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Steroidogenic Enzymes in Leydig Cells

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SUMMARY

This chapter describes the enzymes expressed in Leydig cells that are required for the biosynthesis of testosterone from cholesterol, as well as the two enzymes, steroid 5 α -reductase and P450arom, that metabolize testosterone to dihydrotestosterone and estradiol, respectively. The emphasis is on human and mouse enzymes.

Key Words: CYP11A; CYP17A; CYP19A, 3 β -HSD; 17 β -HSD; Leydig cell; P450arom; P450c17; P450scc; steroidogenesis; steroid- α -reductase.

INTRODUCTION

The Leydig cell is the only cell in the male that expresses all of the enzymes essential for the conversion of cholesterol to testosterone, the major male sex hormone secreted by the testis. Testosterone can be metabolized further in the Leydig cell by S5A (5 α -reductase) to yield dihydrotestosterone (1), or by the enzyme, CYP19A1 (P450arom) to yield estradiol (2,3). Testosterone or its metabolite, dihydrotestosterone, is essential for male sexual differentiation, expression of male secondary sex characteristics (4), and maintenance of spermatogenesis (5). The biosynthesis of testosterone is dependent on both acute and chronic stimulation of Leydig cells by the pituitary hormone luteinizing hormone (LH). LH binds to specific high affinity receptors on the surface of Leydig cells activating adenylate cyclase, resulting in increased production of cyclic AMP. The acute stimulation results in the rapid transport of cholesterol from the outer to the inner mitochondrial membrane, the site of the first enzyme in the pathway of cholesterol to testosterone. This process is mediated by the steroidogenic acute regulatory protein (StAR) (6), see Chapter 9. Chronic stimulation of Leydig cells by LH or cAMP is required for

optimal expression of the enzymes required for the biosynthesis of testosterone from cholesterol. This chapter describes the enzymes involved in the biosynthesis of testosterone from cholesterol as well as the two enzymes, steroid 5 α -reductase and P450arom that metabolize testosterone to dihydrotestosterone and estradiol, respectively (Fig. 1). The enzymes can be divided into two major classes of proteins: the cytochrome P450 heme-containing proteins CYP11A1 (P450scc), CYP17A1 (P450c17), and P450arom, and the hydroxysteroid dehydrogenases 3 β -hydroxysteroid dehydrogenase (3 β -HSD), and 17 β -hydroxysteroid dehydrogenase (17 β -HSD). 5 α -reductase belongs to the steroid 5 α -reductase family (Table 1C; ref. 7).

The initial step in the biosynthesis of testosterone from cholesterol is the conversion of the C27 cholesterol to the C21 steroid, pregnenolone. This reaction is catalyzed by the cytochrome P450 enzyme, cholesterol side-chain cleavage (P450scc), located in the inner mitochondrial membrane. Pregnenolone diffuses across the mitochondrial membrane and is further metabolized by enzymes associated with the smooth endoplasmic reticulum. These include the cytochrome P450 17 α -hydroxylase C17-C20 lyase, P450c17, which catalyzes the conversion of the C21 steroids pregnenolone or progesterone to the C19 steroids dehydroepiandrosterone or androstenedione, respectively, and 3 β -hydroxysteroid dehydrogenase which catalyzes the conversion of the Δ 5 steroids, pregnenolone, or dehydroepiandrosterone to the Δ 4 steroids, progesterone, or androstenedione, respectively, and 17 β -hydroxysteroid dehydrogenase, which catalyzes the final step in the biosynthesis of testosterone (Fig. 1).

CYTOCHROME P450s

The cytochrome P450 enzymes are members of a superfamily of heme-containing proteins (8). They

