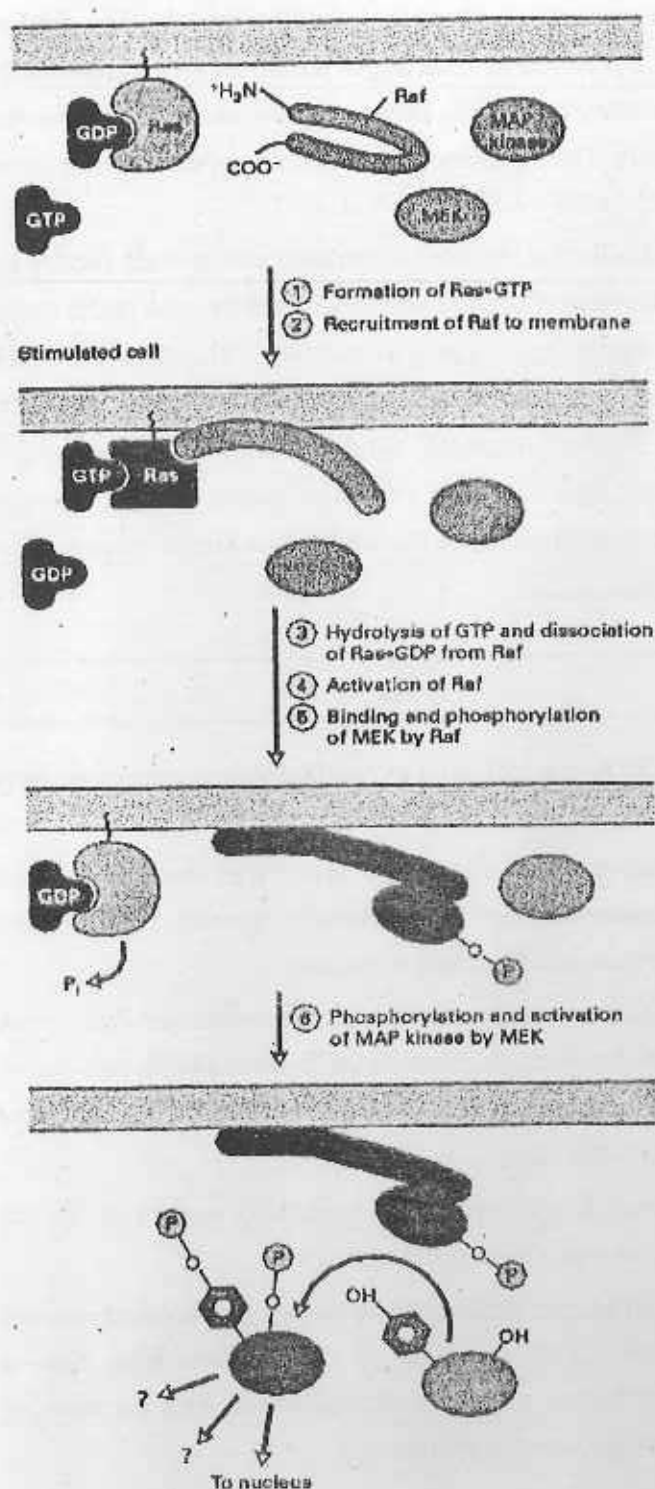


Fig. 7. Figure 20-28. Kinase cascade that transmits signals downstream from activated Ras protein. In unstimulated cells, most Ras is in the inactive form with bound GDP (*top*); binding of a growth factor to its RTK leads to formation of the active Ras \cdot GTP. A signaling complex then is assembled downstream of Ras, leading to activation of MAP \cdot kinase by phosphorylation of threonine and tyrosine residues separated by a single amino acid. Phosphorylation at both sites is necessary for activation of MAP kinase.

in the developing eye, R7 photoreceptors were found to develop normally. This finding indicates that activation of MAP kinase is sufficient to transmit a proliferation or differentiation signal normally initiated by ligand binding to an RTK. Biochemical studies showed that Raf does not activate MAP kinase directly. The signaling pathway thus appears to be a linear one: activated RTK \rightarrow Ras \rightarrow Raf \rightarrow (?) \rightarrow MAP kinase.

Finally, fractionation of cultured cells that had been stimulated with growth factors led to identification of MEK, a kinase that specifically phosphorylates threonine and tyrosine residues on MAP kinase, thereby activating its catalytic activity. (The acronym MEK comes from MAP and ERK kinase, where ERK is another acronym for MAP.) Later studies showed that MEK binds to the C-terminal catalytic domain of Raf and is phosphorylated by the Raf serine/ threonine kinase activity; this phosphorylation activates the catalytic activity of MEK. Hence, activation of Ras induces a kinase cascade that includes Raf, MEK, and MAP kinase.

