

Involvement of Cytochromes P450 in Development

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Cytochrome P450 is generally thought of as a superfamily of oxidative enzymes that functions in xenobiotic metabolism. The fact is, however, that the many forms of cytochrome P450 are found in almost every phylum and have roles in homeostasis, synthesizing biochemicals used in normal functioning, and in signaling in and between cells and tissues. In this review we point out other functions of cytochrome P450 forms, that of participating in the organization and shaping of the developing organism. Examples are provided in a number of phyla, from fungi to mammals, of cytochrome P450 forms functioning in morphogenesis in the developing organism. A recent, related review focusing on the involvement of cytochrome P450 in plant homeostasis and development has been published (Kim and Tsukaya 2002)

Key Words: Development, Cytochrome 450, Morphogenesis, Embryo/foetus

Introduction

We are constantly under challenge by chemicals in the environment, lipophilic compounds that enter the body via the airways, skin, and alimentary canal, the latter in the food as plant products or contaminating agricultural chemicals used as growth enhancers or pesticides. Chemicals with a high oil/water partition coefficient are poorly excreted, and living organisms have evolved enzyme systems that facilitate renal excretion of such compounds by making them more polar (Schenkman 1999). One such enzyme system involves the cytochrome P450 mono-oxygenase superfamily. The indication that members of these families have a major role in the oxidative metabolism of lipophilic xenobiotics, as well as endogenous lipophilic compounds, such as steroid hormones, was an extension of several earlier observations. In the 1950s it was noted that hepatic endoplasmic reticulum fragments, the microsomes, contained enzymes responsible for the oxidation of drugs and chemicals (Brodie, et al. 1958). The identification of cytochrome P450 as a microsomal hemoprotein (Omura and Sato 1962, Omura and Sato 1964) and its function as a terminal oxidase (Cooper, et al. 1965, Estabrook, et al. 1963) responsible for the oxidations sparked several decades of intense investigation into this superfamily of monooxygenases.

Individual species have large numbers of cytochrome P450 forms. Humans, for example, have at the latest listing, 57 different cytochromes P450 (<http://drnelson.utmem.edu/CytochromeP450.html>), contained in 18 families and 33 subfamilies (figure 1). Half of the total number of forms of human cytochrome P450 are found in families 1-3, which are generally thought of as 'xenobiotic metabolizing' enzymes. The enzymes in these three families are responsible for increasing the polarity of exogenous chemicals, taken into the body as drugs or environmental contaminants, as well as endobiotics, chemicals of endogenous origin, such as steroid hormones. Family 1 members are generally considered to be responsible for the metabolism of polycyclic aromatic hydrocarbons and for activation of a large number of procarcinogens (Gonzalez and Gelboin 1994, Shimada, et al. 1996). Members of this family are induced by polycyclic aromatic hydrocarbons and other ligands, like TCDD, of the cytoplasmic aryl hydrocarbon (AH) receptor (Bresnick 1993, Nebert and Jones 1989). Family 2 (figure 1) has the largest number of individual enzyme forms in mammals, and its members are readily, but differentially, induced by a large number of drugs and chemicals, some of which also serve as substrates. For example, members of Subfamily CYP2B are transcriptionally induced by barbiturates, like phenobarbital

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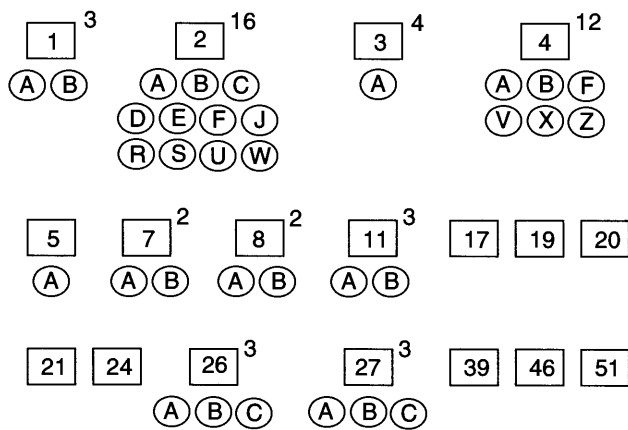


Figure 1. Human cytochrome P450 families and subfamilies. Superscript numbers indicate the number of members in this family.