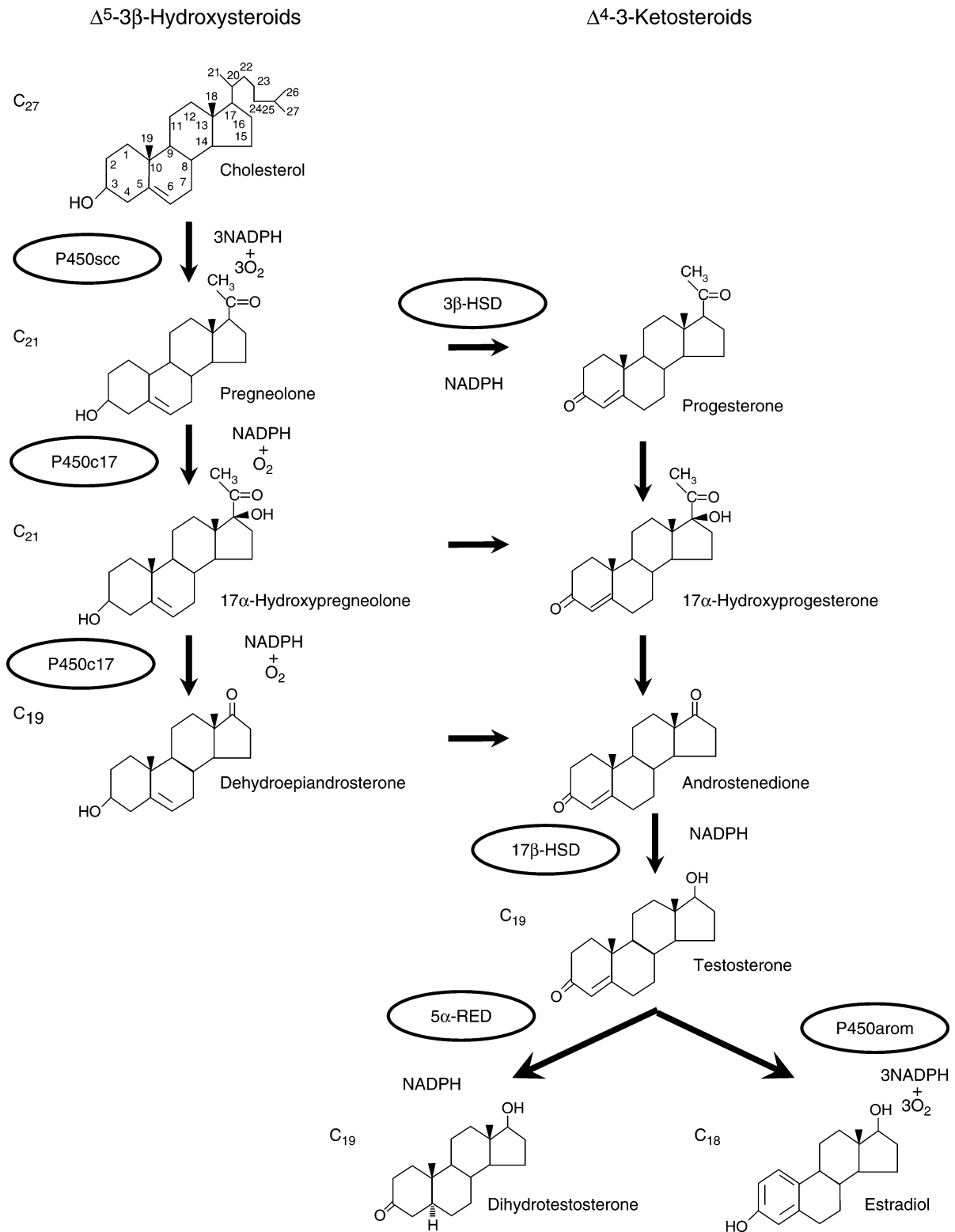


Fig. 1. Steroid biosynthetic pathways in Leydig cells.

derive their name from the characteristic which, when complexed in vitro with exogenous carbon monoxide, absorb light maximally at 450 nm. They function as monooxygenases utilizing reduced nicotinamide adenine dinucleotide phosphate (NADPH) as the donor for the reduction of molecular oxygen. The general reaction is: $\text{RH} + \text{O}_2 + \text{NADPH} + \text{H}^+ \rightarrow \text{ROH} + \text{H}_2\text{O} + \text{NADP}^+$. In this reaction, the oxygen is activated by P450, and one oxygen atom is introduced into the substrate RH as a hydroxyl group, and the other oxygen is reduced to H_2O . The electrons from NADPH are transferred to the substrate by two distinct electron transfer systems. The mitochondrial transfer involves the transfer of high potential electrons to a flavoprotein, adrenodoxin reductase (ferredoxin reductase), and then sequentially to adrenodoxin (ferredoxin), a nonheme iron-sulfur protein, then P450, and finally, to the substrate. The microsomal electron transfer system involves only one protein, cytochrome P450 oxidoreductase, a protein that contains two flavins. The electrons are transferred from NADPH, to flavinadenine dinucleotide, followed sequentially by transfer to flavinmononucleotide and then the substrate (7).

P450scc

REACTION CATALYZED

P450scc catalyzes the conversion of cholesterol to pregnenolone, the first and rate-limiting enzymatic step in the biosynthesis of testosterone (Fig. 1). P450scc catalyzes three sequential oxidation reactions of cholesterol. Each reaction requires one molecule of oxygen and one molecule of NADPH, and the mitochondrial electron transfer system (7). The first reaction is the hydroxylation at C22, followed by hydroxylation at C20 to yield 20,22R-hydroxycholesterol that is cleaved between C22 and C20 to yield the C21 steroid pregnenolone, and isocaproaldehyde (9,10) Isocaproaldehyde is further metabolized to isocaproic acid (11).

Investigations utilizing the purified protein as well as studies on recombinant proteins from P450scc cDNAs have provided conclusive evidence that a single protein catalyzes all three reactions at a single active site (12,13). The pair of electrons required for each of the reactions is transferred from NADPH to a flavoprotein, ferredoxin reductase, and then sequentially to a nonheme iron-sulfur protein, ferredoxin, to P450scc, and finally, to the substrate (14). The P450scc enzyme is typical of all mitochondrial cytochrome P450 enzymes that share the same electron transfer proteins (15). It has been shown that the P450scc enzyme only functions in the mitochondrion. This requirement appears to be for the mitochondrial

environment rather than the specific mitochondrial electron transfer system (16). A model of the interactions between P450scc and the electron transport proteins has been proposed based on the expression of mutants. The results of these studies indicate that the acidic residues, Asp 76, and Asp 79, of ferredoxin interact with the basic residues of ferredoxin reductase and P450scc (17).

