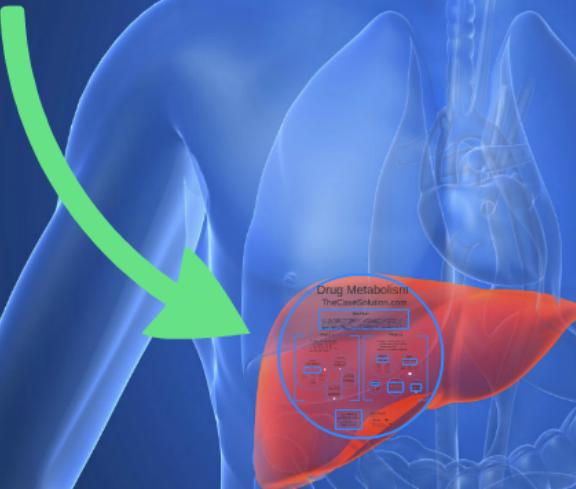


Drug metabolism e-learning module

This e-learning resource is designed to allow you to explore drug metabolism and drug metabolising enzymes. Click on the circle in the liver to start.

Produced by University of Otago and University of Wisconsin.



Drug Metabolism

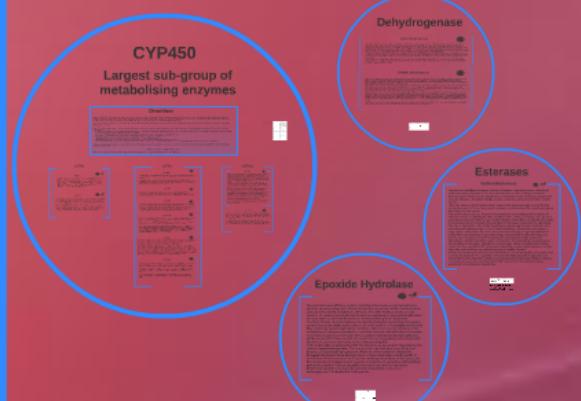
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Overview

In 1947 R. T. Williams noted that enzyme-catalyzed biotransformation of drugs, dietary substances, and other synthetic and environmental agents, i.e., xenobiotics, can be by enzymatic and/or nonenzymatic reactions. Enzymes catalyzing aspartic or so-called Phase 1, reactions are thus classified broadly as all those catalyzing the oxidation, reduction, and hydrolysis of xenobiotics. Enzymes in this group include, but are not limited to, the mixed-function oxidases more commonly known as cytochrome P450 monooxygenases, monoamine and diamine oxidases, aldehyde dehydrogenases, aldehyde oxidase, alcohol dehydrogenases, quinone reductases, short-chain dehydrogenases/reductases, aldo-keto reductases, and esterases. Enzymes catalyzing synthetic, or so-called Phase 2, reactions are thus classified broadly as all those catalyzing the conjugation of xenobiotics to endogenous molecules, e.g., glucuronyl, sulfate, glutathione, acids or a metal group. Representative enzymes in this group include, but are not limited to, the UDP-glycosyltransferases, sulfotransferases, glutathione S-transferases, N-acetyltransferases, and methyltransferases.

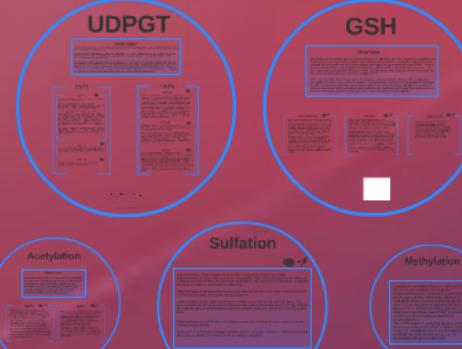
Phase 1

- Introduce a functional group
- Increases water solubility
 - Increases reactivity
- Product can be excreted or metabolised further.



Phase 2

- Conjugates a large group
- Increases water solubility
 - Increases size
- Product is normally excreted.



Drug metabolising enzymes are found throughout the body but the highest concentrations are found in the liver.

These symbols indicate whether the enzyme is relevant to:

- Clinical drug metabolism
- or
- Environmental chemical metabolism.

