

Minireview: Regulation of Steroidogenesis by Electron Transfer

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Cytochrome P450 enzymes catalyze the degradation of drugs and xenobiotics, but also catalyze a wide variety of biosynthetic processes, including most steps in steroidogenesis. The catalytic rate of a P450 enzyme is determined in large part by the rate of electron transfer from its redox partners. Type I P450 enzymes, found in mitochondria, receive electrons from reduced nicotinamide adenine dinucleotide (NADPH) via the intermediacy of two proteins—ferredoxin reductase (a flavoprotein) and ferredoxin (an iron/sulfur protein). Type I P450 enzymes include the cholesterol side-chain cleavage enzyme (P450_{scc}), the two isozymes of 11-hydroxylase (P450_{c11β} and P450_{c11AS}), and several vitamin D-metabolizing enzymes. Disorders of these enzymes, but not of the two redox partners, have been described. Type II P450 enzymes, found in the endoplasmic reticulum, receive electrons from NADPH via P450 oxidoreductase (POR), which contains two flavin

moieties. Steroidogenic Type II P450 enzymes include 17 α -hydroxylase/17,20 lyase (P450_{c17}), 21-hydroxylase (P450_{c21}), and aromatase (P450_{aro}). All P450 enzymes catalyze multiple reactions, but P450_{c17} appears to be unique in that the ratio of its activities is regulated at a posttranslational level. Three factors can increase the degree of 17,20 lyase activity relative to the 17 α -hydroxylase activity by increasing electron flow from POR: a high molar ratio of POR to P450_{c17}, serine phosphorylation of P450_{c17}, and the presence of cytochrome b₅, acting as an allosteric factor to promote the interaction of POR with P450_{c17}. POR is required for the activity of all 50 human Type II P450 enzymes, and ablation of the *Por* gene in mice causes embryonic lethality. Nevertheless, mutation of the human *POR* gene is compatible with life, causing multiple steroidogenic defects and a skeletal dysplasia called Antley-Bixler syndrome. (*Endocrinology* 146: 2544–2550, 2005)

DISCUSSIONS OF THE regulation of steroidogenesis generally center on the CRH/ACTH/glucocorticoid and renin/angiotensin/mineralocorticoid systems, which are classical examples of endocrine feedback loops regulated by circulating factors acting at a distance from their sites of synthesis. Recent work has expanded our understanding of steroidogenesis to include intracellular factors that directly influence steroidogenic enzymes. Perhaps the best studied of these is the steroidogenic acute regulatory protein, which regulates the acute steroidogenic responses to ACTH and angiotensin II (1, 2) by acting on the outer mitochondrial membrane (3). Steroidogenic acute regulatory protein increases the delivery of substrate (cholesterol) to the cholesterol side-chain cleavage enzyme, P450_{scc}, but does not act on the enzyme itself. Another level of regulation is at the level of the catalytic efficiency of the steroidogenic enzymes themselves, which is regulated by electron transfer. Regulation of electron transfer to enzymes by complex electron transfer chains is a common cellular strategy for regulating many of biochemical processes, such as oxidative phosphorylation. Such biochemical regulation is also central to steroidogenic processes.

Cytochrome P450

Steroidogenic enzymes fall into two broad categories: the cytochrome P450 enzymes and the hydroxysteroid dehydrogenases, which are addressed in another review (4). This review will focus on the P450 enzymes. Cytochrome P450 refers to a large group of enzymes that have about 500 amino acids and a single heme group and have a characteristic absorption peak at 450 nm in their reduced states. There are two biochemical classes of P450 enzymes. Type I enzymes are found in mitochondria (and bacteria), where they receive electrons from reduced nicotinamide adenine dinucleotide (NADPH) via an electron transfer chain consisting of two proteins: a flavoprotein termed ferredoxin reductase (also called adrenodoxin reductase) and an iron-sulfur protein termed ferredoxin (adrenodoxin). Type II enzymes are found in the endoplasmic reticulum, where they receive electrons from NADPH via a single intermediate, termed P450 oxidoreductase, sometimes assisted by cytochrome b₅ (5). The human genome project has identified 57 P450 genes: seven encode type I enzymes, all of which play key roles in sterol biosynthesis, and 50 encode type II enzymes. Of these 50 type II enzymes, 20 participate in the biosynthesis of steroids, sterols, fatty acids, and eicosanoids; 15 principally metabolize xenobiotic agents and drugs; and 15 are orphan enzymes whose functions and activities remain unclear.

