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Sex-, age-, and race/ethnicity-dependent variations in drug-processing and NRF2-regulated genes in human livers

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Abbreviations: AHR, aryl hydrocarbon receptor; CAR, constitutive androstane receptor; EH1, epoxide hydrolase 1; FXR, farnesoid X receptor; GCLC, glutamate-cysteine ligase catalytic subunit; GLRX, glutaredoxin; KEAP1, Kelch-like ECH-associated protein 1; LXR α , liver X receptor alpha; NQO1, NAD(P)H-quinone oxidoreductase 1; NRF2, nuclear factor-erythroid 2 related factor 2; PPAR α , peroxisome proliferator-activated receptor α ; PRDX1, peroxiredoxin-1; RXR α , retinoid X receptor alpha; SHP, small heterodimer partner; SOD1, superoxide dismutase 1; TXN, thioredoxin (TXN) and TXNRD1, thioredoxin reductase-1 (TXNRD1).

Abstract

Individual variations in xenobiotic metabolism affect the sensitivity to diseases. In this study, the impacts of sex, age and race/ethnicity on drug-processing genes and NRF2 genes in human livers were examined via QuantiGene multiplex suspension array (226 samples) and qPCR (247 samples) to profile the expression of nuclear receptors, cytochrome P450s, conjugation enzymes, transporters, bile acid metabolism and NRF2-regulated genes. Sex differences were found in expression of about half of the genes, but in general the differences were not large. For example, females had higher transcript levels of *CAT*, *GCLC*, *HO-1*, *KEAP1*, *SOD1*, and *TXNRD1* compared to males via qPCR. There were no apparent differences due to age except children had higher *GCLM* and elderly had higher *MRP3*. African Americans had lower expression of *FXR* but higher expression of *HO-1*, Caucasians had higher expression of *OAT2*, and Hispanics had higher expression of *FXR*, *SULT2A1*, *SHP*, and *BSEP*. An examination of 34 diseased and control human liver samples showed that compared to disease-free livers, fibrotic livers had higher *NQO1*, *GCLC*, *GCLM* and *NRF2*; hepatocellular carcinoma had higher transcript levels of *NQO1* and *KEAP1*, and steatotic livers had lower *GCLC*, *GCLM* and *HO-1* expression. In summary, in drug-processing gene and NRF2 genes, sex differences were the major findings, and there were no apparent age-differences and race/ethnicity differences occurred for a few genes. These descriptive findings could add to our understanding of the sex-, age-, and race/ethnicity -dependent differences in drug-processing genes, as well as NRF2 genes in normal and diseased human livers.

Significance statement

In human liver drug-processing and NRF2 genes, sex differences were the main finding. There were no apparent differences due to age, except children had higher *GCLM* and elderly had higher *MRP3*. African Americans had lower expression of *FXR* but higher expression of *HO-1*, Caucasians had higher expression of *OAT2*, and Hispanics had higher expression of *FXR*, *SHP*, *SULT2A1* and *BSEP*.

Keywords: Drug-Processing genes; NRF2/ARE signaling; Human livers; Sex; Age; Race/ethnicity; Diseased liver samples

Introduction

Individual variations in xenobiotic metabolism can affect the effectiveness of drugs in various diseases. Drug processing genes can include uptake transporters, phase-I and phase-II enzymes, as well as efflux transporters that are responsible for the absorption, distribution, metabolism, and excretion of xenobiotics. The constitutive and/or inducible expression of these drug processing genes is regulated by nuclear receptors and other transcription factors (Aleksunes and Klaassen, 2012; Cui and Klaassen, 2016). Among sex-, age-, and race/ethnicity -differences in physiological functions, the adaptive responses mediated via the NRF2/ARE antioxidant pathway are of great interest (Pomatto et al., 2018).

Nuclear receptor-mediated regulation of xenobiotic-processing genes involves the aryl hydrocarbon receptor (*AHR*), constitutive androstane receptor (*CAR*, *NR1I3*), pregnane X receptor (*PXR*, *NR1I2*), and peroxisome proliferator-activated receptor α (*PPAR α* , *NR1C1*) (Aleksunes and Klaassen, 2012). Liver X receptor alpha (*LXR α* , *NR1H3*), retinoid X receptor alpha (*RXR α* , *NR2B1*), hepatocyte nuclear factors (*HNF1 α* and *HNF4 α*) also participate in the regulation of phase-1, phase-2, and transporters (Aleksunes et al., 2009).