10.6 Summary

- Receptor tyrosine kinases (RTKs), which bind to peptide/protein hormones, may exist as dimers or dimerize during binding to ligands.
- Ligand binding leads to activation of the kinase activity of the receptor and autophosphorylation of tyrosine residues in its cytosolic domain. The activated receptor also can phosphorylate other protein substrates.
- Ras is an intracellular GTPase switch protein that acts downstream from most RTKs. Like G_{sq} , Ras cycles between an inactive GDP-bound form and active GTP-bound form. Ras cycling requires the assistance of two proteins, GEF and GAP, , whereas G_{sq} cycling does not.
- Unlike GPCRs, which interact directly with an associated G protein, RTKs are linked indirectly to Ras via two proteins, GRB2 and Sos.
- The SH2 domain in GRB2, an adapter protein, binds to specific phosphotyrosines in activated RTKs. The two SH3 domains in GRB2 then bind Sos, a guaninenucleotide exchange factor, thereby bringing Sos close to membrane-bound Ras-GDP and activating its exchange function.

- Binding of Sos to inactive Ras causes a large conformational change that permits release of GDP and binding of GTP.
- Normally, Ras activation and the subsequent cellular response is induced by ligand binding to an RTK. However, in cells that contain a constitutively active Ras, the cellular response occurs in the absence of ligand binding.
- Activated Ras promotes formation of signaling complexes at the membrane containing three sequentially acting protein kinases and a scaffold protein Ksr. Raf is recruited to the membrane by binding to Ras · GTP and then activated. It then phosphorylates MEK, a dual specificity kinase that phosphorylates MAP kinase. Phosphorylated MAP kinase dimerizes and translocates to the nucleus where it regulates gene expression.
- RTKs, GPCRs, and other receptor classes can activate MAP kinase pathways. Single-cell eukaryotes, such as yeast, and multicellular organisms contain multiple M/ P kinase pathways that regulate diverse cellular processes.
- Although different MAP kinase pathways share some upstream components, activation of one pathway by extracellular signals does not lead to activation of others containing shared components.
- In MAP kinase pathways containing common components, the activity of shared components is restricted to only a subset of MAP kinases by their assembly into large pathway-specific signaling complexes.
- Some MAP kinases have kinase-independent functions that can restrict signals to only a subset of MAP kinases.

Unit 11 □ Apoptosis

Structure

- 11.1 Introduction
- 11.2 How does apoptosis differ from necrosis
- 11.3 Apoptotic Process
- 11.4 When Cells die?
- 11.5 Basic Apoptotic Machinery
- 11.6 Mechanism of Apoptosis
- 11.7 Procaspases are activated by binding to adaptor proteins
- 11.8 Activation of procaspase from outside the cell
- 11.9 Bcl2 protein and IAP proteins are the main intracellular regulator
- 11.10 Summary

11.1 Introduction

The cells of multicellular organism are members of highly organized community. The number of these cells in this community is tightly regulated - not simply by controlling the rate of cell division, but also by controlling the cell death. If cells are no longer needed, they commit suicide by activating an intracellular death programme. This process is **Programmed Cell Death (PCD)** or **Apoptosis** (from a Greek word, "falling off" as leaves from a tree). Apoptosis when not regulated, can contribute to the various diseases, mainly cancer, autoimmune or neurodegenerative diseases. The biological hallmark of apoptosis includes activations of endonucleases, DNA fragmentation into oligosomal fragments and activation of a family of cysteine protease called caspases.