Mitochondrial (Type I) P450 Enzymes

The type I enzymes include six enzymes familiar to endocrinologists. P450_{scc}, the cholesterol side chain cleavage enzyme (formal gene name CYP11A1), is the enzymatic rate-limiting step in steroidogenesis (6, 7). P450_{c11β} (CYP11B1) is the classic steroid 11 β -hydroxylase that converts 11-deoxy-

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Abbreviations: FAD, Flavin adenine dinucleotide; FMN, flavin mononucleotide; NADPH, reduced nicotinamide adenine dinucleotide; OMB₅, outer mitochondrial membrane cytochrome b₅; POR, P450 oxidoreductase.

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cortisol to cortisol and deoxycorticosterone to corticosterone in the adrenal zona fasciculata; its closely related isozyme P450c11AS (CYP11B2) is the aldosterone synthase that catalyzes 11 β hydroxylation, 18 hydroxylation, and 18 methyl oxidation in the adrenal zona glomerulosa, thus converting deoxycorticosterone to aldosterone (8, 9). P450c1 α (CYP27B1) is the hormonally regulated vitamin D 1 α -hydroxylase that activates vitamin D; P450c24 (CYP24) is the vitamin D 24-hydroxylase that initiates inactivation of vitamin D; and P450c27 (CYP27A1) is a hepatic enzyme principally involved in bile acid biosynthesis that is also a minor vitamin D 25-hydroxylase (10–12).

All type I P450 enzymes receive electrons from NADPH via the same electron-transport chain. First, NADPH binds to ferredoxin reductase, a 54-kDa flavoprotein that is loosely associated with the inner mitochondrial membrane and contains a flavin adenine dinucleotide (FAD) moiety (13). The x-ray crystal structure of bovine ferredoxin reductase shows that it is a bilobed protein with an NADPH-binding site in a tightly packed amino-terminal lobe and an FAD-binding domain in the more loosely packed carboxyl-terminal lobe, with the FAD isoalloxazine ring abutting the bound NADPH (14). The cleft containing the FAD is a Rossman fold with numerous basic residues that appear to be important for interacting with acidic residues near the Fe₂S₂ cluster of ferredoxin. Ferredoxin reductase then interacts with and transfers a pair of electrons to ferredoxin, a small (14 kDa) iron/sulfur protein found in the mitochondrial matrix (15) or loosely associated with the inner mitochondrial membrane (16). Ferredoxin accepts electrons by means of an Fe₂S₂ cluster, which resides in an acidic environment containing one Glu and three Asp residues, which are deprotonated, and hence negatively charged (17). This acidic region protrudes from the molecule and interacts with the basic Rossman fold of ferredoxin reductase to accept a pair of electrons and also interacts with the basic, positively charged redox partner binding site of the mitochondrial P450 to donate electrons. Ferredoxin thus forms a 1:1 complex with ferredoxin reductase, then dissociates, and then subsequently forms a 1:1 complex with the P450 (Fig. 1), thus functioning as an indiscriminate electron-shuttle system to all type I P450 enzymes (18–20).

