

Hepatic Expression of Drug Metabolizing Enzyme in Diabetes

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당뇨병에서 간의 약물대사효소 발현변화

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요 약

간의 약물대사는 흡수된 외인성물질의 배설을 위한 중추적인 역할을 수행하며 이 반응은 일상대사와 이상대사효소로 구성된 약물대사효소계에 의해 매개된다. 약물대사효소의 발현과 활성은 외인성물질의 노출에 의해 유도되거나 억제되며 이 결과는 약물상호작용을 발생시키는 주요한 원인이다. 또한 당뇨, 비만, 영양실조, 음주, 염증반응 등의 병적인 생리상태는 간에서 약물대사효소의 발현과 활성을 조절하는 것으로 보고되고 있다. 이러한 변동은 치료약물 또는 환경오염물질에 대한 인체의 반응성에 영향을 미치며 결과적으로 예측하지 못한 부작용이나 독성을 발생시킬 수 있다. 본 논문에서는 당뇨병에서 약물대사효소의 발현변화를 정리하였다.

Key words : drug metabolizing enzyme, Cytochrome P450, drug interaction, diabetes

INTRODUCTION

Hepatic drug metabolism plays a critical role in metabolic clearance of xenobiotics, which mediated by xenobiotic, or drug, metabolizing enzymes divided classically into two groups, namely, phase I and phase II. Phase I reactions introduce functional groups into xenobiotics, which increases polarity (Kim *et al.*, 2005). Cytochrome P450 (CYP), the flavin-containing monooxygenase, xanthine oxidase, prostaglandin H synthase, amine oxidase, alcohol dehydrogenase,

aldehyde dehydrogenase, microsomal epoxide hydrolyase (mEH) and esterase can mediate phase I reactions. Phase II reactions include glucuronidation, sulfation, methylation, acetylation, glutathione conjugation and amino acid conjugation. These reactions, with the exception of methylation and acetylation, generally result in an increase in xenobiotic hydrophilicity and facilitate elimination via bile or urine.

Xenobiotics often change the expression or capacity of drug metabolizing enzymes and this response, known as induction or inhibition, is a tightly regulated process that is controlled at the levels of transcription, translation and/or posttranslation. Induction of drug metabolizing enzymes in a manner that

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is sensitive to repeated exposure of xenobiotics allows the animal to facilitate elimination of xenobiotics via drug metabolism. It is generally recognized that the expression of drug metabolizing enzymes may be altered in response to development, gender, genetic factors, nutrition, pregnancy and pathophysiological conditions such as diabetes, long-term alcohol consumption, inflammation, protein-calorie malnutrition. Although the mechanisms by which xenobiotics regulate drug metabolizing enzymes have been intensively studied, relatively less is known regarding the cellular mechanisms by which drug metabolizing enzymes are regulated in response to endogenous factors such as hormones, growth factors and cytokines. Recent findings, however, have revealed that hormones, growth factors and cytokines/chemokines play an important role in the regulation of drug metabolizing enzyme expression. Furthermore, several of the cellular signaling pathways involved in hormone- and growth factor-mediated regulation of drug metabolizing enzymes have been identified. The mechanism(s) by which the signaling pathway kinases and phosphatases regulate gene expression in response to agonists are being actively examined. In this review, an overview of hepatic expression of drug metabolizing enzyme in diabetes will be described.

1. Role of liver in glucose homeostasis and insulin signaling pathways

Diabetes is associated with a high risk of atherosclerosis and kidney, nerve, and tissue damage. Also a higher incidence of hepatic disease including hepatic cancer and non-alcoholic hepatitis has been reported to be associated with diabetes (Cherrington, 1999). Liver plays an important role in regulation of metabolic homeostasis and is one of major organ response to insulin and glucagon. Hepatic insulin level and cellular responsiveness are altered in diabetes. It is well established that, regardless of the degree of muscle insulin resistance, glucose levels in diabetic and non-diabetic individuals are determined by the rate of hepatic glucose production, which in turn is

regulated by insulin. Disruption of insulin action in liver by tissue-specific knockout of the insulin receptor leads to severe glucose intolerance and resistance to the blood glucose-lowering effect of insulin. This provides evidence of a direct role of liver in postprandial glucose homeostasis, and suggests that a considerable portion of the decrease in blood glucose following insulin administration is due to a suppression of hepatic glucose production rather than an increase in muscle glucose uptake.