(Honkakoski & Negishi 1998, Honkakoski et al. 1998), and metabolize a wide variety of drugs, while Subfamily CYP2E members are similarly inducible by a number of small molecules, like ethanol, acetone and pyrazole (Ronis et al. 1991, Song et al. 1987), and metabolize alcohol and a number of nitrosamines. In contrast, CYP2D does not appear to be inducible (Johansson et al. 1993), but metabolizes a number of drugs, including propranolol, codeine and antidepressants. As in rodents, (Funae & Imaoka 1993), human Family 3 members are very active in the oxidative metabolism of steroid hormones, like testosterone, estradiol and progesterone (Guengerich et al. 1993, Waxman et al. 1991). Family 3 has but one subfamily, CYP3A, and members are inducible by steroids, like dexamethasone, (Schuetz et al. 1984) and responsible for steroid 6 β -hydroxylations. Being the predominant form of cytochrome P450 in the liver microsomes, CYP3A forms are major contributors in drug metabolism, oxidizing a large number of different drugs (Guengerich 1994). Interestingly, Family 4 is the second largest family of cytochrome P450 in mammals, but unlike Family 2 forms these enzymes do not appear to be important in the metabolism of xenobiotics. In fact, of the fourteen Family 4 human enzymes, only CYP4B1 and CYP4F12 have been reported to be capable of xenobiotic metabolism (Hashizume et al. 2002, Verschoyle et al. 1993). For those other forms tested, only metabolism of lipids e.g., eicosanoids like arachidonate, prostaglandins and leukotrienes have been reported (Bylund et al. 2000, Hardwick 1991, Kikuta et al. 2000, Masters et al. 1993, Sundseth & Waxman 1992). From the very large number of members of this family, and their minimal impact on xenobiotic metabolism, it is

possible they play a role in inactivation or generation of bioactive lipids and lipid-derived compounds.

Cytochromes P450 involved in 'housekeeping' functions

Most of the other families of cytochrome P450 in mammals have important roles in maintaining homeostasis in the adult animal, producing components of intermediary metabolism involved in signaling and/or maintenance of the various functions of the different tissues, i.e., what we consider as 'housekeeping' functions (table 1). Biochemicals produced by these enzymes are sterols and steroids, like cholesterol and the corticosteroids and sex steroids, and lipid-derived compounds, like the prostacyclins and thromboxanes, as well as the bile acids, and certain vitamins. These families generally have only one or two subfamilies, and rarely more than three members. In contrast to the very broad substrate specificities of the Families 1-3 cytochromes P450, these families have more specific substrate dependence, although some may be able to bind and oxidize a few xenobiotics. Some examples of these specific forms include, CYP51, lanosterol 14 α -demethylase, which catalyzes synthesis of cholesterol from lanosterol; orthologous forms of this cytochrome P450 exist in most eukaryotic species, including the unicellular fungi. CYP11A1 cleaves the side chain of cholesterol preparatory for production of a range of steroids. CYP7A1 hydroxylates cholesterol in the 7 α -position, sending the sterol into a pathway toward bile acid synthesis in which other forms of cytochrome P450, like CYP8B1 (12 α -hydroxylation) participate. CYP27A1 activates Vitamin D3 by 25-hydroxylase activity and will also hydroxylate cholesterol in the 27-methyl group, another step in the formation of bile acids. CYP46 acts to form the oxysterol 24-hydroxycholesterol, and also a substrate for bile acid synthesis (Russell 2000). CYP27B1 is necessary in the 1 α -hydroxylation of 25-hydroxy vitamin D3 to the active 1 α , 25-dihydroxy vitamin D3. CYP26 is involved in the metabolism of the active vitamin A metabolite, all-trans retinoic acid. Other examples of housekeeping functions include formation of the prostacyclins (CYP8A) thromboxanes (CYP5A1) and aldosterone (CYP11B2).

Developmental functions of cytochrome P450

Over the last few years evidence has begun to appear suggestive of a role for cytochrome P450 in development of the organism (Stoilov 2001, Stoilov, et al. 2001). In 1997, a study of primary congenital glaucoma, a disease affecting newborns, linked the disease to mutations in the gene of a form of

Table 1. Cytochrome P450 Housekeeping Genes

CYP	Common name	Substrates	Function
CYP5A1	Thromboxane synthase	PGH ₂	Forms thromboxane A ₂
CYP7A1	Cholesterol 7 α -hydroxylase	Cholesterol	Bile acid synthesis
CYP7B1	Oxysterol 7 α -hydroxylase	25OH-Cholesterol & 27OH-Cholesterol	Neurosteroid synthesis
CYP8A1	Prostacyclin synthase	PGH ₂	Prostaglandin synthesis
CYP8B1	Sterol 12 α -hydroxylase	7 α OH 4-cholesten-3-one	Bile acid synthesis
CYP11A1	P450 _{scc}	Cholesterol	Pregnenolone
CYP11B1	11 β -hydroxylase	Deoxycorticosterone 11-deoxycortisol	Corticosteroid synthesis
CYP11B2	Aldosterone synthase	Corticosterone 18OH-Corticosterone	Corticosteroid synthesis
CYP17	17 α -hydroxylase	Pregnenolone Progesterone 17 α OH-Pregnenolone 17 α OH-Progesterone	Steroid synthesis
CYP19	Aromatase	Androstenedione Testosterone	Estrogen synthesis
CYP20	–	–	–
CYP21	Sterol 21-hydroxylase	Progesterone 17OH-Progesterone	Corticosteroid synthesis
CYP24	1 α ,25-Dihydroxyvitamin D ₃ –24-hydroxylase	1 α ,25-Dihydroxyvitamin D ₃	Vitamin D degradation
CYP26	Retinoic acid hydroxylase	Retinoic acid	Retinoate degradation
CYP27A1	Sterol 27-hydroxylase	Cholesterol Vitamin D ₃	Bile acid synthesis Vitamin D ₃ 25-hydrox.
CYP27B1	25OH-vitamin D ₃ -1- α -hydroxylase	25OH-vitamin D ₃	Vitamin D ₃ activation
CYP39	Oxysterol 7 α -hydroxylase	24OH-Cholesterol	Bile acid synthesis
CYP46	Cholesterol 24-hydroxylase	Cholesterol	Bile acid synthesis
CYP51	Lanosterol 14 α -demethylase	Lanosterol	Cholesterol synthesis