Although the same surface of the ferredoxin molecule that interacts with the ferredoxin reductase must also interact with the P450 (21, 22), catalytically active, highly efficient fusion proteins of these three components have been constructed by placing the ferredoxin moiety on a short tether with rotational freedom (23–27). The increased efficiency of fusion proteins suggests that electron transfer is rate limiting in mitochondrial P450 enzymes. In bovine adrenals, in which P450scc and P450c11 β are found in approximately equimolar quantities, the ratio of ferredoxin reductase to ferredoxin to total mitochondrial P450 is about 1:3:8 (28). To convert cholesterol to pregnenolone, P450scc must catalyze three sequential reactions, 20-hydroxylation, 22-hydroxylation, and scission of the 20–22 carbon bond, each of which requires a pair of electrons. Thus, three distinct ferredoxin molecules must dock with the P450scc, give up their electrons, and then exit, making way for the next charged (reduced) ferredoxin. Thus, the rate-limiting enzymatic step in steroidogenesis re-

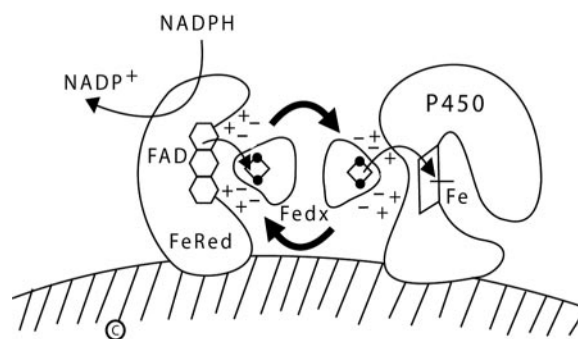


FIG. 1. Diagram of electron transfer by mitochondrial (type I) P450 enzymes. NADPH interacts with ferredoxin reductase (FeRed), which is bound to the inner mitochondrial membrane, and gives up a pair of electrons. The isoalloxazine ring of the FAD moiety of ferredoxin reductase, which lies in a Rossman fold, receives the electrons and in turn passes them to ferredoxin (Fedx). Basic, positively charged residues in ferredoxin reductase, and acidic, negatively charged residues in ferredoxin coordinate the protein interaction, permitting the electrons to be received by the Fe₂S₂ center of ferredoxin, depicted by a ball-and-stick diagram. Ferredoxin then dissociates from ferredoxin reductase and diffuses through the mitochondrial matrix. The same surface of ferredoxin that received the electrons from ferredoxin reductase then interacts with the redox partner binding site of a type I P450, with electrostatic interactions again coordinating the protein-protein interaction. The electrons from the Fe₂S₂ center of ferredoxin then travel through an ill-described protein conduit in the P450 to reach the heme ring of the P450. The heme iron then mediates catalysis with substrate bound in the P450.

lates to the movement of ferredoxin molecules rather than to actual catalysis by P450scc. As a result of this, the turnover number for P450scc is only about six molecules of cholesterol converted to pregnenolone per molecule of P450scc per minute (29).

There is only a single gene for ferredoxin reductase (30, 31) located on chromosome 17q24-q25 (32), which is ubiquitously expressed in all tissues, but is most abundantly expressed in steroidogenic tissues (33). It is alternatively spliced into two forms differing by the presence of six residues (30, 31), but these disrupt the FAD binding site so that the longer form is inactive (34). The single functional gene for ferredoxin (35) is located on chromosome 11q22 (32), although there are also several pseudogenes on chromosome 20 (36). The single functional gene encodes several alternatively spliced mRNAs that are widely expressed and differ in their 3' untranslated regions, possibly resulting in different mRNA half-lives (37).

These proteins are not major sites of hormonal regulation. Adrenodoxin mRNA increases sluggishly in response to treatment of steroidogenic cells with cAMP (37, 38), and adrenodoxin reductase mRNA is posttranscriptionally diminished by cAMP, but its transcription does not appear to be regulated by cAMP (33). Similarly, the consequences of mutations in these genes can only be inferred: no mouse knockouts or human disease-causing mutations have been reported. The lack of human disease suggests embryonic lethality. The production of progesterone by placental P450scc is required to suppress maternal uterine contractility, permitting the maintenance of pregnancy, implying that a genetic lesion in any factor required for its synthesis (P450scc, ferredoxin, ferredoxin reductase) will cause spon-

taneous abortion (39). However, three cases of partial or complete absence of P450_{scc} activity have now been described (40–42), suggesting that similar mutations of ferredoxin and ferredoxin might be compatible with life. Mutations in these genes have been sought but not found in at least two cases (43, 44).