Insulin receptor mediates the numerous and varied biological functions of insulin. The insulin receptor belongs to the large family of receptor tyrosine kinase (RTK) cell surface receptors which possess intrinsic tyrosine kinase activity (Kim and Novak, 2007). Upon binding of corresponding agonist, this receptor undergoes autophosphorylation of tyrosine residues in the cytoplasmic tails and initiates a complex series of intracellular signaling cascades that ultimately results in diverse cellular responses. Insulin stimulates the recruitment of a family of lipid kinases known as class I phosphatidylinositol 3-kinases (PI3Ks) to the plasma membrane. There, the PI3Ks phosphorylate the glycerophospholipid phosphatidylinositol (PI) 4,5-bisphosphate (PI(4,5)P₂) at the D-3 position of the inositol ring, converting it to PI 3,4,5-triphosphate (PI(3,4,5)P₃). Recent evidence indicates that the 3-phosphoinositide-dependent protein kinase-1 (PDK1)-mediated activation of the downstream serine/threonine protein kinase B (Akt/PKB), mammalian target of rapamycin (mTOR), atypical protein kinase C (PKC) and p70 ribosomal protein S6 kinase (p70S6 kinase) mediate many of the downstream events controlled by PI3K. Activation of insulin receptor also leads to activation of the mitogen activated protein kinase signaling cascade. Following tyrosine phosphorylation of the cytoplasmic domain of the receptor, recruitment of adaptor proteins and Ras occurs. Ras is then activated by SOS, Son-of Sevenless, a guanine nucleotide exchange factor, which converts inactive Ras-GDP to activated Ras-GTP. The small guanosine triphosphatase G-protein Ras subsequently recruits and activates Raf, which leads to a

phosphorylation signaling cascade involving recruitment and activation of the MAPKs. RTK signaling is regulated not only by a cascade of phosphorylation via protein kinases but also by dephosphorylation via tyrosine and serine/threonine phosphatases and lipid phosphatases. The growth factor receptor binding protein 2 (Grb2) is constitutively associated with the SOS through binding of the SH3 domain of Grb2 to a SOS proline-rich region.

2. Expression of drug metabolizing enzymes in diabetes

Pathophysiological conditions such as diabetes, obesity, fasting and xenobiotic exposure, including excessive alcoholic consumption, result in altered expression/activity of hepatic drug metabolizing enzymes including CYP1A, 2B, 2C11, 3A, 4A, 2E1, mEH, UDP-glucuronosyltransferase (UGT) and sulfotransferases (Rubin and Lieber, 1968; Duvaldestin *et al.*, 1975; Abernethy *et al.*, 1983; Hong *et al.*, 1987; Bellward *et al.*, 1988; Thomas *et al.*, 1989; Barnett *et al.*, 1990; Song *et al.*, 1990; Donahue *et al.*, 1991; Raucy *et al.*, 1991; Badger *et al.*, 1993; Shimojo *et al.*, 1993; Van de Wiel *et al.*, 1993; Chaudhary *et al.*, 1993; Runge-Morris and Vento 1995; Irizar *et al.*, 1995; Clarke *et al.*, 1996; Visser *et al.*, 1996; Braun *et al.*, 1998; Roe *et al.*, 1999; Kardon *et al.*, 2000; Xiong *et al.*, 2002; Kim *et al.*, 2004; Cowpland *et al.*, 2006; Yoshinari *et al.*, 2006a, b). In contrast, research on expression and activity of the glutathione S-transferases (GSTs) during diabetes are inconclusive, with both increased and decreased GST expression being reported *in vivo* (Rouer *et al.*, 1981; Agius and Gidari, 1985; Grant and Duthie, 1987; Thomas *et al.*, 1989; Mukherjee *et al.*, 1994; Raza *et al.*, 1996). The reason for this discrepancy remains unknown. However, it may, in part, be associated with competing hormonal factors *in vivo* with variations in the mechanisms of inducing diabetes, and with variations in oxidative stress, usually observed in diabetes. It has been reported that transcriptional activation of some GST genes may be associated

with changes in the redox status of the cell in conjunction with oxidative stress (Wasserman and Fahl, 1997; Kang *et al.*, 2001). In addition synthesis of glutathione (GSH), a cofactor for GST, is altered in response to pathophysiological conditions, such as diabetes, protein-calorie malnutrition and alcohol consumption, through regulation of expression of gamma-glutamylcysteine ligase which is the rate-limiting step for catalysis of GSH synthesis, and by the availability of cysteine for GSH synthesis (Yoshida *et al.*, 1995; Lu *et al.*, 1999).