cytochrome P450, CYP1B1 (Stoilov et al. 1998, Stoilov et al. 1997). Confirmation soon followed in reports by other groups (Bejjani et al. 1998, Bejjani et al. 2000, Mashima et al. 2001, Panicker et al. 2002, Plasilova et al. 1998, Plasilova et al. 1999). This gene has orthologous forms in different species of mammals and is the only member of its subfamily. An examination of species in which CYP1B1 has been detected, indicates that Subfamily 1B members are found in mammals, as well as in the earlier evolving bony fishes, such as zebrafish and fugu (<http://drnelson.utmem.edu/CytochromeP450.html>), indicating an early evolutionary appearance. The disease phenotype presents as elevated intraocular pressure and abnormal development of the trabecular meshwork in the eye and also with defects in the Canal of Schlemm (WuDunn 2002). These

studies provide direct evidence that a form of cytochrome P450 is involved in normal eye development in the mammalian organism. An earlier examination of a Cyp1b1-null mouse strain revealed no gross phenotypical defects in the homozygous null animals (Buters et al. 1999). However, more recent histological examination showed anomalies in the trabecular meshwork and Canal of Schlemm in the homozygous Cyp1b1-null mouse (Libby et al. 2003). Studies on Cyp1b1 in the mouse eye revealed an absence of mRNA transcripts around the trabecular meshwork at all in utero stages, but presence in the retinal neuroepithelium at developmental age E15 (Bejjani et al. 2002). The morphogenic pathway and nature of the morphogenic agent affected by CYP1B1 in eye development is, at present, unknown.

Xenobiotic-metabolizing P450 Family Members in the Conceptus

One of the earliest reports of the presence of cytochrome P450 in the conceptus, showed the presence of the hemoprotein in human fetal liver as early as 14 weeks (Yaffe et al. 1970). These investigators also reported the presence of NADPH-cytochrome P450 reductase in this tissue. Early attempts to identify forms of cytochrome P450, which were produced in the embryo, indicated the presence of CYP3A subfamily members. A form of cytochrome P450 not found in the adult liver, CYP3A7, was purified from human fetal liver (Kitada et al. 1985). Attempts to see CYP1A1, and CYP1A2 mRNA in poly(A)-rich RNA extracts of 21-31 day rabbit fetus were negative, while CYP3A6 only appeared just prior to birth (Pineau et al. 1991). In contrast, a number of studies have shown the presence of the Family 1 cytochrome P450 in the conceptus (table 2). Interestingly, *Cyp1a1*- and *Cyp1a2*-null mice showed normal development (Dalton et al. 2000, Liang et al. 1996). Transcripts for *Cyp51* have been found in the pre-implantation developing mouse blastocyst, but transcripts for other 'housekeeping' forms of cytochrome P450, those involved in steroid metabolism, *Cyp17*, *Cyp11a1*, *Cyp19* and *Cyp27*, were not detected at that developmental stage (Stromstedt et al. 1996). To date, a number of forms of cytochrome P450 have been reported to be constitutively present in developing mammals in utero, the majority being identified from mRNA transcripts. These include another member of the CYP1 Family, CYP1B1, as well as a dozen from Family 2, and half that number from Family 3A. Most of the latter have been found in late prenatal developmental stages of the fetus (table 2). The functional role played by the presence of these forms has been suggested to involve xenobiotic metabolism and to be associated with toxicities produced by reactive intermediates (Miller et al. 1996).

Cytochrome P450 is a terminal oxidase that requires for its function the enzyme NADPH-cytochrome P450 reductase. In support of a developmental role for forms of cytochrome P450 in the conceptus, mRNA for NADPH-cytochrome P450 reductase was detected in the 4-day, preimplantation mouse blastocyst (Stromstedt et al. 1996). NADPH-cytochrome P450 reductase was shown to have a specific spatial orientation in the developing mouse embryo (Keeney and Waterman 1999). Further, lethality was associated

with knockout of the NADPH-cytochrome P450 reductase gene (Shen et al. 2002). These studies suggest a role for cytochrome P450 in the development of the embryo. However, the reductase can also participate in lipid metabolism (Schenkman & Jansson 2003), a defect in which might also be lethal to the developing embryo.