Microsomal (Type II) P450 Enzymes

The type II enzymes include hepatic P450 enzymes involved in drug metabolism; several enzymes in the biosynthetic pathways leading to cholesterol, bile acids, and prostaglandins; and three steroidogenic enzymes familiar to endocrinologists. P450_{c17} (CYP17) catalyzes steroid 17 α -hydroxylase and 17,20 lyase activities (45–50) and hence is essential for the synthesis of glucocorticoids (17 α -hydroxylase activity) and sex steroids (17,20 lyase activity). P450_{c21} (CYP21A2) is the single enzyme catalyzing the 21-hydroxylation of both glucocorticoids and mineralocorticoids and is the enzyme that is disordered in the common form of congenital adrenal hyperplasia (51–53). P450_{aro} (CYP19) is the aromatase that converts androgens to estrogens: androstenedione to estrone, testosterone to estradiol, and 16 α -hydroxytestosterone to estriol (54, 55).

P450 oxidoreductase

All type II P450 enzymes receive electrons from NADPH through the intermediacy of P450 oxidoreductase (POR), sometimes with the assistance of cytochrome *b*₅. POR is an 82-kDa, membrane-associated protein first isolated in 1969 (56); the cDNA was cloned in 1989 (57), but the gene was not characterized and sequenced until the human genome project showed it consists of 15 exons spanning 32 kb on chromosome 7q11.2 (GenBank sequences GI: 4508114, GI: 11181841, and GI: 24307876). Like ferredoxin reductase, POR contains a molecule of FAD that accepts a pair of electrons from NADPH, but unlike ferredoxin reductase, POR also contains a molecule of flavin mononucleotide (FMN), which can accept the electrons from the FAD moiety and donate them one at a time directly to the P450 enzyme so that POR is a self-contained electron transfer system that does not need another protein such as the ferredoxin used by type I P450 enzymes. The first electron is always transferred more rapidly than the second (58); in some type II P450 systems, cytochrome *b*₅ can substitute for POR and donate the second but not the first electron, but the presence of POR is mandatory (59, 60).

The structure and function of POR are well understood, in large measure from the x-ray crystal structure of a soluble, amino-terminally deleted form of rat POR (61). The FAD and FMN moieties are contained in distinct domains separated by a flexible hinge region. It appears that binding of NADPH and receipt of electrons by the FAD moiety elicits flexion of the hinge, aligning the isoalloxazine rings of the FAD and FMN moieties so that electrons can pass from FAD to FMN. On doing so, the hinge flexes once more, permitting the FMN domain to become associated with the redox partner binding site of the cytochrome P450 (Fig 2). The surface charge of the FMN domain of POR is negative, produced by acidic residues (61–63), whereas the redox partner binding sites of