MOLECULAR STRUCTURE

P450scc is the product of a single gene. The cDNA was first isolated in 1984 from bovine adrenal cortex mRNA (18). Subsequently, P450scc cDNA has been cloned from human (19), rat (20), mouse (21), and numerous other species. The deduced amino acid (aa) sequence displays high homology among species, equal to or more than 71%. The open reading frame of human cDNA encodes a peptide consisting of 521 aa (19,22). The 39 aa at the amino-terminus includes the N-terminal leader sequence essential for the translocation of the protein to the inner mitochondrial membrane. The removal of this leader sequence yields a protein of 482 aa (16,19). The aa sequence contains a heme-binding region common to the P450 superfamily located close to the carboxyl terminus containing a single cysteine residue (18), and a specific 20 aa region of high homology among species located at the amino-terminus which is proposed to be the P450scc-specific substrate binding region (23).

The structure of the cholesterol-side chain cleavage gene designated as *CYP11A1* has been determined in human (22) and rat (24). The gene is at least 20 kb in length, and consists of nine exons containing an unusual exon/intron junctional sequence that begins with GC found in the sixth intron of both the human gene (22) and the rat gene (24). The human gene is located on chromosome 15q23-q24 (19), and the mouse gene is found on chromosome 9 at 31 cM (25).

P450c17

Reaction Catalyzed

P450c17 catalyzes two mixed function oxidase reactions, 17α -hydroxylation, and C17-C20 cleavage. Each reaction requires one molecule of NADPH, and one molecule of oxygen, and the microsomal electron transfer protein, cytochrome P450 oxidoreductase (7). The two reactions catalyzed by P450c17 are the 17α -hydroxylation of either the Δ^5 -C21 steroid, pregnenolone, or the Δ^4 -C21 steroid, progesterone, followed by cleavage of the C17-20 bond to yield either the C19 steroids, dehydroepiandrosterone (DHEA), or androstenedione, respectively (Fig. 1). In this two

Table 1
Leyding Cell Steroidogenic Enzymes

Gene	Chromosomal location		Protein name (molecular mass)	Subcellular location	Synonyms	Protein Gene ID (accession no)	
	Human	Mouse				Human	Mouse
A. Cytochrome P450							
<i>CYP11A1</i>	15q23-q24	9 (31 cM)	CYP11A1 (56 kDa)	Mitochondria (146)	P450 _{scc} , cholesterol side chain cleavage, cholesterol desmolase, cytochrome P450 cholesterol side chain cleavage, cholesterol 20-22 desmolase	1583 (P05108)	13070 (Q9QZ82)
<i>CYP17A1</i>	10q24.3	19 (46 cM)	CYP17A1 (57 kDa)	Microsomal (146)	P450 _{c17} , 17 α -hydroxylase/17,20 lyase, P450 17 α -hydroxylase/c17-20 lyase	281739 (P05093)	13074 (P27786)
<i>CYP19A1</i>	15q21.1	9 (31 cM)	CYP19A1 (58 kDa)	Microsomal (57)	Aromatase, P450 _{arom} , cytochrome P450 _{arom} , estrogen synthase	1588 (P11511)	13075 (P28649)
B. Hydroxysteroid dehydrogenases							
<i>HSD3B1</i>	Hsd3b6	1p13.1	3 β -HSDI human 3 β -HSDVI mouse (42 kDa)	Microsomal	3 β -HSD type-I (type-VI), 3 β -HSD/ Δ 4- Δ 5 isomerase, 3 β -hydroxy Δ 5-steroid dehydrogenase, 3 β -hydroxy-5-ene steroid dehydrogenase	3283 (P14060)	15497 (O35469)
<i>HSD3B2</i>	Hsd3b1	1p13.1	3 β -HSDII human 3 β -HSDI mouse (42 kDa)	Mitochondria and microsomal (146)	See previous entry	3284 (P26439)	15492 (P24815)
<i>HSD17B3</i>	Hsd17b3	9q22	17 β -HSD3 (34.5 kDa)	Microsomal (147)	17 β -HSD 3, testicular 17 β -HSD	3293 (P37058)	15487 (P70385)
C. Steroid 5α-reductases							

<i>SRDA1</i>	<i>Srda1</i>	5p15	13 (39 cM)	SRDA1 (29.5 kDa) human (24.9 kDa) mouse	Microsomal (148)	3-oxo-5 α -reductase, 5 α -reductase	6715 (P18405)	24950
<i>SRDA 2</i>	<i>Srda1</i>	2p23	17 (E2)	SRDA2 (28.4 kDa) human (24.9 kDa) mouse	Microsomal (148)	See previous entry	6716 (P31213)	94224 (Q99N99)

Swiss-Prot <http://us.espasy.org/cgi-bin/sprot-search.ac>.