In the examination of human 17-23 week embryonic cDNA libraries of different tissues (figure 2), selective and differential expression of CYP1B1 transcripts was observed, suggestive of a role for this enzyme in the human embryo. CYP1B1 transcripts were seen in lung, skeletal muscle, and heart, and levels were especially prominent in spleen (Lane 8), thymus (Lane 9) and kidney (Lane 5). Signals were absent in cDNA libraries of brain and liver. While a number of forms of cytochrome P450 have been reported to be expressed in the human embryo and fetus, to date, only a few of forms of cytochrome P450 have been detected in the mouse conceptus (table 2). However, an examination of mouse embryo cDNA libraries at different stages of development revealed a temporal component to the developmental appearance of a number of different cytochrome P450 forms (Choudhary et al. 2003). This is exemplified by the data shown in (figure 3) for *Cyp1b1*, where the signal for *Cyp1b1* did not appear until post-conception day 11 (E11). In mouse 93 forms of cytochrome P450 have been identified. These are contained in 18 families and 33 subfamilies (figure 4). Recent studies from our laboratory, using gene-specific RT-PCR methodology, indicate the appearance of at least 27 different cytochromes P450 at different stages of embryonic development (Choudhary et al. 2003). Since only 40 gene-specific primers were utilized in that study, it is clear that the number of forms appearing will be considerably higher, when the complete complement of forms is examined.

Forms of Cytochrome P450 Involved in Morphogenesis

The role of a gene product in development is more readily identified when a mutation in the gene results in a mutational phenotype. The effects of cytochrome P450 gene mutations illustrating a role in development in several phyla are indicated below and in (figure 5). A recent essay reviewing concepts on morphogens and pattern formation (Neumann and Cohen 1997) provides criteria for a compound to meet in order to be considered a morphogen: a) the agent must have a direct effect on target cells and b) the influence of the agent must be concentration dependent. A known morphogen,

Table 2. Cytochromes P450 in the Conceptus

CYPs	Species (age)	Reference
CYP1A1	Mouse (E7)	(Kimura et al. 1987)
	Rat (late prenatal)	(Rich and Boobis 1997)
	Rabbit (late prenatal)	(Rich et al. 1993)
	Human (E45-60)	(Omiecinski et al. 1990, Yang et al. 1995)
	Human (11-13 wks)	(Shimada et al. 1996)
CYP1A2	Rat (late prenatal)	(Rich et al. 1993)
	Rabbit (late prenatal)	(Rich and Boobis 1997)
CYP1B1	Mouse (E11-17)	This study
	Human (12-19 wks)	(Hakkola et al. 1997)
	Human (17-23 wks)	(Jansson et al. 2001)
CYP2A6	Human (91-125d)	(Gu et al. 2000)
CYP2A13	Human (91-125d)	(Gu et al. 2000)
CYP2B6	Human (91-125d)	(Gu et al. 2000)
CYP2B15	Rat (?)	(Keeney et al. 1998)
CYP2B19	Mouse (E15.5-postnatal)	(Keeney et al. 1998)
CYP2C8	Human (11-17 wks)	(Hakkola et al. 1994)
CYP2C9	Human (16-40 wks)	(Hines and McCarver 2002)
CYP2C18	Human (16-40 wks)	(Hines and McCarver 2002)
CYP2D6	Human (17-40 wks)	(Treluyer et al. 1991)
	Human (11-17wks)	(Hakkola et al. 1994)
CYP2E1	Human (7-16 wks)	(Brzezinski et al. 1999)
	Human (16-24 wks)	(Carpenter et al. 1996)
CYP2J2	Human (91-125d)	(Gu et al. 2000)
CYP2J5	Mouse (E18)	(Ma et al. 1999)
CYP3A1	Rat (late prenatal)	(Simmons and Kasper 1989)
CYP3A4	Human (9-12 wks)	(Hakkola et al. 2001)
CYP3A5	Human (9-12 wks)	(Hakkola et al. 2001)
CYP3A6	Rabbit (E30)	(Pineau et al. 1991)
CYP3A7	Human (55-81d)	(Kitada 1991 Yang et al. 1994)
CYP3A16	Mouse (E17)	(Itoh et al. 1994)
CYP7B	Mouse (12.5-18.5)	(Bean et al. 2001)
CYP11A	Mouse (13.5-17.5)	(Keeney et al. 1995) ^a
CYP17A	Mouse (E11-15)	(Keeney et al. 1995)
	Rat (E10.5-19.5)	(Compagnone et al. 1995)
CYP19	Equine (E12-15)	(Walters et al. 2000)
CYP21	Mouse (E14-18)	(Raschella et al. 1989)
CYP26A1	Mouse (E6-17)	(Fujii et al. 1997)
	Human (E57-110)	(Trofimova-Griffin et al. 2000)
	Human (20-26wks)	(Trofimova-Griffin and Juchau 1998)
CYP26B1	Mouse (E8-postnatal)	(Abu-Abed et al. 2002, MacLean et al. 2001)
	Human (E57-224)	(Trofimova-Griffin and Juchau 2002)
CYP51	Mouse (E4)	Stromstedt et al. 1996