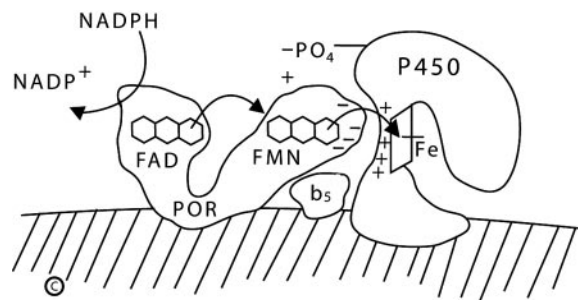


FIG. 2. Diagram of electron transfer by microsomal (type II) P450 enzymes. NADPH interacts with POR, bound to the endoplasmic reticulum, and gives up a pair of electrons, which are received by the FAD moiety. Electron receipt elicits a conformational change, permitting the isoalloxazine rings of the FAD and FMN moieties to come close together so that the electrons pass from the FAD to the FMN. After another conformational change that returns the protein to its original orientation, the FMN domain of POR interacts with the redox partner binding site of the P450. Electrons from the FMN domain of POR reach the heme group to achieve catalysis, as described for type I P450 enzymes. The interaction of POR and the P450 is coordinated by negatively charged acidic residues on the surface of the FMN domain of POR and positively charged basic residues in the redox partner binding site of the P450. In the case of human P450_{c17}, this interaction was facilitated by the allosteric action of cytochrome *b*₅ and the serine phosphorylation of P450_{c17}.

microsomal P450 enzymes have a positive surface charge produced by basic (Lys and Arg) residues (64–69). The redox partner binding site of the P450 is on the opposite side of the plane of the P450 heme group from the substrate-binding site; hence, electrons from the FMN moiety of the POR must travel about 18 Å to reach the heme iron of the P450 (70). It appears likely that there are multiple pathways for this electron flow in various P450 enzymes.

The availability of electrons from POR is limiting in most microsomal P450 reactions. In both the liver and steroidogenic tissues, the microsomal P450 component is found in a great molar excess to POR (71), possibly as high as 20:1; this has a profound influence on steroidogenesis. P450_{c17} catalyzes both the 17 α -hydroxylation required to produce 17-hydroxy 21-carbon precursors to cortisol (17-hydroxyprenolone and 17-hydroxyprogesterone) and the 17,20 lyase activity needed to produce 19-carbon precursors of sex steroids. In posing the question of why most adrenal steroidogenesis stops at C21 steroids, Yanagibashi and Hall (72) found that the ratio of POR to P450_{c17} was 3- to 4-fold higher in testicular microsomes than adrenal microsomes, and that addition of exogenous POR increased the 17,20 lyase reaction far more than the 17 α -hydroxylase reaction, although the hydroxylase to lyase ratio never fell below 2.0. This key finding has been confirmed for human P450_{c17} (73) and forms the basis for the view that the onset of adrenal androgen synthesis (adrenarche) is regulated by events that govern electron flow from POR to P450_{c17} (74, 75).

Cytochrome *b*₅

Because a single POR molecule interacts with the redox partner binding sites of five distinct microsomal P450 enzymes, it seems logical to infer that different P450 enzymes will have different affinities for POR. In this situation it is easy to conceptualize how another factor, in this case cyto-

chrome b_5 can act allosterically to optimize the positioning of the POR and P450 with respect to one another and thus foster catalysis indirectly. Similarly, one would predict that the allosteric effect would be greater for some P450 enzymes than for others, depending on the surface geometry and charge distribution in the redox partner binding site of the P450. Modeling and mutagenesis studies with hepatic P450 2B4 indicate that cytochrome b_5 and POR interact with overlapping portions of the negatively charged redox partner binding site of the P450 (76). By optimizing the interaction of POR and the P450, one would expect to see an increased reaction velocity, but one would not expect to see significant changes in substrate binding or product dissociation because these parameters reflect events on the far side of the plane of the heme group, away from the redox partner binding site. Substantial experimental data support this allosteric mechanism for the action of cytochrome b_5 with selected hepatic drug-metabolizing P450 enzymes (77–79).

Recent work has highlighted the central role of cytochrome b_5 and other factors regulating electron flux from POR to P450c17 in the intracellular regulation of human androgen synthesis. Early studies suggested that cytochrome b_5 increased the 17,20 lyase activity of P450c17, but it was thought that its mechanism of action was to function as an alternative donor for the second electron in the P450 catalytic cycle (80, 81), as can happen with some hepatic P450 enzymes (59, 60). However, work with a humanized yeast system that expresses human P450c17 and human (rather than yeast), POR has now established that cytochrome b_5 exerts no action on the 17 α -hydroxylase reaction of human P450c17. Instead, cytochrome b_5 profoundly stimulates the 17,20 lyase reaction through an allosteric mechanism, rather than as an electron donor (82, 83). Thus, cytochrome b_5 promotes the association of P450c17 with POR to increase the efficiency of electron donation from POR.