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Drug Metabolism

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Overview

In 1947 R. T. Williams noted that enzyme-catalyzed biotransformation of drugs, dietary substances, and other synthetic and environmental agents, i.e., xenobiotics, can be by asynthetic and/or synthetic reactions. Enzymes catalyzing asynthetic, or so-called Phase 1, reactions are thus classified broadly as all those catalyzing the oxidation, reduction, and hydrolysis of xenobiotics. Enzymes in this group include, but are not limited to, the mixed-function oxidases more commonly known as cytochrome P450 monooxygenases, monoamine and diamine oxidases, aldehyde dehydrogenases, aldehyde oxidase, alcohol dehydrogenases, quinone oxidoreductases, short-chain dehydrogenases/reductases, aldo-keto reductases, and esterases. Enzymes catalyzing synthetic, or so-called Phase 2, reactions are thus classified broadly as all those catalyzing the conjugation of xenobiotics to endogenous molecules, e.g., glucuronic acid, sulfate, glutathione, acetate, or a methyl group. Representative enzymes in this group include, but are not limited to, the UDP-glycosyltransferases, sulfotransferases, glutathione S-transferases, N-acetyltransferases, and methyltransferases.

Phase 1

• Adds a functional group
• Increases water solubility
• Reduces reactivity
• Product can be excreted or
• Further metabolism

Phase 2

• Conjugates a large group
• Increases water solubility
• Increases size
• Product is normally excreted.

Phase 1

Introduce a functional group

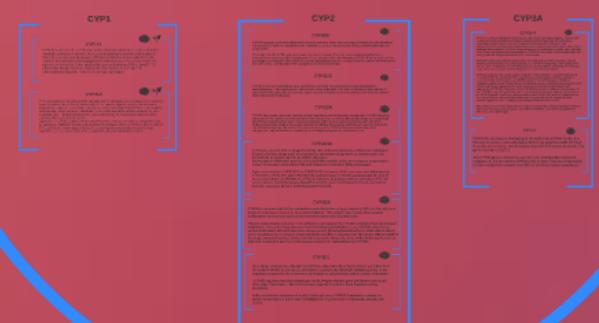
- Increases water solubility
- Increases reactivity

Product can be excreted or metabolised further.

CYP450

Largest sub-group of metabolising enzymes

Overview



Dehydrogenase

Alcohol Dehydrogenase

Alcohol dehydrogenase (ADH) is an enzyme that catalyzes the oxidation of alcohols to aldehydes or ketones, and the reduction of aldehydes or ketones to alcohols. ADH is found in many tissues, but it is particularly abundant in the liver, where it plays a major role in the metabolism of ethanol. ADH is also found in the stomach, small intestine, and colon. ADH is a monomeric protein composed of a single polypeptide chain. It has a molecular weight of approximately 45 kDa. The active site of ADH contains a histidine residue that is involved in the reduction of aldehydes. ADH is inhibited by disulfiram and other drugs that bind to the active site.

Aldehyde Dehydrogenase

Aldehyde dehydrogenase (ALDH) is an enzyme that catalyzes the oxidation of aldehydes to carboxylic acids. ALDH is found in many tissues, but it is particularly abundant in the liver, where it plays a major role in the metabolism of acetaldehyde. ALDH is also found in the stomach, small intestine, and colon. ALDH is a monomeric protein composed of a single polypeptide chain. It has a molecular weight of approximately 45 kDa. The active site of ALDH contains a histidine residue that is involved in the oxidation of aldehydes. ALDH is inhibited by disulfiram and other drugs that bind to the active site.

Epoxide Hydrolase

Epoxide hydrolases (EHs) are a class of enzymes that cleave certain derivatives to yield the corresponding diol. If we think from the perspective of the classical phase I reactions, EHs are not really phase I enzymes, but they do play a role in the first phase. If so, epoxide hydrolase may as well be regarded as a conjugation with water because it is related to the same metabolic pathway as hydroxylation. The final EH step happens after the most common mammalian microsomal epoxide hydrolase which plays a major role in the control of chemically reactive and thus potentially carcinogenic epoxides. These epoxides are formed during the metabolism of numerous substances, and their metabolic detoxification is therefore of primary importance. A few years after a sizable number of epoxide hydrolase (EH) genes were identified, it was discovered that the epoxide hydrolase gene encodes for a hormone, i.e., an estrogen derivative, to the corresponding diol.