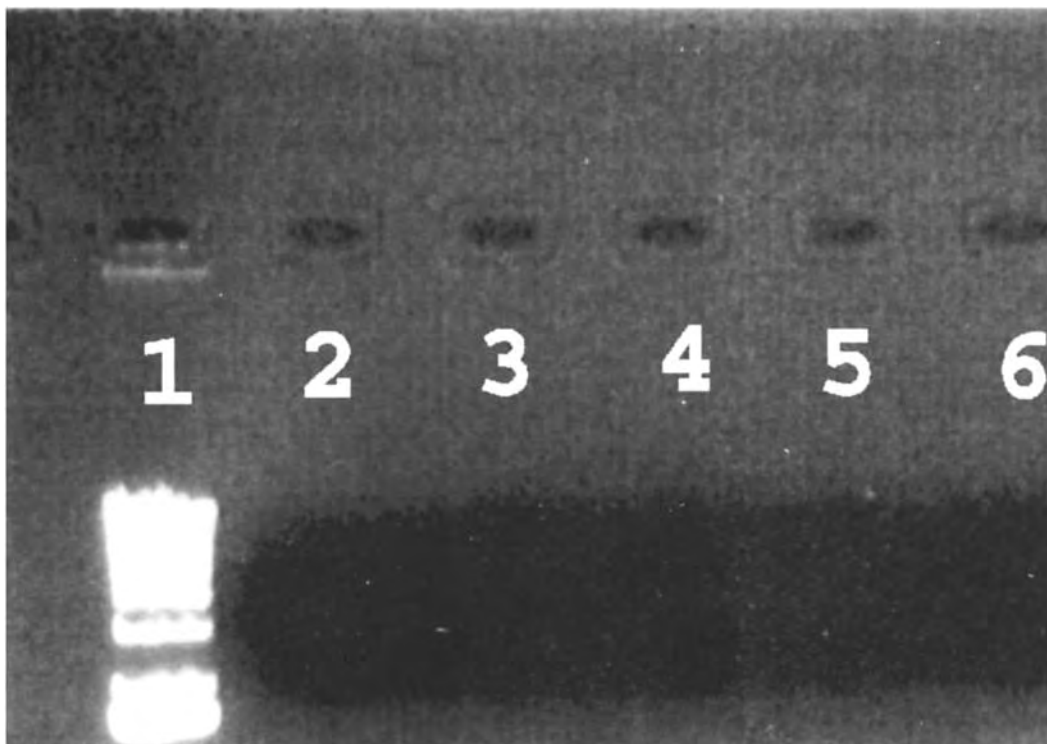


Figure 2. Profile of expression of CYP1B1 transcripts in human fetal tissue cDNA libraries. Lane 2: Fetal Brain. Lane 3: Fetal Lung. Lane 4: Fetal Liver. Lane 5: Fetal Kidney. Lane 6: Fetal Heart. Lane 7: Fetal Skeletal Muscle. Lane 8: Fetal Spleen. Lane 9: Fetal Thymus. Lanes 1 and 10: 1 Kb Plus DNA Ladder (GibcoBRL). PCR of each cDNA library was carried out for 27 cycles of amplification to allow comparison of relative amounts of transcript in the libraries. 10 μ l of each amplification reaction was applied to the 1% agarose gel and after electrophoresis was visualized by fluorescence of ethidium bromide. G3PDH band (1Kb) is seen in lanes 2-9. The number of amplification cycles was optimized in a preliminary experiment to ensure that the PCR reaction had not reached its plateau in order to be able to compare amounts of signal from the different tissues. [after Jansson et al. (2001) *Pharmacogenetics* 11 1-9, with permission from the publishers (Williams & Wilkins)].

retinoic acid (RA), the active metabolite of vitamin A, has been studied for over 60 years. Deficiency of vitamin A results in a wide range of malformations, while excess of RA during pregnancy also leads to developmental defects. Retinoic acid has a role in development in patterning and formation of the anterior-posterior axis [see review (Maden 1999)]. Retinoic acid exerts its effects by serving as a ligand for nuclear retinoic acid receptors (RAR) and retinoate X receptor (RXR). The level of retinoic acid in tissues is regulated by a balance in the rate of synthesis and oxidative degradation by retinoic acid oxidase, Cyp26, which catalyzes removal of the retinoic acid (Fujii et al. 1997, Hollemann et al. 1998, Swindell et al. 1999). In order for RA to exert its effects properly there has to be an uneven distribution of the RA, and this is provided by a differential expression of CYP26. In fact, the presence of RA in regions where Cyp26 would normally prevent its elevation resulted in severe developmental defects in the Cyp26-null mouse,

including caudal truncation, resulting in embryonic and fetal lethality (Sakai et al. 2001). In this case, and unlike the effect of destructive CYP1B1 mutation, the identity of the morphogenic agent and the role of the cytochrome P450 is known. A number of other forms of cytochrome P450 have been shown to