Diabetes may lead to chronic non-alcoholic liver diseases including nonalcoholic steatohepatitis (NASH) that may progress to hepatic cirrhosis and hepatocellular carcinoma. An increased risk factor for development of diabetes is associated with the metabolic syndrome, which is characterized by insulin resistance (Sanyal, 2005). Diabetes is associated with a 2-3-fold increase in the risk of hepatocellular carcinoma, regardless of the presence of other major hepatocellular carcinoma risk factors (Davila *et al.*, 2005). Insulin resistance is produced by a complex interplay of genetic and environmental factors, resulting in inhibition of insulin signaling/action in peripheral tissues, such as muscle, adipose tissue and liver. The resultant disequilibrium in lipid homeostasis causes triglycerides to accumulate in the liver. An increase in oxidative stress, defined as an imbalance between the production of highly reactive molecular species and antioxidant defenses, could be one mechanism by which the nonalcoholic fatty liver develops into nonalcoholic steatohepatitis (Videla *et al.*, 2004a). Insulin resistance in type 2 diabetes, cirrhosis and other hepatic diseases result in decreased insulin signaling and diminished signaling through downstream components, such as PI3Ks, Akt, mTOR and p70S6 kinase. Induction of CYP2E1 as well as depression of antioxidant system has been observed in NASH patients (Videla *et al.*, 2004b). From a pathological point of view, CYP2E1 is considered of particular interest due to its poor coupling with NADPH-cytochrome P450 reductase, with NADPH oxidase activity generating reactive oxygen species

(Lieber *et al.*, 1997). Leclercq *et al.* (2000) showed that CYP4A10 and CYP4A14 were upregulated in Cyp2e1^{-/-} mice and served as alternative initiators of oxidative stress in NASH. These results indicate that altered expression of xenobiotic metabolizing enzyme gene plays a progressive role in hepatic diseases.

Because pathophysiological states such as diabetes result in alteration of secretion and/or cellular response of hormone, including insulin, glucagon and growth hormone, these hormones may be etiologic factors affecting the expression of hepatic drug-metabolizing enzymes. It has been reported that insulin or growth hormone administration to chemically-induced or spontaneously diabetic rats restores drug-metabolizing enzyme activity and expression to control values (Dong *et al.*, 1988; Yamazoe *et al.*, 1989a, b; Thomas *et al.*, 1989; Donahue *et al.*, 1991; Tunon *et al.*, 1991; Runge-Morris and Vento 1995). Our laboratory and others have demonstrated that the activity and/or expression of hepatic drug metabolizing enzymes, such as CYP2B, CYP2E1, CYP2C11, CYP-2A5, GST alpha class, GST pi class, UGT and mEH are differentially regulated in response to insulin and glucagon (De Waziers *et al.*, 1995; Constantopoulos and Matsaniotis, 1978; Woodcroft *et al.*, 2002; Kim *et al.*, 2003a, b). These results indicate that changes in drug-metabolizing enzyme mRNA or protein levels observed in pathophysiological conditions, such as diabetes or inflammation, may be attributed to alterations in the efficiency of agonist activation of intracellular signaling pathways and components. Thus, it is of interest to identify which cellular signaling pathways are involved in regulating the expression of these genes in response to hormones and cytokines.

CONCLUSION

Endogenous factors including hormones, growth factors and cytokines play an important role in regulating drug metabolizing enzyme gene and protein expression in normal physiological conditions and

well as in pathophysiological conditions. These results warrant studies for determining what signaling pathways and components are involved in endogenous factor-mediated regulation of drug metabolizing enzyme expression. Studies of cellular signal transduction events elicited by hormones and cytokines yield important insights into the regulation of drug metabolism in pathophysiological conditions. Consequently, understanding the role of signaling pathways and components in the regulation of xenobiotic metabolizing gene expression will advance our understanding of differences in xenobiotic metabolism with diseases, as well as the consequent effects on efficacy and safety of many therapeutics. In addition, understanding the signaling pathways and components that may regulate xenobiotic metabolizing enzyme gene expression will assist in understanding the progressive risk of an altered phenotype and xenobiotic metabolism and toxicity in the treatment of disease.

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