There are two human genes for cytochrome b_5 . The gene on chromosome 18q23 has six exons that undergo alternative splicing: exons 1, 2, 3, and 4 encode the 98AA soluble form of cytochrome b_5 found principally in erythropoietic tissues, whereas exons 1, 2, 3, 5, and 6 encode the widely expressed 134AA form bound to the endoplasmic reticulum (84, 85). A second gene on chromosome 16q22.1 consists of five exons that encode OMB $_5$, a 146AA form of cytochrome b_5 that is bound to the mitochondrial outer membrane (86). Because some domains of OMB $_5$ share 70% amino acid sequence identity with microsomal cytochrome b_5 , it is likely that antisera raised against one will cross-react with the other. Rat OMB $_5$ can facilitate 17,20 lyase activity *in vitro* but exerts an even greater effect on 17 α -hydroxylase activity (87). Because the principal form of cytochrome b_5 found in the adrenal is the 134AA microsomal form (88) and because cytochrome b_5 has no apparent effect on human 17 α -hydroxylase activity, it appears that the 134AA microsomal form is largely responsible for the observed effects on 17,20 lyase activity.

Whereas most information about the activity and presumed role of cytochrome b_5 in human androgen synthesis derives from biochemical studies *in vitro*, physiologic support for this role is beginning to emerge. Immunocytochemical analysis of human (89–91) and rhesus monkey (92, 93) adrenals show that cytochrome b_5 is overwhelmingly more

abundant in the zona reticularis than in the other zones and that its degree of expression increases in parallel with the increased secretion of 19-carbon steroids during adrenarche, *i.e.* in parallel with increased 17,20 lyase activity. A proposed role for cytochrome b_5 in the 17,20 lyase activity of P450c17 would suggest that mutations in the gene for cytochrome b_5 might present clinically as isolated 17,20 lyase deficiency. Only a single case of cytochrome b_5 deficiency has been reported (94), having a splice-site mutation between exons 1 and 2 (95). Because a major physiologic role of cytochrome b_5 is in the reduction of methemoglobin, the principal clinical manifestation in this patient was methemoglobinemia, which is most commonly caused by disordered cytochrome b_5 reductase. Unlike individuals with cytochrome b_5 reductase disorders, the patient with mutant cytochrome b_5 also had ambiguous genitalia in a 46,XY male, but unfortunately, androgen synthesis was not assessed in this patient. Hence, it is possible that cytochrome b_5 deficiency will disrupt androgen synthesis, but this is not established.

Phosphorylation of P450c17

In addition to high molar ratios of POR to P450c17 and the allosteric action of cytochrome b_5 , a third mechanism that increases 17,20 lyase activity is the serine/threonine phosphorylation of P450c17 (96). Very few P450 enzymes undergo posttranslational modification. P450aro (aromatase) can be glycosylated, but this does not appear to affect its catalytic ability (97). To date, P450c17 is one of the few cytochrome P450 enzymes that is known to undergo phosphorylation and the only case in which a posttranslational modification has been shown to exert a major influence on catalysis. Serine/threonine phosphorylation of P450c17 confers 17,20 lyase activity on the enzyme, and dephosphorylation by treating human adrenal microsomes with alkaline phosphatase ablates 17,20 lyase activity without affecting 17 α -hydroxylase activity (96). The responsible kinase appears to be responsive to cAMP but remains unidentified. A kinase-enriched cytoplasmic fraction of human adrenal NCI-H295A cells can phosphorylate dephospho-P450c17 expressed in eukaryotic cells or in bacteria and can confer 17,20 lyase activity to the P450c17 (98). Treatment with inhibitors of various protein phosphatases, RNA interference studies, and protein transfection studies indicate that the phosphorylation of P450c17 is counterbalanced by protein phosphatase 2A, which, in turn, is negatively regulated by phosphoprotein SET (98). Because serine phosphorylation of the β -chain of the insulin receptor will produce insulin resistance (99, 100), it appears likely that serine phosphorylation is the mechanistic link between the insulin resistance and hyperandrogenism that characterize some forms of the polycystic ovary syndrome (75, 96, 101). Serine phosphorylation of P450c17 apparently increases 17,20 lyase activity by increasing the association of P450c17 with POR and increasing the efficiency of electron transfer. Strong evidence for this model comes from the recent observation that serine phosphorylation of P450c17 and addition of cytochrome b_5 can each saturate the 17,20 lyase activity of P450c17, *i.e.* the effects are neither additive nor cooperative (88). Thus, three mechanisms, the abundance of POR,