step reaction, 17α -hydroxypregnenolone or 17α -hydroxyprogesterone is synthesized as an intermediate. Initially, it was believed that each reaction was catalyzed by a distinct enzyme, but studies by Hall and colleagues (26,27) demonstrated that a single purified protein catalyzed both 17α -hydroxylation and C17–C20 cleavage (lyase) activity. Subsequent cloning of a bovine P450c17 cDNA and expression of this cDNA confirmed that both reactions were catalyzed by the same protein (28). Although, the P450c17 enzyme from various species catalyzes both the hydroxylation and the lyase reaction, there are marked species-dependent differences in the utilization of either 17α -hydroxypregnenolone ($\Delta 5$) or 17α -hydroxyprogesterone ($\Delta 4$) as substrate for the lyase reaction. The human and bovine enzymes use 17α -hydroxypregnenolone as the preferential substrate yielding DHEA as the product, whereas the rodent enzyme utilizes 17α -hydroxyprogesterone as the substrate yielding androstenedione as the product (29). Auchus and colleagues provided conclusive evidence that human testes synthesize testosterone predominantly by the $\Delta 5$ pathway (30). These species-dependent differences in substrate preference for the C17–C20 lyase activity are not related to differences in the aa sequence of the bovine and human enzyme, compared with the rodent enzyme. However, the differences are a property of the human and bovine enzyme required for high molar concentration of cytochrome P450 reductase (31,32), serine/threonine phosphorylation of P450c17 (33,34), and the accessory protein cytochrome b_5 in promoting lyase activity of 17α -hydroxypregnenolone, but not of 17α -hydroxyprogesterone (29,35).

Additional activities to that of the classic 17α -hydroxylation/C17–C20 cleavage have been observed. Swart et al. (36) reported that human P450c17 also expresses 16α -hydroxylase activity at the same site as 17α -hydroxylase activity. More recent study by Liu et al. (37) using a P450c17 deficient MA10 mouse tumor Leydig cell culture indicated that P450c17 expresses a secondary activity, squalene monooxygenase (epoxidase) activity, suggesting that this enzyme may also be involved in cholesterol biosynthesis as proposed several years earlier by Lieberman and Warne (38).

MOLECULAR STRUCTURE

Genomic Southern blotting and/or cloning has established that in mouse (39), rat (40), and human (41,42) as well as in other species there is a single gene designated as *CYP17A1* in human and *Cyp17a1* in mouse. The *CYP17A1* gene is approx 6 kb in length and contains eight exons with the location of intron–exon boundaries

conserved among species. The 5' upstream region of the human, bovine, porcine, rat, and mouse gene share a high homology over the first 550 bp including the same nonconsensus TATA box (41–46). The human *CYP17A1* gene has been mapped to chromosome 10q24.3 (47,48) and the mouse *Cyp17a1* gene to chromosome 19 at 46 cM (39). The human P450c17 protein contains 508 aa (49) compared with 507 aa in the mouse (39) and rat (40) proteins. The molecular mass of the P450c17 protein is approx 57 kDa. Comparison of the mouse aa sequence to rat and human sequences indicates that they are 83 and 66% identical, respectively. The P450c17 protein of different species contains regions of high homology common to members of the P450 gene family (39). These are the putative binding regions for mouse aa 434–454 (39), human aa 435–455 (50), and the ozols tridecapeptide sequence (343–372 aa) (51) that may play a role in substrate specificity (52). In addition, there is a region that is specifically conserved among different species of P450c17 (296–319) that may function in catalysis (53). Arginine346 in the rat enzyme (54,55) and arginine347 in the human enzyme were found to be critical for catalyzing lyase activity.

P450AROM

Reaction Catalyzed

P450arom catalyzes the conversion of the C19 androgens, androstenedione, and testosterone, to the C18 estrogens, estrone, and estradiol, respectively. The reaction requires three molecules of oxygen and three molecules of NADPH using the microsomal electron transfer system. The first two oxygen molecules are required for the oxidation of the C19 methyl group by standard hydroxylation reactions, whereas the third oxygen molecule is required for a reaction proposed to be a peroxidative attack on the C19 methyl group combined with elimination of the 1β hydrogen to yield a phenolic A ring and formic acid (7).

Molecular Structure

P450arom (*CYP19A1*) is the product of a single gene in human (56,57), mouse (58), and rat (59). The human gene has been mapped to 15q21.1 (60), and the mouse gene is located on chromosome 9 at 31 cM (25). The human gene contains 10 exons, nine of which includes the coding region spanning approx 30 kb (56). Upstream of exon II are several alternative exon 1s that are spliced into the 5' untranslated region, which determines the tissue-specific expression of the protein (56). The proximal promoter II determines testicular and ovarian expression of P450arom, and the transcript originates immediately upstream of the

translational start site, approx 26 bp downstream of the putative TATA sequence (57,61,62). Although, the transcripts have different termini in the different tissues, the coding region of the expressed protein is identical.