11.2 How does apoptosis differ from necrosis

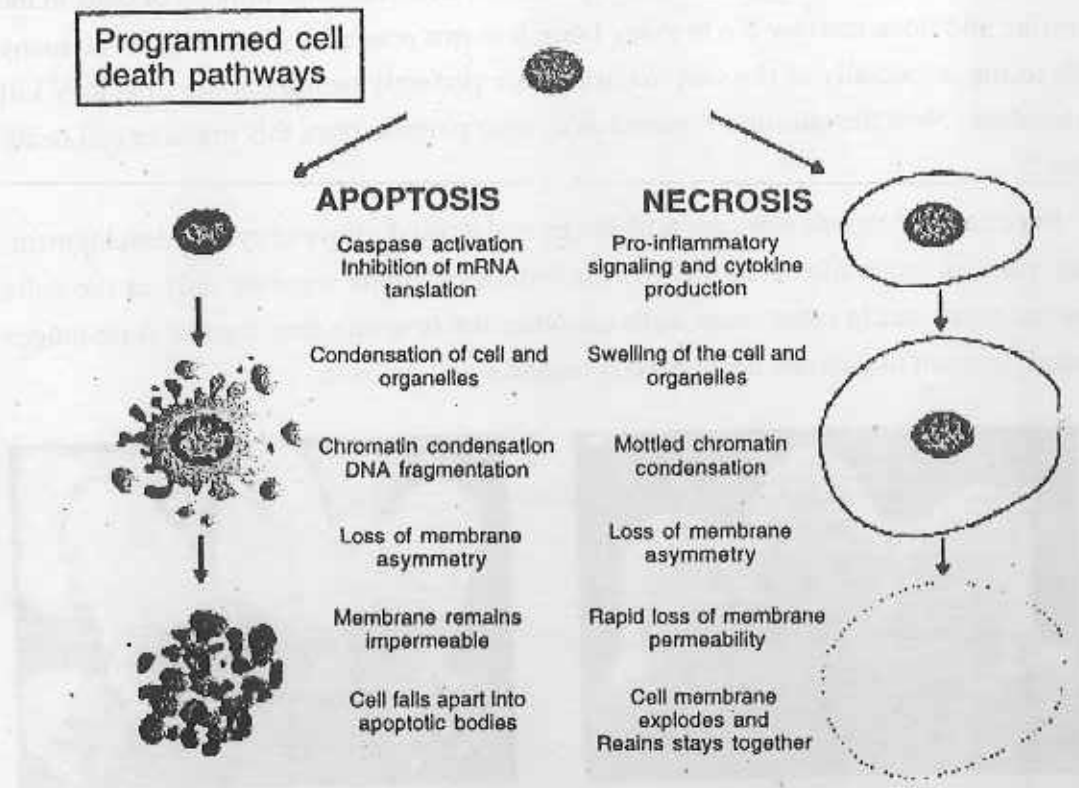


Fig. 1 : Basic differences between apoptosis and necrosis

Cells that die as a result of injury typically, swell and burst. They spill over their contents over their neighbours - a process called **cell necrosis** causing a potentially damaging inflammatory response. By contrast, a cell undergoes apoptosis dies neatly, without damaging its neighbour. The cell shrinks and condenses, the cytoskeleton collapses, the nuclear envelop disassembles and the nuclear DNA breaks up into fragments. Most importantly, the cell surface is altered, displaying property that causes the dying cell to be rapidly phagocytosed, either by neighbouring cells or by macrophages before any leakage of its content occurs. These events not only avoid the damaging consequence of the cell necrosis, but also allow the organic components of the dead cells to be recycled by the cells that ingest them.

The amount of apoptosis in developing and adult animal tissues can be astonishing. For example, in the developing vertebrate nervous system about half of the nerve cells normally die soon after they are formed. In healthy adult humans, billions of cells in the intestine and bone marrow die in every hour. It seems reasonably wasteful for so many cells to die, especially as the vast majorities are perfectly healthy at the time they kill themselves. Now the question is: what purpose does this massive cell death serve?

For example, mouse paws are sculpted by cell death during embryonic development. They start as spade like structure and the individual digits separate only as the cells between them die. In other cases, cells die when the structure they formed is no longer needed. In adult tissues cell death exactly balances cell division.

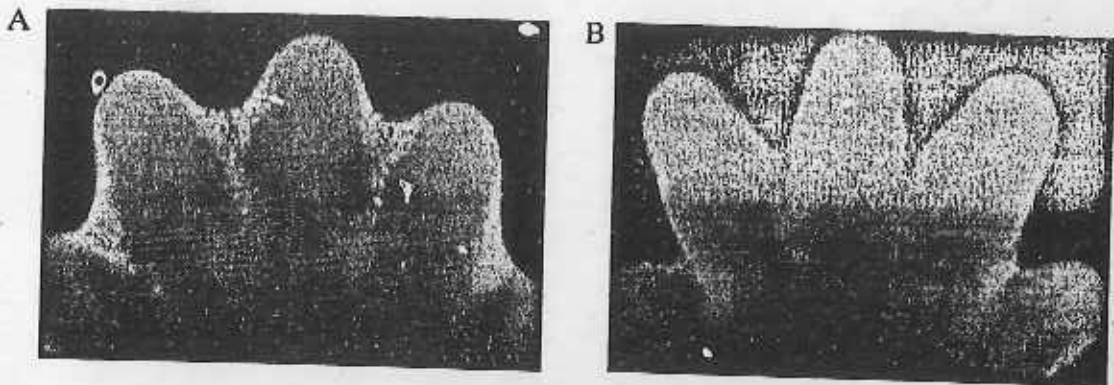


Fig 2. : Sculpting the digits in the developing mouse paw by apoptosis. (A) The paw in this mouse embryo has been stained with a dye that specifically labels cells that have undergone apoptosis. The apoptotic cells appear as *bright green* dots between the developing digits. (B) This inter-digital cell death eliminates the tissue between the developing digits, as seen one day later, when few, if any, apoptotic cells can be seen.

11.3 Apoptotic process

The process of apoptosis can be divided into three distinct phases namely **i) initiation**, **ii) effectors**, and **iii) degradation**. During initiation cell receives death inducing signals. The cells at this stage lack the obligatory survival factors and the cells have shortage of

metabolic supply which is followed by appearance of death-signal transducing receptors. During the effector phase the signals are translated into metabolic reaction and the decision to die is taken. Beyond this stage i.e., during degradation phase an increase in the overall entropy, including activation of catabolic enzymes, DNA fragmentation and massive protein degradation become apparent. Fragmented DNA encapsulated to form apoptotic bodies that are quietly consumed by the adjacent cells. Thus pathway of apoptotic cell death is demarcated when the cells sense or receive the death signals depending on the type of stimulus of the particular cell type.

Biochemically, apoptotic cells are characterized by reduction in the mitochondrial transmembrane potential, intracellular acidification, production of reactive oxygen species (ROS), externalization of phosphatidyl serine residues in the membrane bilayer, selective proteolysis of subset of cellular proteins and degradation of DNA into internucleosomal fragments.