the presence of cytochrome b_5 , and the serine phosphorylation of P450c17, all regulate 17,20 lyase activity, and hence androgen production, by modulating the flow of electrons from NADPH to P450c17.

P450 oxidoreductase deficiency

Because POR is required for the activity of all 50 human type II (microsomal) P450 enzymes, one might presume that ablation of POR would have dire consequences. In fact, mice lacking only the membrane-anchoring amino-terminal domain of POR (but retaining residues 107–677, which can reduce cytochrome *c in vitro*) die by embryonic d 13.5 (102), and mice lacking the entire POR gene suffer embryonic lethality by d 9.5 (103). This lethality is apparently a consequence of disordered extrahepatic P450 enzymes because liver-specific POR knockout mice have normal development and normal reproductive capacity, despite severely impaired drug metabolism (104). Thus, it was most surprising when Flück *et al.* (105) reported POR missense mutations in both a phenotypically normal adult woman with primary amenorrhea and three children with disordered steroidogenesis and a severe skeletal malformation disorder called Antley-Bixler syndrome. These patients have steroidal findings suggesting partial combined deficiencies of 17 α -hydroxylase and 21-hydroxylase and occasionally evidence of fetoplacental aromatase deficiency as well (106). Several other groups have also reported similar cases (107–109).

Although this steroidal profile was first reported in 1985 (110) and it was suggested that the disorder might be in POR (111, 112), POR was not investigated until the human genome project made the gene sequence available. All patients studied to date have had a missense (amino acid replacement) mutation on at least one allele; hence, it is not clear whether total ablation of POR is compatible with human life. With the completion of a large international series, a total of 21 POR missense mutations have been identified, providing excellent scanning mutagenesis of POR and the opportunity to correlate clinical, biochemical, and genetic findings (113). All affected individuals have disordered 17,20 lyase activity; the defects in 17 α -hydroxylase, 21-hydroxylase, and aromatase activities are more variable. This is consistent with the observations that the 17,20 lyase activity of P450c17 is sensitive to mutations in its redox partner binding site that do not affect 17 α -hydroxylase activity and the observations that the 17,20 lyase activity of P450c17 requires the assistance of either serine phosphorylation or the allosteric action of cytochrome b_5 . Not surprisingly, the biochemical assay of POR activity that most closely correlates with the clinical findings is the degree to which a mutant form of POR is able to support the 17,20 lyase activity of P450c17 *in vitro*, in the presence of saturating amounts of cytochrome b_5 (105, 106, 113). The potential effects of such POR mutations or POR polymorphisms on drug metabolism by hepatic P450 enzymes has not yet been investigated but may become an important area of pharmacogenomics.

Conclusion

Whereas endocrinology has traditionally emphasized regulation by circulating hormonal factors, regulation by intra-

cellular factors has assumed equal importance. Many biochemical pathways including steroidogenic pathways are delicately regulated by electron-donation and redox state. The elucidation of the structures of these redox partner proteins, their biochemical activities, and their genetic deficiency states are opening a major new area of endocrine investigation.

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