The deduced aa sequence of human P450arom in comparison to the rat and mouse protein exhibits 81% homology (56). Both the human and mouse protein consist of 503 aa with a molecular mass of 58 kDa (56). The P450arom proteins from different species contain the same structural features described for the other cytochrome P450 enzymes: the heme-binding region containing a conserved cysteine residue that serves as the fifth coordinating ligand of the heme iron, and the substrate binding site in the amino-terminal I-helix region.

HYDROXYSTEROID DEHYDROGENASES

The hydroxysteroid dehydrogenases, 3 β -HSD and 17 β -HSD, involved in the biosynthesis of testosterone from cholesterol, belong to the same phylogenetic protein family, namely the short-chain alcohol dehydrogenase reductase superfamily. In general, they are involved in the reduction and oxidation of steroid hormones, requiring NAD⁺/NADP⁺ as acceptors and their reduced forms as donors of reducing equivalents. One of the major differences between the P450 enzymes and the hydroxysteroid dehydrogenases is that each of the P450 enzymes is a product of a single gene, whereas there are several isoforms for 3 β -HSDs and several isozymes of the 17 β -HSDs, each a product of a distinct gene. The number of isoforms or isozymes varies in different species, in tissue distribution, catalytic activity (whether they function predominantly as dehydrogenases or reductases), substrate and cofactor specificity, and sub-cellular distribution. The 3 β -HSD isoform expressed in Leydig cells is 3 β -HSD II in human (63), 3 β -HSD I (64) and VI (65) in mouse, and 3 β -HSD I in rat (66). The 17 β -HSD3 is the 17 β -HSD isoform exclusively expressed in both human (67) and rodent adult Leydig cells (68,69).

3 β -Hydroxysteroid Dehydrogenase

REACTION CATALYZED

The 3 β -HSD isoforms expressed in Leydig cells catalyze the conversion of the Δ 5-3 β -hydroxysteroids, pregnenolone, 17 α -hydroxypregnenolone, and DHEA, to the Δ 4-3-ketosteroids, progesterone, 17 α -hydroxyprogesterone, and androstenedione, respectively. Two sequential reactions are involved in the conversion of the Δ 5-3 β -hydroxysteroid to a Δ 4-3-ketosteroid. The first

reaction is the dehydrogenation of the 3 β -equatorial hydroxysteroid, requiring the coenzyme NAD⁺, yielding the Δ 5-3-keto intermediate, and reduced NADH. The reduced NADH, activates the isomerization of the Δ 5-3-keto steroid to yield the Δ 4-3-ketosteroid (7,70,71). This reaction is catalyzed by a single dimeric protein without the release of the intermediate or coenzyme (71). Four isoforms in rat have been identified (7,72). Each of these isoforms is the product of a distinct gene. Human *HSD3B* genes are found on chromosome 1p31.1 (73) and the *Hsd3b* mouse genes are located in a cluster on mouse chromosome 3 close to the centromeric region that shows conservation of gene order and physical distance with the centromeric region of human chromosome 1 (74,75). All of the *HSD3B* genes consist of four exons, with the start site of translation found in exon 2 (75). The two human genes are approx 7.8 kb, and their nucleotide sequences are highly homologous including their intronic sequences and the 1250 bp sequence of the 5' flanking region that exhibits 81.9% identity (72). The size of the mouse genes varies as result of differences in the size of their introns (75,76). Intron 1 of the mouse *Hsd3b6* gene was found to be 3.1 kb (76) compared with 126, 125, and 132 bp found in mouse *Hsd3b1* and human *HSD3B1* and *HSD3B2* (75). The open reading frames of mouse I and mouse VI 3 β -HSD, the isoforms expressed in Leydig cells, encode a protein including the initiator methionine of 373 aa (65), whereas human II 3 β -HSD encodes a protein of 372 aa (72). The aa sequences among the different isoforms and between mouse and human isoforms show a high degree of identity. Mouse 3 β -HSD I is 84% identical to mouse VI, and 71% identical to human II (65,72). Although the aa sequence predicts a molecular mass of 42 kDa for all of the 3 β -HSD proteins, when subjected to sodium dodecyl sulfate-polyacrylamide gel electrophoresis, the mobilities of mouse 3 β -HSD I and VI are distinct, exhibiting an apparent molecular mass of 42 and 44 kDa, respectively (65). The cofactor binding site is located in the amino-terminal sequence. Investigations using homology modeling of human 3 β -HSD I demonstrated that Asp36 is responsible for the NAD(H) binding site (71). In earlier studies investigating the difference in the aa sequence of mouse 3 β -HSD I, which requires NAD⁺ as a cofactor, and mouse 3 β -HSD IV and V, which require NADP⁺ as cofactor, it was found that Asp36 was essential for NAD⁺-mediated dehydrogenation/isomerization, and replacement of Asp36 with phenylalanine at position 36 changed the cofactor specificity to NADP⁺. (77,78) The dehydrogenase activity has been localized to the Y154-P-H-S-K158 domain and the isomerase site to Tyr269 and Lys273 of the human 3 β -HSD protein (79).