Farnesoid X receptor (*FXR*, *NR1H4*) and small heterodimer partner (*SHP*, *NROB2*) regulate bile acid homeostasis (Cui et al., 2012; Liu et al., 2014). FXR signaling and gut microbiota have been linked to fatty liver disease and hepatocellular carcinoma (Klaassen and Cui, 2015; Chiang and Ferrell, 2018). Bile acid receptors (FXR, SHP and TGR5) regulate not only bile acid synthesis and transport but also energy metabolism (Klaassen and Cui, 2015). Alteration of bile acid homeostasis contributes to cholestatic liver diseases, inflammatory diseases in the digestive system, obesity, and diabetes (Chiang and Ferrell, 2018).

Transporters influence the disposition of xenobiotics resulting in individual variations in the accumulation of xenobiotics in the body. The hepatic uptake transporters include organic anion transporting *peptides* *OATP1A2* (*SLCO1A2*), *OATP1B1*, *OATP1B3* and *OATP2B1*; while the main efflux transporters are multidrug

resistance protein families *MRP2* (*ABCC2*), *MRP3*, and *MRP4*. Transporters of the solute carrier family (SLC) comprise a variety of proteins, including organic cation transporter *OCT1* (*SLC22A1*), organic cation/carnitine transporters *OCTN1* (*SLC22A5*), organic anion transporter *OAT2* (*SLC22A7*), multidrug and toxin extrusion transporter *MATE1* (*SLC47A1*) and equilibrative nucleoside transporter *ENT1* (*SLC29A1*). The ATP-binding cassette superfamily, such as *ABCA1*, *ABCG5*, *ABCG8* and *ATP8B1*, are responsible for the unidirectional export of endogenous and exogenous substances (Klaassen and Aleksunes, 2010). The function of hepatic transport systems can be affected by interspecies differences and inter-individual variability (polymorphism) and have been altered with the therapeutic effects and toxicity of drugs (Pan, 2019).

Nuclear factor erythroid 2-related factor 2 (NRF2) regulates the antioxidant system of cells (Klaassen and Reisman, 2010). The NRF2-regulated redox homeostasis includes the glutathione system such as glutamate-cysteine ligase, catalytic and modifiers subunits (*GCLC*, *GCLM*), glutathione reductase (*GSR*), and glutathione peroxidase (*GPX1*), as well as various antioxidant enzymes such as catalase (*CAT*), superoxide dismutase (*SOD1*), heme oxygenase 1 (*HO-1*) to maintain cellular redox balance (Truong et al., 2018). NAD(P)H:quinone oxidoreductase 1 (*NQO1*), peroxidase (*PRDX1*) (Kobayashi and Yamamoto, 2006), glutaredoxin (*GLRX*) (Holmgren et al., 2005), thioredoxin and thioredoxin reductase-1 (*TXN*, *TXNRD1*) (Lu and Holmgren, 2014), and epoxide hydrolase 1 (*EH1*) (Cornejo et al., 2013) play important roles in cellular detoxifying systems, and are also under NRF2 regulation. NRF2 activation induces a number of phase-II drug metabolizing enzymes directly and metabolic activities downstream of AhR (Yeager et al., 2009; Wu et al., 2012), or CAR activation (Rooney et al., 2019). The non-enzymatic thiol-rich protein metallothionein and its regulators (MTF-1, MT-1A, MT-2A) play important roles in heavy metal detoxification (Klaassen et al., 1999), and are also under influence of Nrf2 (Gu et al., 2017). Thus, the Nrf2/ARE signaling is considered as a primary defense system against xenobiotic insults.

In order to better understand sex-, age- and race/ethnicity-dependent differences in drug-processing and NRF2 genes, this study utilized 247 human liver samples to

profile the constitutive expression of nuclear receptors, cytochrome P450, as well as bile acid metabolism, transporter, and NRF2-regulated genes using QuantiGene multiplex suspension array and real-time RT-qPCR. An additional 34 samples from diseased patients were examined for the expression of NRF2-regulated genes in steatosis, fibrosis and hepatocellular carcinoma (HCC) via real-time RT-PCR.

Materials and Methods

Normal liver sample demographics

Normal human liver samples (n = 247) were purchased from Xenotech LCC (Lenexa, KS, USA). The demographics are shown in Table 1 including sex (42.5% are females), age (0-86 years old), and race/ethnicity (8.09% African Americans, 7.28% Hispanics, 83.0% Caucasians). This study received Institutional Review Board exemption status by the University of Kansas Medical Center Human Subject Committee because the specimens were obtained commercially and not identified to the authors of the study.