11.4 When cells die?

The cell dies by apoptosis in the developing embryo during morphogenesis and in the adult animal during tissue turn over, immune regulation or at the end of immune response. So aberration of this process is detrimental. Thus unscheduled apoptosis of certain brain neurons contribute to cause disorder such as Alzheimer's and Parkinson's disease, whereas failure of the dividing cells to initiate apoptosis after sustaining DNA damage contribute to the cancer. PCD has also been reported in the pathological dysfunction, such as T-cell depletion in HIV infection and mononuclear cell loss in *Plasmodium falciparum* infection.

11.5 Basic apoptotic machinery

Genetic studies of nematode *C. elegans* contribute a conceptual frame work involving three genes. Two of these genes are cell death defective genes (*ced*) – *ced3* and *ced4* are both required for the apoptosis in worm whereas another gene *ced9*,

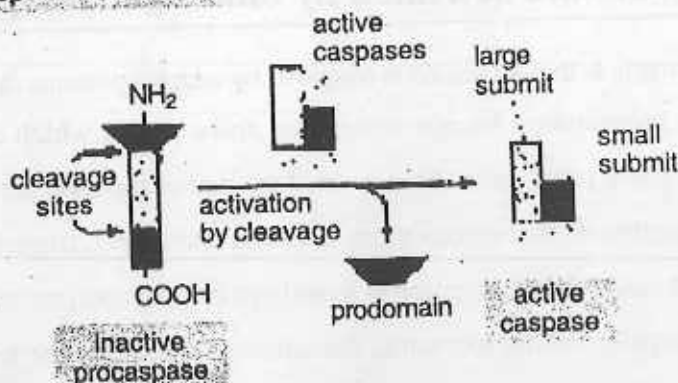
inhibits action of *ced3* and *ced4* by helping cell survival. Gene product of *ced3* is a caspase that cleaves certain proteins after specific aspartic amino acid residue. This is activated through self cleavage. Normally *ced4* binds *ced3* and promotes *ced3* activation, whereas *ced9* binds to *ced4*, and prevents it from activating *ced3*. Normally *ced9* is combines with *ced3* keeping *ced3* inactive. Apoptotic stimuli cause *ced9* dissociation, allowing *ced4* to activate *ced3* and thereby causing cell death by apoptosis. Vertebrate animals have evolved the entire gene families that resemble the cell death genes of *C. elegans*. Mammalian caspases are similar to *ced3*. Apoptotic activation factor (Apaf-1) is the only mammalian *ced4* homologue known so far. The products of the mammalian *Bcl2* gene family are related to *ced9*, but include two subgroups of proteins that either inhibit or promote apoptosis.

11.6 Mechanism of apoptosis

All nucleated animal cells contain the seed of their own destruction in the form of various inactive procaspases that lie waiting for a signal to destroy cells. The basic mechanism is similar in animal cells. This machinery depends on family of proteases that have a cystine at their active site and cleaves their target protein at specific aspartic acids. These enzymes are called caspases.

Caspases are synthesized in the cell as inactive "procaspases", which are usually activated by cleavage at aspartic acids by other caspase. Once activated caspases cleave and thereby activate other procaspases, resulting in an amplifying proteolytic cascade. Some activated caspases then cleave other key proteins in the cells. Some cleave the nuclear lamina, for example causing irreversible breakdown of the nuclear lamina, and other cleaves a protein that normally holds a DNA degrading enzyme (DNAase) in an active form freeing the DNAase to cut out the DNA in the cell nucleus. In this way the cell dismantles itself quickly and neatly, and its corpse is rapidly taken up and digested by another cell. The protease cascade is not only destructive and self amplifying but also irreversible, so that once a cell reaches a critical point it can not be turned back.