17-HYDROXYSTEROID

Till date, 11 distinct 17 β -HSDs have been identified. Unlike the 3 β -HSDs described earlier, there is little homology among the different 17 β -HSD isozymes (7). But unlike the 3 β -HSDs, the orthologs among the different species are assigned the same number. Thus, the isozyme expressed in Leydig cells is 17 β -HSD 3 in human, rat, and mouse.

Reaction Catalyzed

The 17 β -HSD catalyzes the last step in the biosynthesis of testosterone. It converts androstenedione, a weak androgen, to testosterone, a potent androgen. 17 β -HSD 3 prefers NADPH as a cofactor, and its primary activity is reductive.

Molecular Structure

The human gene *HSD17B3* maps to chromosome 9q22 (67) and the mouse gene *Hsd17b3* is located on chromosome 13 (68). The human gene is 60 kb in length and contains 11 exons (67). It encodes a protein of 310 aa with a molecular mass of 34.5 kDa and no apparent membrane spanning region (67). The mouse gene encodes a protein of 305 aa, five fewer than the human with a molecular mass of 33.7 kDa (68). The mouse protein is missing four of the aa at the amino-terminus and Val245 of the human sequence; the aa identity between the mouse and the human protein is 72.5%, and similarity is 94.8% (68). Site-directed mutational analysis of human 17 β -HSD 3 demonstrated that arginine at position 80 was critical for binding of the cofactor NADPH (80).

STEROID 5 α -REDUCTASE

Reaction Catalyzed

Steroid 5 α -reductase (3-oxo-5 α -steroid reductase) catalyzes the irreversible conversion of a 3-keto Δ^4 - Δ^5 structure to the corresponding 5 α -reduced metabolite, e.g., testosterone to 5 α -dihydrotestosterone (Fig. 1) or progesterone to 5 α -dihydroprogesterone. NADPH is the donor of the electrons. Conversion of testosterone to dihydrotestosterone is predominant in androgen target tissues, although, it is also present in the testis. In several species, including rat (81,82) and mouse (83,84), there is a peak of 5 α -reductase activity in Leydig cells during pubertal development. The major androgen produced in mouse Leydig cells during pubertal development is 5 α -androstane diol reaching a maximal production between 25 and 30 d postnatal (83).

Molecular Structure

Two isoforms of steroid 5 α -reductase, each a product of a distinct gene, have been identified in human

(85), rat (85), and mouse (86). Both the human, and most likely the mouse and rat genes, contain five exons with the positions of the introns being essentially identical in the two isoforms (85). The two genes, human *SDR5A1* and *SDR5A2*, are located on distinct chromosomes. *SDR5A1* maps to the distal arm of chromosome 5p15 (87), whereas *SDR5A2* is located on chromosome 2p23 (88), the mouse *Sdr5a1* maps to chromosome 13 39.0 cM and mouse *Sdr5a2* to 17E2.

The steroid 5 α -reductases are hydrophobic intrinsic membrane-bound proteins: the human 5 α isozyme type-1 consists of 259 aa whereas the type-2 consists of 254 aa with a molecular mass of 29.5 kDa and 28.4 kDa, respectively (Table 1C; 89). The respective mouse 5 α -reductases 1 and 2 consist of 217 and 254 aa, and a molecular mass of 24.9 kDa and 28.6 kDa, respectively (Table 1C; ref. 90). The enzymes show aberrant electrophoretic mobilities in sodium dodecyl sulfate polyacrylamide gels. The human isozymes migrate with molecular weights of 21–27 kDa instead of the predicted 28 and 29 kDa (85).

REGULATION OF EXPRESSION OF STEROIDOGENIC ENZYMES IN LEYDIG CELLS

P450 Enzymes

A major nuclear factor that is essential for cell-specific expression for P450 steroidogenic enzymes was identified by two laboratories in 1992. This nuclear DNA-binding protein, referred to as SF-1 by Lala et al. (91) or Ad4BP by Morohashi et al. (92) belongs to the orphan nuclear receptor family and binds to variants of an AGGTCA sequence motif found in the proximal promoter of all P450 steroidogenic enzymes (93,94). Although SF-1 is essential for cell-specific gonadal expression, other factors are necessary for determining maximal as well as cell-specific expression of these enzymes.

Chronic stimulation of Leydig cells by the pituitary hormone LH is required for the maintenance of optimal expression of the enzymes. LH, acting via G protein-coupled receptors, activates adenylate cyclase thereby, increasing cAMP, which in turn, leads to increased synthesis of P450 steroidogenic enzymes. The regulation of LH stimulation via cAMP is not mediated by the cAMP response element (CRE/CRE-binding protein [CREB]) system with the exception of *CYP19A1*. It has been reported that cAMP acts via CRE/CREB in the rat *Cyp19a1* promoter expressed in rat granulosa cells and in R2C Leydig cells (95) and in the PII human *CYP19A1* promoter expressed in human granulosa cells

(96). cAMP-responsive sequences found in the promoters of *CYP11A1* and *CYP17A1* differ among these *CYP* genes and among the same genes of different species (45,97). Although, hormone-stimulated increases in cAMP enhance the expression of all of steroidogenic P450 enzymes, additional factors are involved in maintaining maximal expression. Recent studies have provided evidence for a role of GATA-4 and GATA-6 as phosphorylated intermediates in cAMP-stimulated expression of P450_{scc}, P450c17, P450_{arom}, and 3 β -HSD (98–100).