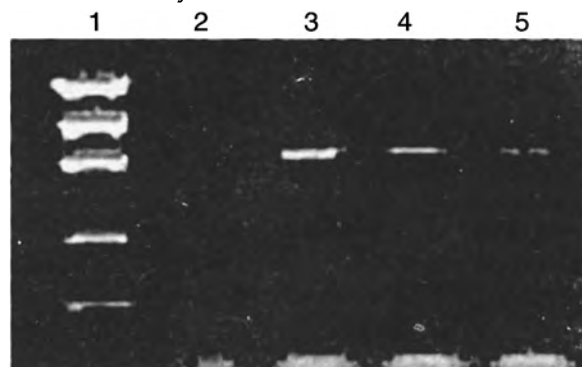


Figure 3. Expression of Cyp1b1 transcripts in mouse fetal tissue cDNA libraries (Clontech) at E7, E11, E15 and E17 (tracks 2-5 respectively). Conditions were as in Figure 2. Track 1 contains a low DNA mass ladder (Invitrogen).

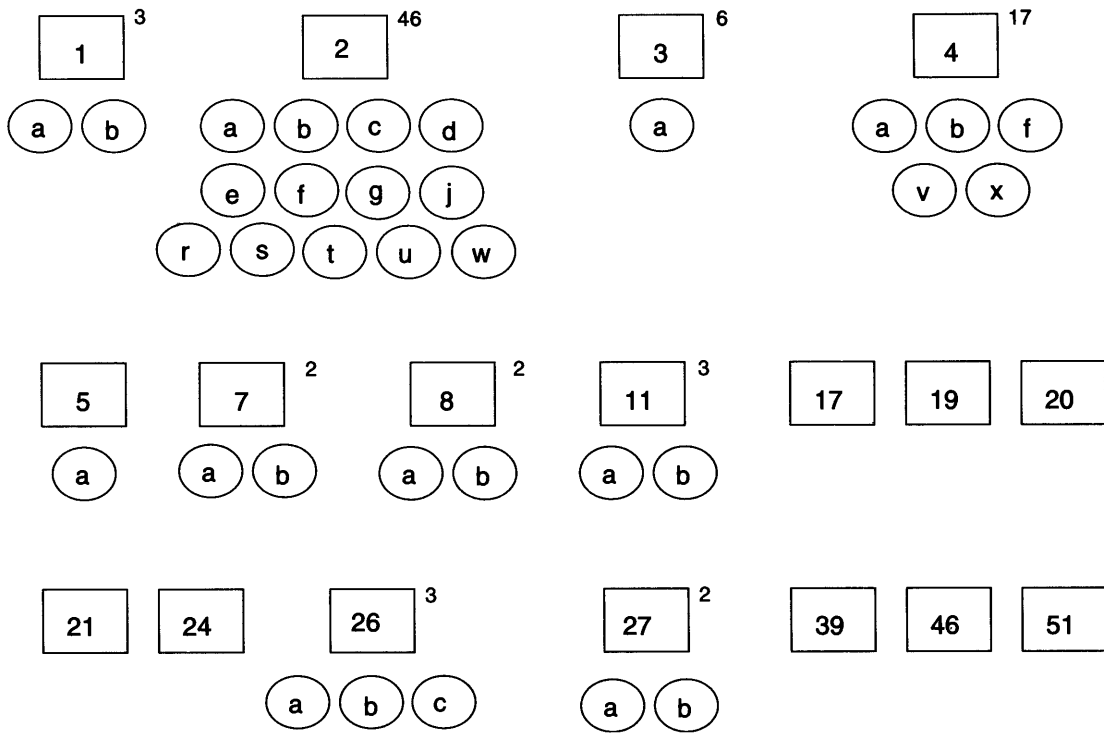


Figure 4. Mouse cytochrome P450 families and subfamilies. Superscript numbers indicate the number of members in this family.