(A) procaspase activation



(B) caspase cascade

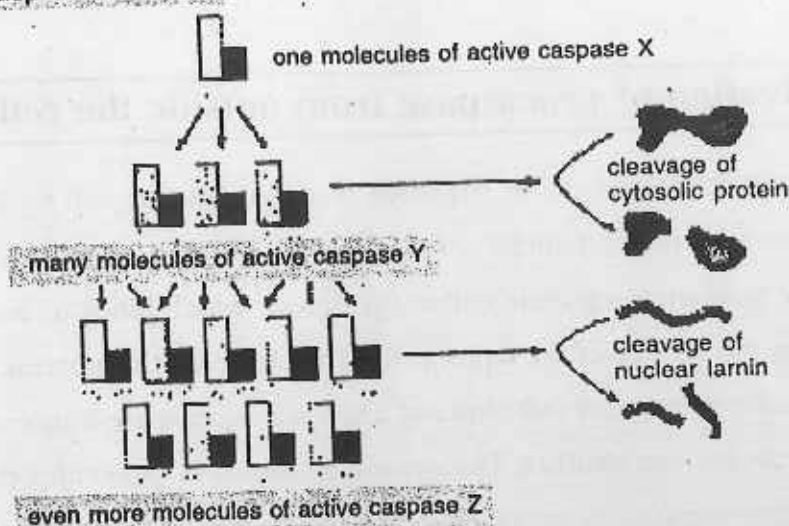


Fig 3. The caspase cascade involved in apoptosis. (A) Each suicide protease is made as an inactive proenzyme (procaspase), which is usually activated by proteolytic cleavage by another member of the caspase family. As indicated, two of the cleaved fragments associate to form the active site of the caspase. The active enzyme is thought to be a tetramer of two of these units (not shown). (B) Each activated caspase molecule can cleave many procaspase molecules, thereby activating them, and these can then activate even more procaspase molecules. In this way, an initial activation of a small number of procaspase molecules (called initiator caspases) can lead, via an amplifying chain reaction (a cascade), to the explosive activation of a large number of procaspase molecules. Some of the activated caspases (called effector caspases) then cleave a number of key proteins in the cell, including specific cytosolic proteins and nuclear lamins, leading to the controlled death of the cell.

11.7 Procaspases are activated by binding to adaptor proteins

A general principle is that activation is triggered by adaptor proteins that brings multiple copies of specific procaspases, known as *initiator procaspases*, which can aggregate. In some cases, the initiator procaspases have a small amount of protease activity, and forcing them together to aggregate that causes them to cleave each other, triggering their mutual activation. In other cases, the aggregation is thought to cause a conformational change that activates the procaspase. Within moments, the activated caspase at the top of the cascade cleaves downstream procaspases to amplify the death signal and spread it throughout the cell.

11.8 Activation of procaspase from outside the cell

Procaspase activation can be triggered from outside the cell by activation of death receptors on the cell surface. For example, killer lymphocytes can induce apoptosis by producing a protein called fas ligand, which binds to death receptor protein fas on the surface of the target cells. The clustered fas proteins then recruit intracellular adaptor proteins that bind and aggregate procaspase-8 molecules, which cleave and activate one another. The activated caspase-8 molecules then activate downstream procaspases to induce apoptosis. Some stressed or damaged cells kill themselves by producing both fas ligand and fas protein, thereby triggering an intracellular caspase cascade.

When cells are damaged or stressed, they can also kill themselves by triggering procaspase activation and activation from within the cell. In a best understood pathway mitochondria are involved and induce to release the electron carrier protein cytochrome C into cytosol, where it binds and activate an adaptor protein called Apaf-1. This mitochondrial pathway of procaspase activation is recruited in most of the apoptosis to initiate or to accelerate and amplify caspase cascade. This response

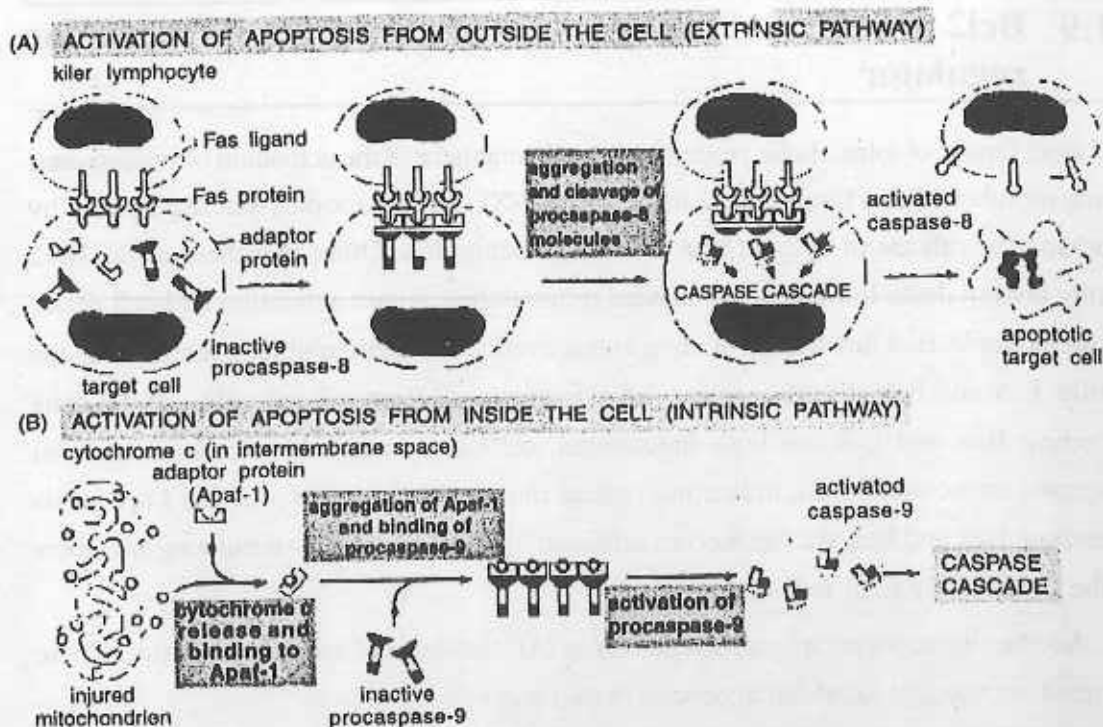


Fig 4. Induction of apoptosis by either extracellular or intracellular stimuli. (A) Extracellular activation. A killer lymphocyte carrying the Fas ligand binds and activates Fas proteins on the surface of the target cell. Adaptor proteins bind to the intracellular region of aggregated Fas proteins, causing the aggregation of procaspase-8 molecules. These then cleave one another to initiate the caspase cascade. (B) Intracellular activation. Mitochondria release cytochrome C, which binds and causes the aggregation of the adaptor protein Apaf-1. Apaf-1 binds and aggregates procaspase-9 molecules, which leads to the cleavage of these molecules and the triggering of a caspase cascade. Other proteins that contribute to apoptosis are also released from the mitochondrial intermembrane space (not shown).