In the last few years, it has been shown that epoxide hydrolase is particularly important for the control of genotoxic epoxides. The enzyme has broad substrate specificity and displays a surprisingly high apparent affinity to a wide variety of epoxides.

During the metabolism of epoxides, the resulting hydrodiols, in few cases, are the most potent mutagens.

The epoxide hydrolase gene is located on chromosome 16 and encodes a 45-kDa

glycoprotein consisting of 394 amino acid residues.

Esterases

Carboxylesterases

Carboxylesterases (CES) are enzymes that catalyze the hydrolysis of esters, amides, thioesters, and carbamates. These are common metabolites of many drugs, including psychotropic drugs, antihistamines, and central nervous system agents. The CES enzymes prefer esters with a large, fatty acyl group and a small alcohol group, and amides with a large, substituted amide group, associated with a small acyl group and a large alcohol group. The surface of esterases is highly conserved among all esterases, and most esterases including the liver, small intestine, kidney, and lungs. The present question is found in the liver and small intestine, where they can significantly lower the bioavailability of many drugs. The CES enzymes are also found in the brain, heart, and other organs. The rate of hydrolysis of the CESs is estimated to range from 100 to 1000 nmol/min/mg protein. Engaging a similarity to the CYP system in demonstrating a large interindividual variation in activity, the CESs are also subject to genetic polymorphisms, including lack of expression, lack of induction, and altered activity in regard to disease. The use of inhibitors of CESs can affect the expression of the CESs, which is influenced by the pregnane X receptor and constitutive androstane receptor proteins. Carboxylesterases are also involved in the metabolism of organophosphates, pyrethroids and carbamate insecticides.



Largest sub-group of metabolising enzymes

Overview

Cytochromes P450 (CYPs) belong to the superfamily of proteins containing a haem co-factor and, therefore, are haemoproteins. CYPs use a variety of small and large molecules as substrates in enzymatic reactions. They are, in general, the terminal oxidase enzymes in electron transfer chains, broadly categorised as P450-containing systems. The term P450 is derived from the spectrophotometric peak at the wavelength of the absorption maximum of the enzyme (450 nm) when it is in the reduced state and complexed with carbon monoxide.

CYP enzymes have been identified in all domains of life - animals, plants, fungi, protists, bacteria, archaea, and even in viruses. However, the enzymes have not been found in *E. coli*. More than 21,000 distinct CYP proteins are known.

Most CYPs require a protein partner to deliver one or more electrons to reduce the iron (and eventually molecular oxygen). Based on the nature of the electron transfer proteins, CYPs can be classified into several groups:

- Microsomal P450 systems in which electrons are transferred from NADPH via cytochrome P450 reductase (variously CPR, POR, or CYPOR). Cytochrome b5 (cyb5) can also contribute reducing power to this system after being reduced by cytochrome b5 reductase (CYB5R).
- Mitochondrial P450 systems, that employ adrenodoxin reductase and adrenodoxin to transfer electrons from NADPH to P450.
- Bacterial P450 systems, that employ a ferredoxin reductase and a ferredoxin to transfer electrons to P450.
- CYB5R/cyb5/P450 systems in which both electrons required by the CYP come from cytochrome b5.
- FMN/Fd/P450 systems originally found in *Rhodococcus* sp. in which a FMN-domain-containing reductase is fused to the CYP.
- P450 only systems, which do not require external reducing power. Notable ones include CYP5 (thromboxane synthase), CYP8 (prostacyclin synthase), and CYP74A (allene oxide synthase).

The most common reaction catalyzed by cytochromes P450 is a monooxygenase reaction, e.g., insertion of one atom of oxygen into the aliphatic position of an organic substrate (RH) while the other oxygen atom is reduced to water:



Humans have 57 genes and more than 59 pseudogenes divided among 18 families of cytochrome P450 genes and 43 subfamilies.[

CYP2

CYP2B6

CYP2B6 enzymes synthesise cholesterol, steroids and other lipids. Its expression is induced by phenobarbital. The enzyme is known to metabolize some xenobiotics, such as the anti-cancer drugs cyclophosphamide and ifosfamide.