In vitro studies using isolated Leydig cells in culture have contributed to our understanding of the regulation of steroidogenic enzymes. Early studies reported that treatment of immature porcine Leydig cells in culture with hCG increased the *de novo* synthesis of P450_{scc} and adrenodoxin (101). Similar studies using rat Leydig cells in culture demonstrated that treatment with hCG or cAMP increased the synthesis of P450_{scc} and adrenodoxin (102).

Studies by this author and colleagues using primary culture of mouse Leydig cells demonstrated that LH or cAMP are essential for the expression of P450c17 enzyme activity (103,104), *de novo* synthesis of P450c17 protein (105,106), and the expression of P450c17 mRNA (107). The synthesis of P450c17 ceases in the absence of cAMP (105). In a subsequent study, Youngblood and Payne identified the cAMP-responsive region between -346 and -245 bp upstream of the start site of transcription of the *Cyp17a1* promoter (45). The essential role of cAMP for the expression of P450c17 in other species has been reviewed by Waterman and Keeney (108). In contrast to the absolute requirement for cAMP for the expression of P450c17 in mouse Leydig cells, expression of P450_{scc} and 3 β -HSD are not dependent on cAMP (105). Although LH, hCG, or cAMP may not be critical for expression of P450_{scc} in Leydig cells in culture, treatment of mouse MA-10 Leydig tumor cells with cAMP (106,109) or forskolin (110) increases the amount of P450_{scc} protein and mRNA.

In the studies on the requirement of cAMP for the expression of P450c17, evidence was obtained that testosterone produced during LH or cAMP stimulation repressed cAMP induction of P450c17 activity (104), *de novo* synthesis (106), and the amount of mRNA (107). This negative effect of testosterone could be mimicked by the androgen agonist mibolerone (107) and prevented by the androgen antagonist hydroxyflutamide (106) indicating that androgen-mediated repression of P450c17 expression was mediated by the androgen receptor. A subsequent study demonstrated that androgen-mediated repression involved the binding

of the androgen receptor to sequences within the cAMP-responsive region of the *Cyp17a1* promoter (111).

Glucocorticoids have been implicated in the regulation of testicular steroidogenesis. Increased production of glucocorticoids in pathological conditions of the adrenal cortex, such as Cushing's syndrome, can be associated with decreased circulating testosterone and reproductive dysfunction (112). Studies by Hales and Payne (109) and Payne and Sha (107) demonstrated that the glucocorticoids, cortisol, corticosterone, or the synthetic glucocorticoid, dexamethasone, repress both basal and cAMP-induced synthesis of P450_{scc} protein and mRNA. The glucocorticoid-mediated decrease in P450_{scc} synthesis was prevented by the antiglucocorticoid, RU486, suggesting that glucocorticoid repression of P450 synthesis is mediated by the glucocorticoid receptor found in Leydig cells (113).

For regulation of P450c19 in Leydig cells, see Chapter 19.

HYDROXYSTEROID DEHYDROGENASES

3 β -HSD

Gonadal expression of human 3 β -HSD II and mouse 3 β -HSD I is dependent on SF-1 as described for the gonadal-specific expression of the P450 steroidogenic enzymes (114,115). A study on the mouse *Hsd3b1* promoter identified three potential SF-1 consensus binding sites in the proximal promoter of the gene (75). In a subsequent study, it was shown that SF-1, also, was required for the expression of mouse 3 β -HSD I protein (76).

Studies involving the regulation of 3 β -HSD mRNA in mouse Leydig cells in culture, demonstrated high constitutive expression of 3 β -HSD (107). In a subsequent study, it was found that mouse Leydig cells express two distinct isoforms of 3 β -HSD, 3 β -HSD I, and VI (65). Investigations using gonadotropin-deficient mice to study the role of LH/hCG in regulating the expression of 3 β -HSD I and VI mRNA in the adult Leydig cell lineage revealed that the expression of 3 β -HSD I is independent of LH stimulation (116). In contrast, the expression of 3 β -HSD VI mRNA is highly dependent on LH/hCG stimulation. GATA factors appear to be important in the expression of human 3 β -HSD II in steroidogenic cells (100). In a recent study, Martin et al. identified a proximal element in the *HSD3B2* promoter that interacts with GATA 4 and 6 which physically interact with SF-1 or LHR-1 to determine cell-specific and maximal expression of *HSD3B2* in Leydig cells (117). In addition, Martin and Tremblay (118) identified a response element located at -130 bp specific for another orphan nuclear receptor, Nur 77, which was found to be important for both basal- and

hormone-induced human *HSD3B2* promoter activity Nur 77 expression is induced in vivo by LH/hCG in the testis and appears to be an important mediator in the action of LH on steroidogenesis (119).