usually requires p53 which can activate the transcription of gene that encodes the protein and promote the release of cytochrome C from mitochondria. This protein belongs to Bcl2 family.

11.9 Bcl2 protein and IAP proteins are the main intracellular regulator

Bcl2 family of intracellular protein is the main regulator of the activation of procaspases. Some member of this family, Bcl2 itself and Bcl-XL inhibit apoptosis at least partly by blocking the release of cytochrome C from mitochondria. Other members of the Bcl2 family are not death inhibitors, but instead promote procaspase activation and cell death. As for example, Bad function by binding to inactivating the death inhibiting members of the family. Bax and Bak stimulate release of cytochrome C from mitochondria. If the gene encoding Bax and Bak are both inactivated, cells are remarkably resistant to most apoptosis inducing stimuli, indicating crucial importance of these proteins I apoptosis induction. Bax and Bak are themselves activated by other apoptosis stimulating members of the Bcl2 family such as Bid.

Another intracellular apoptosis regulator is IAP (inhibitor of apioptosis) family. These proteins are thought to inhibit apoptosis in two ways :

- 1) they bind to some procaspases to prevent their activation and
- 2) they bind to caspases to inhibit their activities.

IAP protein was originally discovered as protein induced by certain insect virus, which use them to prevent the infected cells from killing itself before the virus have had time to replicate. When mitochondria release cytochrome C to activate Apaf-1, they also release a protein to block IAPs, thereby greatly increasing the efficiency of death activating process. Signals, which can either activate apoptosis or inhibit it. These signal molecules mainly act by regulating the levels or activity of members of Bcl2 and IAP families.

11.7 Summary

In multicellular organisms, cells that are no longer needed or are a threat to the organism are destroyed by a tightly regulated cell suicide process known as programmed cell death, or apoptosis. Apoptosis is mediated by proteolytic enzymes called caspases, which trigger cell death by cleaving specific proteins in the cytoplasm and nucleus.

Caspases exist in all cells as inactive precursors, or procaspases, which are usually activated by cleavage by other caspases, producing a proteolytic caspase cascade. The activation process is initiated by either extracellular or intracellular death signals, which cause intracellular adaptor molecules to aggregate and activate procaspases. Caspase activation is regulated by members of the Bcl-2 and IAP protein families.

Procaspase activation can be triggered from outside the cell by the activation of death receptors on the cell surface. Killer lymphocytes, for example, can induce apoptosis by producing a protein called **Fas ligand**, which binds to the death receptor protein **Fas** on the surface of the target cell. The clustered Fas proteins then recruit intracellular adaptor proteins that bind and aggregate procaspase-8 molecules, which cleave and activate one another. The activated caspase-8 molecules then activate downstream procaspases to induce apoptosis. Some stressed or damaged cells kill themselves by producing both the Fas ligand and the Fas protein, thereby triggering an intracellular caspase cascade.

Unit 12 □ Synthesis, Sorting, Trafficking of Protein hormone

Structure

12.1 Introduction

12.2 Steps in Expression of a Protein-encoding Gene

12.3 Subcellular Structure of Cells that Secrete Protein Hormones

12.4 Intracellular Segregation and Transport of Polypeptide Hormones

12.4.1 Signal Sequences in Peptide Prohormone Processing and Secretion

12.1 Introduction

The polypeptide hormones constitute a critically important and diverse set of regulatory molecules encoded by the genome whose functions are to convey specific information among cells and organs. This type of molecular communication appear early in the development of life and evolves a complex system for the control of growth, development and reproduction, and for the maintenance of metabolic homeostasis. These hormones consist of approximately 400 or more small proteins ranging from as few as three amino acids (thyrotropin-releasing hormone, TRH) to 192 amino acids (growth hormone). In a broader sense, these polypeptides function as hormones, whose actions on distant organs are mediated by way of their transport through the blood stream, and act locally as cell-to-cell communicators. The latter function of the polypeptide hormones is exemplified by their elaboration and secretion within neurons of the central, autonomic, and peripheral nervous systems, where they act as neurotransmitters. These multiple modes of expression of the polypeptide hormone genes have aroused great interest in the specific functions of these peptides and the mechanisms of their synthesis and release.