Transcript variants for this gene have been described; however, it has not been resolved whether these transcripts are in fact produced by this gene or by a closely related pseudogene, CYP2B7. Both the gene and the pseudogene are located in the middle of a CYP2A pseudogene found in a large cluster of cytochrome P450 genes from the CYP2A, CYP2B and CYP2F subfamilies on chromosome 19q.

CYP3A4 is induced by glucocorticoids and is involved in the metabolism of many drugs, including acetaminophen, carbamazepine, erythromycin, and theophylline. The enzyme can undergo deactivation by CYP2D6 and CYP2C19. Also, many substances are metabolized by CYP3A4, including many protoxins being toxic to humans.

CYP3A4 is the most common member of this family, it is found in the liver and is involved in the metabolism of many drugs, including acetaminophen, carbamazepine, erythromycin, and theophylline. The enzyme can undergo deactivation by CYP2D6 and CYP2C19. Also, many substances are metabolized by CYP3A4, including many protoxins being toxic to humans.

Table of CYP450 isoforms

Family	Function	Members	Names
CYP1	drug and steroid (especially estrogen) metabolism, benzo(a)pyrene toxicification	3 subfamilies, 3 genes, 1 pseudogene	CYP1A1, CYP1A2, CYP1B1
CYP2	drug and steroid metabolism	13 subfamilies, 16 genes, 16 pseudogenes	CYP2A6, CYP2A7, CYP2A13, CYP2B6, CYP2C8, CYP2C9, CYP2C18, CYP2C19, CYP2D6, CYP2E1, CYP2F1, CYP2J2, CYP2R1, CYP2S1, CYP2U1, CYP2W1
CYP3	drug and steroid (including testosterone) metabolism	1 subfamily, 4 genes, 2 pseudogenes	CYP3A4, CYP3A5, CYP3A7, CYP3A43
CYP4	arachidonic acid or fatty acid metabolism	6 subfamilies, 12 genes, 10 pseudogenes	CYP4A11, CYP4A22, CYP4B1, CYP4F2, CYP4F3, CYP4F8, CYP4F11, CYP4F12, CYP4F22, CYP4V2, CYP4X1, CYP4Z1
CYP5	thromboxane A2 synthase	1 subfamily, 1 gene	CYP5A1
CYP7	bile acid biosynthesis 7-alpha hydroxylase of steroid nucleus	2 subfamilies, 2 genes	CYP7A1, CYP7B1
CYP8	varied	2 subfamilies, 2 genes	CYP8A1 (prostacyclin synthase), CYP8B1 (bile acid biosynthesis)
CYP11	steroid biosynthesis	2 subfamilies, 3 genes	CYP11A1, CYP11B1, CYP11B2
CYP17	steroid biosynthesis, 17-alpha hydroxylase	1 subfamily, 1 gene	CYP17A1
CYP19	steroid biosynthesis: aromatase synthesizes estrogen	1 subfamily, 1 gene	CYP19A1
CYP20	unknown function	1 subfamily, 1 gene	CYP20A1
CYP21	steroid biosynthesis	2 subfamilies, 1 gene, 1 pseudogene	CYP21A2
CYP24	vitamin D degradation	1 subfamily, 1 gene	CYP24A1
CYP26	retinoic acid hydroxylase	3 subfamilies, 3 genes	CYP26A1, CYP26B1, CYP26C1
CYP27	varied	3 subfamilies, 3 genes	CYP27A1 (bile acid biosynthesis), CYP27B1 (vitamin D3 1-alpha hydroxylase, activates vitamin D3), CYP27C1 (unknown function)
CYP39	7-alpha hydroxylation of 24-hydroxycholesterol	1 subfamily, 1 gene	CYP39A1
CYP46	cholesterol 24-hydroxylase	1 subfamily, 1 gene	CYP46A1
CYP51	cholesterol biosynthesis	1 subfamily, 1 gene, 3 pseudogenes	CYP51A1 (lanosterol 14-alpha demethylase)