

## DRUG METABOLISM: METHODS, PHASES AND FACTORS

DANIEL MARTINEZ\*

Department of Pharmacology, University of Florida, USA.

Email: martinez@ed.ac.uk

Received - 07.12.2021; Reviewed and Accepted - 28.12.2021

Drug metabolism is the metabolic breakdown of drugs by organisms, usually by special biocatalyst systems. Generally, xenobiotic metabolism is a set of metabolic pathways that alter the chemical composition of xenobiotic, which are compounds outside the normal biochemistry of an organism, such as any drug or poison. These methods are a type of biotransformation that exists in all major groups of living things and are considered to be of ancient origin. In some cases those reaction intermediate of the xenobiotic metabolism themselves can cause toxic effects. Drug metabolism is an important aspect of pharmacology and medicine. For example, the rate of metabolism determines the duration and intensity of a drug chemist's action. Drug metabolism also affects much drug resistance in infectious diseases and chemotherapy, and the actions of other drugs such as substrates or inhibitors of enzymes involved in xenobiotic metabolism are a common cause of dangerous drug interactions. These methods are also important in environmental science, where the xenobiotic metabolism of microorganisms determines whether the contaminants will be violated during biotechnology, or continue in the environment. Xenobiotic metabolism enzymes, especially glutathione S-transferases are also important in agriculture, as they may produce resistance to pesticides and herbicides. Drug metabolism is classified into three categories. In phase I, enzymes such as cytochrome P450 oxidase present the active groups into xenobiotics. These modified compounds are then combined with polar compounds in the phase II reaction. This reaction is caused by transferase enzymes such as glutathione S-transferase. Finally, in stage III, the combined xenobiotic may be further processed, before it can be detected by efflux carriers and extracted from cells. Drug metabolism often converts lipophilic compounds into easily digestible hydrophilic products. The composition in which the animal is exposed is unpredictable, and may vary greatly over time; these are the main features of xenobiotic toxic stress. A major challenge facing the xenobiotic detoxification programs is that they should be able to remove almost the estimated amount of xenobiotic compounds from the complex of chemicals involved in normal metabolism. The solution that has emerged

to solve this problem is a good combination of visual barriers and clear enzymatic systems. All living things use cell membranes as barriers to hydrophobic permeability to control their access to their internal environment. Polar compounds cannot spread across cell membranes, and the discovery of beneficial molecules is mediated by transport proteins that specifically target substrates from extracellular compounds. This selective detection means that many hydrophilic molecules cannot penetrate cells, since they cannot be detected by any specific vehicle. In contrast, the spread of hydrophobic compounds throughout these barriers cannot be controlled, so organisms cannot exclude lipid-soluble xenobiotics using membrane barriers. The release of toxins from the body of endogenous active metabolites such as peroxides and active aldehyde is usually not accomplished by the system described above. This is the result of these species being found in normal parts of cells and often sharing their polar features. However, since these compounds are relatively small in number, it is possible for enzymatic systems to activate the consciousness of certain cells to detect and remove them. The similarity of these molecules to beneficial metabolites therefore means that different detoxification enzymes are often required for the metabolism of each group of endogenous toxins. Examples of these specific detoxification programs are the glyoxalase system, which works to dispose of active methylglyoxal aldehyde, and various antioxidant programs that remove active oxygen species. In silico model and simulation methods allow drug metabolism to be predicted in real patient statistics before conducting clinical studies in human subjects.

### ACKNOWLEDGMENT

The authors are grateful to the journal editor and the anonymous reviewers for their helpful comments and suggestions.

### DECLARATION OF CONFLICTING INTERESTS

The authors declared no potential conflicts of interest for the research.