12.2 Steps in Expression of a Protein-encoding Gene

The steps involved in transfer of information encoded in the polynucleotide language of DNA to the poly-amino acid language of biologically active proteins involve gene transcription, post-transcriptional processing of ribonucleic acids (RNAs), translation, and post-translational processing of the proteins. The expression of genes and protein synthesis can be considered in terms of several major processes, any one or more of which may serve as specific control points in the regulation of gene expression :

1. *Rearrangements and transpositions of DNA segments.* These processes occur over many years in evolution, with the exception of uncommon mechanisms of somatic gene rearrangements such as the rearrangements in the immunoglobulin genes during the lifetime of an individual.
2. *Transcription.* Synthesis of RNA results in the formation of RNA copies of the two gene alleles and is catalyzed by the basal RNA polymerase II-associated transcription factors.
3. *Post-transcriptional processing.* Specific modifications of the RNA include the formation of messenger RNA (mRNA) from the precursor RNA by way of excision and rejoining of RNA segments (introns and exons) and modifications of the 3' end of the RNA by polyadenylation and of the 5' end by addition of 7-methylguanine "caps."
4. *Translation.* Amino acids are assembled by base pairing of the nucleotide triplets (anticodons) of the specific "carrier" aminoacylated transfer RNAs to the corresponding codons of the mRNA bound to polyribosomes and are polymerized into the polypeptide chains.
5. *Post-translational processing and modification.* Final steps i.e protein synthesis may involve one or more cleavages of peptide bonds, which result in the

conversion of biosynthetic precursors (prohormones), to intermediate or final forms of the protein; derivation of amino acids (e.g., glycosylation, phosphorylation, acetylation, myristoylation); and the folding of the processed polypeptide chain into its native conformation. Each of the specific steps of gene expression requires the integration of precise enzymatic and other biochemical reactions. These processes have developed to provide high fidelity in the reproduction of the encoded information and to provide control points for the expression of the specific phenotype of cells. The post-translational processing of proteins creates diversity in gene expression through modifications of the protein. Although the functional information contained in a protein is ultimately encoded in the primary amino acid sequence, the specific biologic activities are a consequence of the higher orders of the secondary, tertiary, and quaternary structures of the polypeptide. Given the wide range of possible specific modifications of the amino acids, such as glycosylation, phosphorylation, acetylation, and sulfation, any one of which may affect the conformation or function of the protein, a single gene may ultimately encode a wide variety of specific proteins as a result of post-translational processes. Polypeptide hormones are synthesized in the form of larger precursors that appear to fulfill several functions in biologic systems, including (1) intracellular trafficking, by which the cell distinguishes among specific classes of proteins and directs them to act their sites of action, and (2) the generation of multiple biologic activities from a common genetically encoded protein by regulated or cell-specific variations in the post-translational modifications.

All the peptide hormones and regulatory peptides studied thus contain signal or leader sequences at the amino termini; these hydrophobic sequences recognize specific sites on the membranes of the rough endoplasmic reticulum, which results in the transport

of nascent polypeptides into the secretory pathway of the cell. The consequence of the specialized signal sequences of the precursor proteins is that proteins destined for secretion are selected from a great many other cellular proteins for sequestration and subsequent packaging into secretory granules and export from the cell. In addition, most, if not all, of the smaller hormones and regulatory peptides are produced as a consequence of post-translational cleavages of the precursors within the Golgi complex of secretory cells.

12.3 Subcellular Structure of Cells that Secrete Protein Hormones

Cells whose principal functions are the synthesis and export of proteins contain highly developed, specialized subcellular organelles for the translocation of secreted proteins and their packaging into secretory granules. The subcellular pathways utilized in protein secretion have been elucidated largely through the early efforts of Palade and colleagues. Secretory cells contain an abundance of endoplasmic reticulum, Golgi complexes, and secretory granules. The proteins that are to be secreted from the cells are transferred during their synthesis into these subcellular organelles, which transport the proteins to the plasma membrane. Protein secretion begins with translation of the mRNA encoding the precursor of the protein on the rough endoplasmic reticulum, which consists of polyribosomes attached to elaborate membranous saccules that contain cavities (cisternae). The newly synthesized, nascent proteins are discharged into the cisternae by transport across the lipid bilayer of the membrane. Within the cisternae of the endoplasmic reticulum, proteins are carried to the Golgi complex by mechanisms that are incompletely understood. The proteins gain access to the Golgi complex either by direct transfer from the cisternae, which are in continuity with the membranous channels of the Golgi

complex, or by way of shuttling vesicles known as transition elements. Within the Golgi complex, the proteins are packaged into secretory vesicles or secretory granules by their budding from the Golgi stacks in the form of immature granules. Immature granules undergo maturation through condensation of the proteinaceous material and application of a specific coat around the initial Golgi membrane. On receiving the appropriate extracellular stimuli (regulated pathway of secretion), the granules migrate to the cell surface and fuse to become continuous with the plasma membrane, which results in the release of proteins into the extracellular space, a process known as exocytosis. The second pathway of intracellular transport and secretion involves the transport of proteins contained within secretory vesicles and immature secretory granules. Although the use of this alternative vesicle-mediated transport pathway remains to be demonstrated conclusively (it is generally considered to be a constitutive, or unregulated, pathway), different extracellular stimuli may modulate hormone secretion differently, depending on the pathway of secretion. For example, in the parathyroid gland and in the pituitary cell line derived from corticotrophic cells (AtT-20), newly synthesized hormone is released more rapidly than hormone synthesized earlier. These findings suggest that the newly synthesized hormone may be transported by way of a vesicle-mediated pathway without incorporation into mature storage granules.

