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Role of Epoxide Hydrolases and Cytochrome P450s on Metabolism of KZR-616, a First-in-Class Selective Inhibitor of the Immunoproteasome Ying Fang¹, Jinhai Wang¹, Christopher J. Kirk¹, Christophe Morisseau², and Bruce D. Hammock²

Ying Fang¹, Jinhai Wang¹, Christopher J. Kirk¹, Christophe Morisseau², and Bruce ¹Kezar Life Sciences, Inc. ²University of California, Davis, Davis, California

CONTACT INFORMATION: yfang@kezarbio.com

PURPOSE

KZR-616 is a tripeptide ketoepoxide-based selective inhibitor of the human immunoproteasome. It is an analog of carfilzomib (KYPROLIS[™]), which inhibits all forms of the proteasome and is FDA/EMA approved for the treatment of multiple myeloma. Inhibition of the immunoproteasome blocks cytokine production in multiple immune cell types, reduces the activity of inflammatory T-helper cell subsets, increases the number of regulatory T-cells, and blocks plasma cell numbers and autoantibody production. Based on promising therapeutic activity in animal models of rheumatoid arthritis (RA) and systemic lupus erythematosus (SLE), KZR-616 is being developed for potential treatment of multiple autoimmune and inflammatory diseases. KZR-616 currently is being evaluated in a Phase1b/2 clinical trial in patients with SLE and lupus nephritis. The aim of this study was to identify the major enzymes involved in the metabolism and elimination of KZR-616 in humans. The information gained will help to understand its pharmacokinetic (PK) variability and drugdrug interaction potential.

METHOD(S)

- Metabolic stability of KZR-616 in liver microsomes (LMs) was assessed in the presence and absence of NADPH and intrinsic clearance (Clint) was monitored by the rate of parent compound disappearance.
- Epoxide hydrolysis of KZR-616 by recombinant epoxide
 hydrolases (EH) was conducted at pH 9.0 for microsomal EH
 (mEH) and pH 7.5 for soluble EH (sEH). Cis-stilbene oxide (cis-SO) and trans-stilbene oxide (trans-SO) were used as probe
 substrates for mEH and sEH, respectively.
- The kinetics of KZR-616 metabolism was studied in female and male HLMs, recombinant human mEH and human hepatocytes.
- 4) The effect of inhibition of EH and CYP activity by KZR-616 in HLM and/or human hepatocytes on KZR-616 clearance was performed using known inhibitors: 2-Nonylsulfanylpropionamide (NSPA), 1-trifluoromethoxypheny1-3(1propionylpiperidin-4-yl) urea (TPPU), and 1aminobenzotriazole (1-ABT), for mEH, sEH and CYP activity, respectively.



As shown in above Table 1, the CLint increased by 2.6 and 6 folds for HLMs and MLMs, respectively, in the presence of NADPH comparing with that in the absence of NADPH, suggesting CYP activity may play a role in the metabolism of KZR-616, which is not consistent with what we found in the in vivo studies.

2. To confirm the role of CYP on KZR-616 metabolism using a pan CYP inhibitor (1-ABT) in human hepatocytes.



- Figure 1. KZR-616 metabolism in human hepatocytes As shown in above Figure 1:
- A pan CYP inhibitor (1-ABT) does not affect the elimination rate(k), indicating that CYPs did not play an important role in the metabolism of KZR-616 in human hepatocytes.
- KZR-59587, a diol form of KZR-616, was found to be the major metabolite in hepatocytes.

3. KZR-616 epoxide hydrolysis pathway study



No formation of KZR-59587 merceased incearly with increasing incermising increasing increasing increasing increasing its formation of KZR-59587 was observed when KZR-616 was incubated in human hepatocyte cytosol, indicating its formation was not from sEH.
Using the recombinant enzyme mEH or sEH, KZR-59587 was confirmed to be formed via mEH.



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The diol KZR-59587 was resulted from direct epoxide hydrolysis of KZR-616. The epoxide hydrolysis of KZR-616 was therefore investigated in human liver microsomes (mEH), hepatic cytosols (sEH)

and recombinant EHs. As shown in Figure 2:
Formation of KZR-59587 increased linearly with increasing liver microsomal proteins, suggesting it formed via mEH:

4.Inhibition of KZR-616 epoxide hydrolysis in HLMs by a selective mEH inhibitor (NSPA)



Figure 3. KZR-616 epoxide hydrolysis was inhibited by NSPA, a selective mEH inhibitor, confirming mEH plays a significant role in KZR-616 metablism.

5. Inhibition of KZR-616 epoxide hydrolysis in human hepatocytes by mEH inhibitor NSPA and sEH inhibitor TPPU

Figure 4. The formation of KZR-59587 was significantly affected by addition of mEH inhibitor NSPA with IC50 of 0.42 μ M, but not affected by sEH inhibitor TPPU, confirming the predominant KZR-616 metabolic pathway is via mEH hydrolysis.

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6. Investigation of KZR-616 as inhibitor on epoxide hydrolases in liver microsomes, cytosol and recombinant EHs.



Figure 5 data shows that KZR-616 did not inhibit cis-SO and trans-SO hydrolysis in either human, monkey LM, hepatic cytosols or with recombinant EHs at concentrations up to 100µM, suggesting that KZR-616 is unlikely to cause clinically drug-drug interaction.

CONCLUSION(S)

- KZR-616 metabolism predominantly driven by mEH
 CYP450 and sEH play little/no role in metabolism
- Hepatocytes serve as a good in vitro system to assess the metabolic profiles of KZR-616
- PK of KZR-616 is unlikely to be affected by co-administration of CYP450 and sEH inhibitors/inducers
- KZR-616 is unlikely to alter epoxide hydrolysis of other mEH and sEH substrate drugs.

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