17βHSD. Studies on the regulation of 17βHSD 3 are limited. Baker et al. (120) examined the expression of 17β-HSD 3 mRNA during development in normal mice, and mice lacking circulating gonadotropins (*hpg*), or functional androgen receptors (*Tmf*). The results showed that during neonatal development expression of 17β-HSD 3 mRNA is independent of gonadotropin action, but becomes dependent on androgen action at the time of puberty (120).

5α-Steroid Reductase

During puberty in rat (82) and mouse (83,84) Leydig cells, 5α-steroid reductase is highly expressed resulting in 5α-androstanediol being the major androgen produced. Hypophysectomy of 21-d-old rats elicited a marked decrease in 5α-reductase activity (121). Treatment of the rats with LH, initiated 6 d posthypophysectomy, resulted in a sharp increase in 5α-reductase activity. Treatment with FSH did not increase or prevent the decrease in 5α-reductase activity following hypophysectomy. Similarly, LH, but not FSH, increased 5α-reductase activity in *hpg* mice (122,123).

Additional studies provided evidence that prolactin (PRL) is involved in the maintenance of high 5α-reductase activity in testes of immature mice (124,125). PRL treatment of mice had no effect on 5α-reductase activity, but enhanced the LH-induced increase in activity (125). Muroso and Washburn tested several hormones in 25-d-old rat Leydig cells in culture and found only hCG increased 5α-reductase activity (126). Additional studies by Muroso et al. showed that the acidic fibroblast growth factor, as well as the platelet-derived growth factor repressed basal and hCG-stimulated 5α-reductase activity in cultured immature rat Leydig cells (127). Basic fibroblast growth factor repressed hCG-stimulated 5α-reductase activity, but had no effect on basal activity (128). In a subsequent study, Viger and Robaire examined the type and developmental expression of 5α-reductase mRNA and protein in the testis of rat (129). At all ages examined, they identified type-1 5α-reductase in Leydig cells. Type-1 5α-reductase mRNA was found to be the most abundant in the immature rat between 21 and 28 d of age. Immunohistochemical staining with a specific antiserum to the type-1 enzyme localized the type-1 protein in the cytoplasm of Leydig cells with the highest expression between 21 and 28 d, followed by a progressive decrease closely paralleling the enzyme activity reported earlier by other investigators.

CLINICAL FEATURES OF MUTATIONS IN STEROIDOGENIC ENZYMES

P450 Enzymes

CYP11A1. Mutations, homozygous in the *CYP11A1* gene in human, are lethal (130). Such mutations result in the inability of the placenta to produce progesterone, which is essential for maintenance of pregnancy beginning at 6–7 wk gestation when production of progesterone by the corpus luteum wanes.

CYP17A1. Numerous reports have been published describing patients with mutations in the *CYP17A1* gene. Mutations have been identified that cause either complete, partial, or isolated 17,20 lyase activity (131–137). The patients exhibit a range of phenotypes depending on the mutation. Both male and female patients are hypertensive because of the overproduction of mineralocorticoids as well as impaired production of cortisol. Affected females exhibit abnormal sexual development resulting in primary amenorrhea. Male patients are phenotypic females due to the deficiency of testosterone production.

CYP19A1. To date five male patients with mutations in *CYP19A1* have been reported (138–143). Defects observed in these patients are not because of the absence of aromatase activity in Leydig cells but, the absence of conversion of testosterone to estradiol in peripheral tissues. Male patients developed very high stature in their late twenties owing to the failure of epiphyseal fusion. Furthermore, they exhibited severely delayed bone age resulting in osteopenia and undermineralization. In addition, these patients experienced marked metabolic defects in carbohydrate and lipid metabolism.

HYDROXYSTEROID DEHYDROGENASES

HSD3B. Homozygous mutations in *HSD3B1* are lethal in human because the 3β-HSD I protein is required for progesterone synthesis in the placenta as described above for *CYP11A*. Many mutations in the *HSD3B2* gene have been identified and are summarized in a review by Simard et al. (72). The major defect observed in males with mutations in the *HSD3B2* gene is either perineal hypospadias or perineoscrotal hypospadias and ambiguous external male genitalia or micropallus. These features in the male are because of decreased biosynthesis of testosterone that is required for normal development of external male genitalia (72).

HSD17B3. Autosomal-recessive mutations in *HSD17B3* have been identified and characterized in numerous male patients (144). The product of the *HSD17B3* gene is essential for Leydig cell biosynthesis

of testosterone during fetal development. Mutations result in phenotypic males with female external genitalia. These males have abdominal testes, epididymides, vas deferentia, seminal vesicles, and ejaculatory ducts. Plasma testosterone concentrations rise at the time of puberty resulting in many of these individuals undergoing marked virilization. The explanation for this phenomenon is most likely result of the peripheral conversion of circulating androstenedione by one of the other 17 β -HSD isoforms (145).

5 α -Reductases

In males, SDR5A2 is expressed in external genitalia. Thus, mutations in *SDR5A2* result in various degrees of male pseudohermaphroditism with undermasculinized external genitalia (see Chapter 12).

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