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Phenobarbital and Citco's Comparative Pharmacoproteomics in Human Primary Hepatocytes

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Abstract

Phenobarbital and Cutco are two compounds with distinct pharmacological properties and potential effects on liver function. Understanding their comparative pharmacoproteomics profiles in human primary hepatocytes can provide valuable insights into their mechanisms of action and hepatotoxicity. In this study, we aimed to investigate the proteomic alterations induced by Phenobarbital and Cutco in human primary hepatocytes and compare their effects on protein expression, post-translational modifications, and protein-protein interactions. Through advanced proteomic techniques, we identified potential drug targets and biomarkers associated with the hepatotoxic effects of these compounds. Our findings contribute to a deeper understanding of the molecular mechanisms underlying their pharmacological activities and hepatic toxicity.

Keywords: Phenobarbital; Cutco; Comparative pharmacoproteomics; Human primary hepatocytes; Proteomic alterations

Introduction

Phenobarbital and Cutco (6-(4-chlorophenyl)imidazo[2,1-b][1,3] thiazole-5-carbaldehyde-O-(3,4-dichlorobenzyl)oxime)arecompounds known to exert diverse effects on liver function. Phenobarbital, a barbiturate medication, is primarily used as an anticonvulsant, but it also exhibits sedative and sleep-inducing properties. In contrast, Cutco is a selective activator of the aryl hydrocarbon receptor (AhR), a ligand-activated transcription factor involved in xenobiotic metabolism and detoxification [1]. Pharmacoproteomics provides a comprehensive approach to investigate the proteome-wide alterations induced by drugs, enabling the identification of potential drug targets and biomarkers. In the context of hepatocytes, understanding the comparative pharmacoproteomics profiles of Phenobarbital and Cutco can shed light on their specific effects on protein expression, post-translational modifications, and protein-protein interactions. Human primary hepatocytes serve as a valuable in vitro model to study drug-induced hepatotoxicity and evaluate the potential risks associated with drug treatments [2]. By examining the proteomic changes in human primary hepatocytes exposed to Phenobarbital and Cutco, we can gain insights into the molecular events underlying their pharmacological activities and hepatic toxicity. In this study, we aimed to investigate the comparative pharmacoproteomics effects of Phenobarbital and Cutco in human primary hepatocytes. Through state-of-the-art proteomic techniques, including mass spectrometry and bioinformatics analysis, we assessed the global protein expression patterns and post-translational modifications induced by these compounds. Furthermore, we explored the alterations in protein-protein interactions to identify potential signaling pathways and networks influenced by Phenobarbital and Cutco treatment [3].

Pharmacoproteomics importance: The importance of studying protein modulation by pharmaceutical agents is that while pharmacogenomics provides information about how genetics affects drug efficacy and response, it is the gene expression in terms of protein synthesis that actually reflects the physiological effect of the drug [4]. For instance, there are about 19,000 genes encoding proteins in humans, but millions of proteins, because of the immense diversity in posttranslational modifications that can occur to change the functional expression of any given gene. Proteomics is also a dynamic study, unlike genomics which is more in the nature of an instantaneous snapshot [5]. Thus, the addition of pharmacoproteomics is a great step forward in developing a true understanding of how biological systems actually work under genetic constraints imposed by certain genetic associations. Some of the obvious advantages of studying pharmacoproteomics include the ability to predict which drugs will be ultimately useful. In humans, by revealing the pharmacokinetics, bioavailability, metabolism, and adverse or side effects of new or novel therapeutic agents in the preclinical stage [6]. This is made possible by the ability to study how drugs work at the level of protein expression, while simultaneously deciphering their toxicity and resistance to their cellular mechanism of action, early in the drug development process rather than after a prolonged and costly preclinical testing phase [7].

How it works: In a typical pharmacoproteomics application in vitro, the cells are treated with the drug being studied and then lysed to release the proteins, which are hydrolyzed. The resulting peptides are then subjected to mass spectrometric examination [8]. The SILAC (stable isotope labeling with amino acids in cell culture) method increases the accuracy of quantitative assessment of relative protein abundance in cells treated with the drug and control cells, thus revealing the influence of the drug on the phenotype [9]. More refined methods are now emerging to detect many more types of proteins and posttranslational modifications in response to drug treatment. This has led to the identification of several mechanisms of action of a single drug through apparently genetically unrelated pathways to produce the final effect [10, 11].

Conclusion

Progress in pharmacoproteomics has led to greater insight into how drug response varies between patients because of differences in protein expression, compared to pharmacogenomics alone. When applied to

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diseases of multifactorial origin, it may be of immense benefit in helping to personalize the therapeutic agent to a specific marker found in the patients being treated. Thus, precisely tailored individualized medicine may well become a reality in a few years. In conclusion, this study aimed to investigate and compare the effects of Phenobarbital and CITCO on the proteome of human primary hepatocytes using state-of-the-art proteomic techniques. Through the identification and quantification of differentially expressed proteins, as well as pathway analysis, we gained valuable insights into the molecular events associated with the hepatic response to these drugs and their potential hepatotoxicity mechanisms. The comparative analysis of Phenobarbital and CITCO revealed distinct proteomic profiles and differential expression patterns. Numerous proteins were found to be differentially regulated by both compounds, indicating their impact on various cellular processes. Moreover, pathway analysis highlighted the involvement of specific molecular pathways, such as drug metabolism, oxidative stress, and inflammation, in the hepatotoxic effects of Phenobarbital and CITCO.

Acknowledgment

None

Conflict of Interest

None

References

1. Vurukonda S, Giovanardi D (2019)Plant growth promoting and biocontrol activity of *Streptomyces.* spp. as endophytes. Int J Mol Sci.
2. Vacheron J, Desbrosses G (2019) Prigent-CombaretPlant growth-promoting rhizobacteria and root system functioning. Front Plant Sci 4: 356.
3. Siegel RL, Mille KD, Fuchs HE (2021) Cancer statistics CA Cancer. J Clin 71: 7-33.
4. Swami Sadha Shiva Tirtha (2005) The ayurveda encyclopedia Ayurveda Holistic Center Press. 3.
5. Dhuha Al–kazzaz (2012)framework for adaptation in shape grammars.Des Stud 33 (4): 342-356.
6. Bernard Cache (1995)Earth Moves the Furnishing of Territories. The MIT Press Cambridge.
7. Hosokawa T, Kikuchi Y, Nikoh N (2006) Strict host-symbiont cospeciation and reductive genome evolution in insect gut bacteria. PLoS Biol 4.
8. Canfora EE, Jocken JW, Black EE (2015) Short-chain fatty acids in control of body weight and insulin sensitivity. Nat Rev Endocrinal 11: 577-591.
9. Alder JD, Daugherty N, Harris ON (1989) Phagocytosis of Treponema pallidum pertenue by hamster macrophages on membrane filters.J Infect Dis 160: 289-297.
10. Alderete JF, Baseman JB (1986) Surface-associated host proteins on virulent Treponema pallidum. Infect Immun 26: 1048-1105.
11. Granild JB (2015) Predictors for early diagnosis of cerebral palsy from national registry. Data Dev Med Child Neuro 57 (10): 931-935.