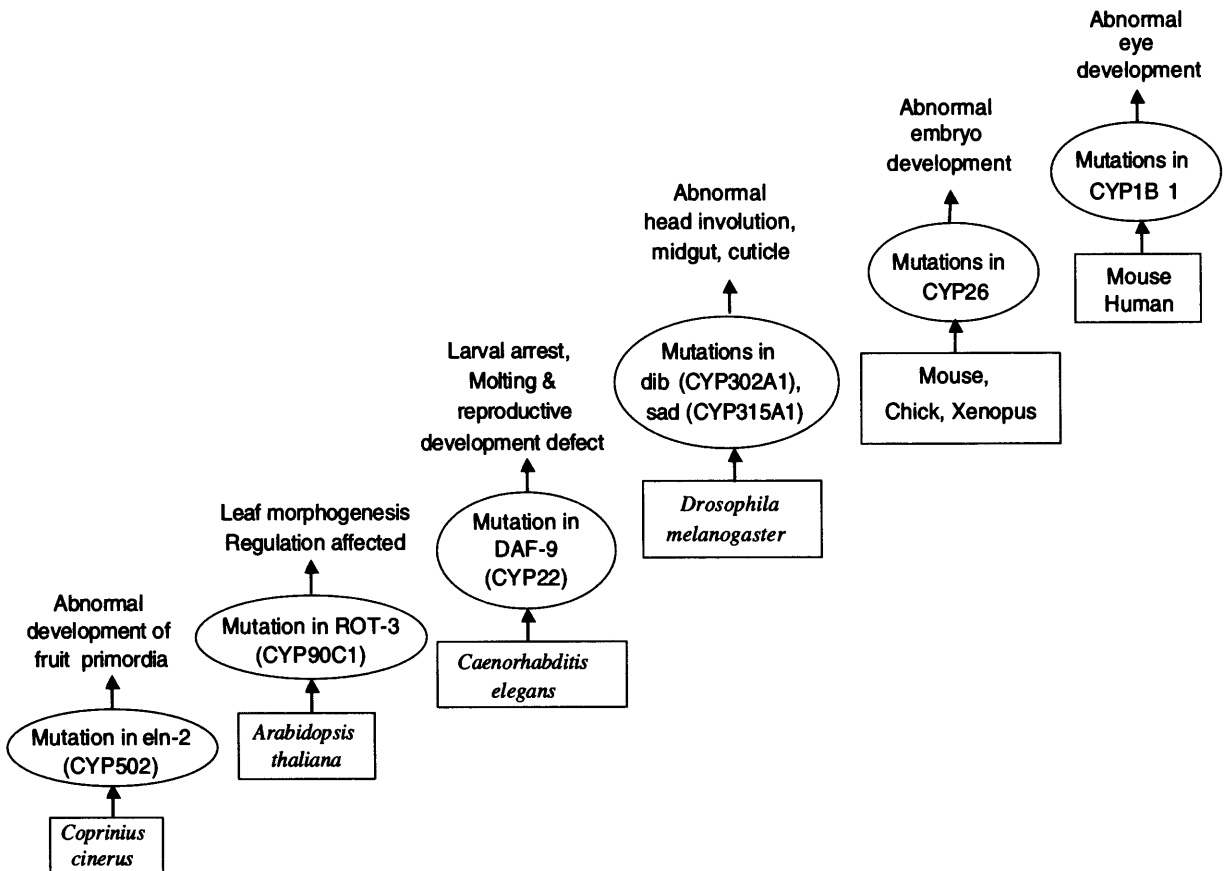


Figure 5. Developmentally active forms of cytochrome P450 in different phyla.

be capable of retinoic acid degradation, such as CYP3A7, CYP3A5, CYP2C18, CYP2C8, and CYP3A4 (Marill et al. 2000). However, for these forms to function in development, they would need a spatial and temporal expression pattern paralleling that of retinoic acid synthesis, as indicated above. A number of other examples of cytochrome P450 influencing development have appeared in recent years (figure 5). As with CYP1B1, the developmental influence of the cytochrome P450 in these examples was determined from examination of the basis of mutation phenotypes:

CYP502. The mushroom *Coprinus cinereus* develops a fruit body by differentiation of its tissues, and an expansion of differentiated cells causing elongation of its stipe. A dominant mutation (*eln2-1*) in the *elongationless2* (*eln2*) gene results in 'dumpy primordia' with mature fruit bodies on short stipes (Maraguchi & Kamada 2000). The gene was shown to code for a form of cytochrome P450, CYP502, and the mutation, a truncating one causing loss of 18 residues from the carboxy-terminal end, might be producing a deleterious effect on the cellular morphogenesis. Since the mutation is a dominant one, the possibility exists that the mutated protein produces an abnormal metabolite or amount of metabolite that prevents the normal morphogenic response of the stipe cells. As with CYP1B1, the nature of the critical metabolite influenced by the wild-type enzyme is unknown at this time.

CYP90C1. In *Arabidopsis thaliana*, the homozygous *rot3* mutant had shortened leaves, a defect in the polar elongation of the leaves. Molecular cloning of the *ROT3* gene revealed it to encode a form of cytochrome P450, named CYP90C1 (Kim et al. 1998). Structurally, the deduced sequence had domains that were homologous to substrate recognition domains of steroid hydroxylase forms of cytochrome P450, and it was suggested that it plays a role in leaf polarization by generating a steroid, perhaps a brassinosteroid known to influence plant development (Kim et al. 1999).