12.4 Intracellular Segregation and Transport of Polypeptide Hormones

Specific amino acid sequences encoded in the proteins serve as directional signals in the sorting of proteins within subcellular organelles. A typical eukaryotic cell synthesizes an estimated 5000 different proteins during its life span. These different proteins are synthesized by a common pool of polyribosomes. However, each of the different proteins is directed

to a specific location within the cell, where its biologic function is expressed. For example, specific groups of proteins are transported into mitochondria, membranes, the nucleus, or into the other subcellular organelles, where they serve as regulatory proteins, enzymes, or structural proteins. A subset of proteins is specifically designed for export from the cell (e.g., immunoglobulins, serum albumin, blood coagulation factors, and protein and polypeptide hormones). This process of directional transport of proteins involves sophisticated informational signals. Because the information for these translocation processes must reside either wholly or in part within the primary structure or in the conformational properties of the protein, sequential post-translational modifications may be crucial for determining the specificity of protein function.

12.4.1' Signal Sequences in Peptide Prohormone Processing and Secretion

The early processes of protein secretion that result in the specific transport of exported proteins into the secretory pathway are now becoming better understood. Initial clues to this process came from determinations of the amino acid sequences of the proteins programmed by the cell-free translation of mRNAs encoding secreted polypeptides. Secreted proteins are synthesized as precursors that are extended at their NH₂ termini by sequences of 15 to 30 amino acids, called *signal* or *leader sequences*. Signal sequence extensions, or their functional equivalents, are required for targeting the ribosomal or nascent protein to specific membranes and for the vectorial transport of the protein across the membrane of the endoplasmic reticulum. On emergence of the signal sequence from the large ribosomal subunit, the ribosomal complex specifically makes contact with the membrane, which results in translocation of the nascent polypeptide across the endoplasmic reticulum membrane into the cisterna as the first step in the transport of the polypeptide within the secretory pathway. These observations initially left unanswered the question of

how specific polyribosomes that translate mRNAs encoding secretory proteins recognize and attach to the endoplasmic reticulum. Because microsomal membranes in vitro reproduce the processing activity of intact cells, it was possible to identify macromolecules responsible for processing of the precursor and for translocation activities. The endoplasmic reticulum and the cytoplasm contain an aggregate of molecules, called a *signal recognition particle complex*, that consists of at least 16 different proteins, including three guanosine triphosphatases to generate energy and a 7S RNA. This complex, or particle, binds to the polyribosomes involved in the translation of mRNAs encoding secretory polypeptides when the NH₂-terminal signal sequence first emerges from the large subunit of the ribosome. The specific interaction of the signal recognition particle with the nascent signal sequence and the polyribosome arrests further translation of mRNA. The nascent protein remains in a state of arrested translation until it finds a high-affinity binding protein on the endoplasmic reticulum, the signal recognition particle receptor, or docking protein. On interaction with the specific docking protein, the translational block is released and protein synthesis resumes. The protein is then transferred across the membrane of the endoplasmic reticulum through a proteinaceous tunnel. At some point, near the termination of synthesis of the polypeptide chain, the NH₂-terminal signal sequence is cleaved from the polypeptide by a specific signal peptidase located on the cisternal surface of the endoplasmic reticulum membrane. The removal of the hydrophobic signal sequence frees the protein (prohormone or hormone) so that it may assume its characteristic secondary structure during transport through the endoplasmic reticulum and the Golgi apparatus. Interestingly, after its cleavage from the protein by signal peptidase, the signal peptide may sometimes be further cleaved in the endoplasmic reticulum membrane to produce a biologically active peptide. The signal sequence of preprolactin of 30 amino acids, for example, is cleaved by a signal peptide peptidase to give a charged peptide of 20 amino acids that is released into the cytosol, where it binds to calmodulin and inhibits Ca²⁺-calmodulin-dependent phosphodiesterase.

This sequence in the directional transport of specific polypeptides ensures optimal cotranslational processing of secretory proteins, even when synthesis commences on free ribosomes. The presence of a cytoplasmic form of the signal recognition particle complex that blocks translation guarantees that the synthesis of the presecretory proteins is not completed in the cytoplasm; the efficient transfer of proteins occurs only after contact has been made with the specific receptor or docking protein on the membrane. Although the identification of the signal recognition particle and the docking protein explains the specificity of the binding of ribosomes containing mRNAs encoding the secretory proteins, it does not explain the mode of translocation of the nascent polypeptide chain across the membrane bilayer. Further dissection and analysis of the membrane have identified other macromolecules that are responsible for the transport process.

NOTES

মানুষের জ্ঞান ও ভাবকে বইয়ের মধ্যে সঞ্চিত করিবার
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