Daf-9. *Caenorhabditis elegans* has the ability to go into a developmentally dormant or dauer larval stage in which it may exist for several months under unfavorable environmental conditions. Entrance into this stage is affected by a nuclear hormone receptor, DAF-12, that responds to sensory transduction pathway signals and controls dauer and non-dauer morphogenesis of the larval development. The natural ligand for DAF-12 is at present unknown. However, a mutation in a *C.*

elegans gene, *daf-9*, was found to cause the entrance into a dauer larval state, indicating it was upstream in the pathway, perhaps producing some DAF-12 ligand. *Daf-9* was found to encode a cytochrome P450 protein, similar to forms of cytochrome P450 with phylogenetic similarity to CYP2C3, a rabbit progesterone hydroxylase, human CYP17, and CYP21 and to *Drosophila* CYP18. The similarity suggested the possibility that the *daf-9* gene product is a steroid hydroxylase responsible for production of a steroid receptor ligand (Jia et al. 2002), the nature of which is, as yet, unknown. The CYP designation for *daf-9* has been assigned as CYP22 on the Nelson's Web Page (<http://drnelson.utm.edu/C.elegans.RNAi.html>), where it is indicated that inactivation of another *C. elegans* cytochrome P450 form, CYP13A8, has been found to result in embryonic lethality.

CYP 302A1 and CYP315A1. In *Drosophila* a mutation in the *disembodied* (*dib*) gene was shown to result in poorly differentiated embryonic cuticle. Mutations were also shown to prevent dorsal closure, midgut morphogenesis and headinvolution. The deduced sequence of *dib* revealed that it coded for a form of cytochrome P450, which was named CYP302A1 (Chavez et al. 2000). Ecdysteroids are necessary for cuticle formation. Since *dib* mutations cause cuticle defects, it was suggested that this form of cytochrome P450 might be involved in ecdysteroid biosynthesis or breakdown. Examination of the ecdysteroid titers in the mutants revealed severely reduced levels of ecdysone and 20-hydroxyecdysone, suggesting CYP302A1 is involved in the biosynthesis of the ecdysteroid (Chavez et al. 2000). CYP302A1 has subsequently been shown to catalyze 22-hydroxylation of 2,22-dideoxyecdysone (ketotriol) to 2-deoxyecdysone and 22-deoxyecdysone to ecdysone (Warren et al. 2002). Another gene, *sad*, has also been found to code for a form of cytochrome P450, CYP315A1. *Sad* catalyzes the hydroxylation of ketotriol to 22-deoxyecdysone, and 2-deoxyecdysone to ecdysone (Warren et al. 2002). Thus, *sad* and *dib* appear to function together in the pathway of 20-hydroxyecdysone biosynthesis. Ecdysteroids bind to nuclear receptors (EcR) which heterodimerize with the *Drosophila* retinoate X receptor (RXR) for transcriptional regulation and might explain the strong developmental impairment in *dib* mutations. A form of cytochrome P450, CYP6H1, has been isolated from the insect *Locusta migratoria*, that may function as ecdysone 20-hydroxylase in the locust (Winter et al. 1999), but has only about 20% sequence identity with CYP302A.

Future Developments

Other developmental forms of cytochrome P450 also exist, such as the DIF-3 hydroxylase in the slime mold, *Dictyostelium discoideum*, which facilitates removal of the differentiation-inducing factor DIF-1 (Kay et al. 1999, Morandini et al. 1995). The function of this form of cytochrome P450 is similar to that of CYP26. Obviously, the very large number of cytochrome P450 families in the many species will eventually be shown to contain many more developmentally active forms of cytochrome P450 and should be the subject of a more inclusive review. The use of newer tools, such as microarray and proteomics will help in clearly delineating the complete complement of constitutive gene expression profiles at each time-point in specific developing tissues. The knowledge gathered from such data will be useful not only in understanding the role of CYPs in normal physiological processes, but also under clinical conditions, and understanding the pharmacokinetics of administered drugs during pregnancy.

Conclusions

Data accumulated to date point to a role for cytochrome P450 forms in the development of living organisms in the different phyla. In some manner this very versatile enzyme has interdigitated itself into the developmental process aiding in the

morphogenesis of different tissues in the different species (figure 5). In some instances, the ability of cytochrome P450 to perform such functions appears to be by modifying lipophilic chemicals of endogenous origin, such as steroids, or developmentally important compounds such as vitamins. Perhaps the very broad substrate specificity of members of this superfamily is what makes it such a useful tool. However, such a versatile tool has proven it can also be a sword of Damocles, ready to doom developing organisms by its very presence, during exposure to certain chemicals. The ability to metabolize such a large range of chemicals means that it is only a matter of time before a metabolite of some chemical is produced which can inadvertently imitate a developmentally active chemical, thereby triggering teratologies or exerting neoplastic transformation. Many examples of such effects are known today. The future, however, is a bright one. As more is learned about the forms of cytochrome P450 present in the embryo and fetus it should be possible to generate lists of drugs and chemical agents that should be contraindicated or to be avoided during pregnancy.

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