Diseased liver samples from KU Liver Bank

Thirty-four diseased human liver samples (8 fibrosis, 8 steatosis, 8 HCC, and 10 normal controls) were obtained from the KU Liver Bank (University of Kansas Medical Center, Kansas City, KS). All liver samples were provided with the approval of the Institutional Review Board.

QuantiGene multiplex suspension array

Multiplex suspension array was performed on 226 human sample analysis (excluding children samples) as described (Renaud et al., 2011). Total RNA was isolated using TRIzol reagent (Invitrogen, Carlsbad, CA, USA). RNA quality was determined by the 260/280 ratio (>1.8) and by formaldehyde-agarose gel electrophoresis for visualization of 18S and 28S rRNA bands. Individual bead-based oligonucleotide probe sets specific for each human gene examined were developed by Panomics, Inc (Fremont, CA, USA). Glyceraldehyde 3-phosphate dehydrogenase (*GAPDH*) mRNA expression was used as an internal control. Samples were analyzed using a Bio-Plex System array reader with Luminex 100 xMAP technology (multi-analyte profiling beads). Briefly, 3 µg of total RNA was incubated overnight at 53°C with X-MAP beads containing oligonucleotide capture probes, label extenders, and blockers. The beads and bound target RNA were washed and subsequently incubated with streptavidin-conjugated R-phycoerythrin (Affymetrix/Panomics, Santa Clara CA).

Fluorescence was analyzed using a Bio-Plex reader and analyzed with Bio-Plex Data Manager Software (BioRad, Hercules, CA). All data were standardized to the internal control *GAPDH*.

Real-time RT-PCR analysis.

Total RNA was extracted with Trizol and purified with RNeasy Mini Kit (Qiagen, Valencia, CA). RNA quality and quantity were determined via spectrophotometry, with 260/280 ratio > 1.8. One µg of total RNA was reverse transcribed with Multiscript reverse transcriptase using High Capacity RT kits from Applied Biosystems (Foster City, CA). Primers were designed with Primer3 software (version 4). The Power SYBR Green Master Mix (Applied Biosystems, Foster City, CA, USA) was used for real-time RT-PCR analysis. Differences in gene expression between groups were calculated using cycle threshold (Ct) values which were calculated by the $2^{-\Delta\Delta Ct}$ method and normalized with *GAPDH* and *RPL13A* of the same sample (averaged).

Principle Component Analysis

Principle Component Analysis (PCA) was performed via Partek Flow (Partek Inc., St. Louis, MO). The qPCR results of 14 genes in 247 samples were imported into the Partek Flow Server with sex, age, and race as contributors, respectively. The feature contributors were set equally, and normalization were set by log base, and images of PCA were generated to visualize the distribution differences.

Statistical analysis

Data were expressed as relative mRNA levels (% of housekeeping genes) and calculated as mean ± SEM. One-way ANOVA was used for statistical analysis via SigmaPlot v.14. Dunn's multiple range test was used for comparisons. The significance level was set at $p < 0.05$ in all cases.

3. Results

3.1. QuantiGene multiplex suspension array analysis

3.1.1 Nuclear receptor and drug metabolism genes

Figure 1 shows sex-, age- and race/ethnicity -dependent expression of nuclear receptor, phase-1 and phase-2 metabolism genes. Compared to males, females had lower expression of *AHR*, *CYP1A2*, *CAR*, *FXR (NR1I2)*, *PPAR α* , *LRH1 (NR5A2)*, *LXR α (NR1H3)*, *RXR α (NR2B1)*, *HNF1 α* , *HNF4 α* , and *CPT1A* except for higher expression of *CREBBP* and *ME1*. There were no differences in the expression of *CYP2B6*, *CYP3A4*, *PAPPSS2*, *CEBPb* and *FABP1* between sexes. There were no age differences. African Americans had lower, while Hispanics had higher *FXR* expression as compared to Caucasians. Hispanics also had higher expression of *SULT2A1* compared to Caucasians.

Insert Figure 1

3.1.2 Bile acid metabolism and homeostasis genes

Figure 2 shows sex-, age- and race/ethnicity-dependent expression of genes involved in bile acid metabolism and homeostasis. Females had lower expression of *CYP27A1*, *CYP7B1*, *CYP39A1*, *FXR (NR1H4)*, *SHP (NROB2)*, and *FGF19* than males; There were no differences in the expression of *CYP7A1*, *CYP8B1*, *FGFR4*, *BSEP (ABCB11)*, *FATP5 (SLC27A5)*, *TAUT (SLC6A6)*, *BAAT* and *APEX1* between sexes. There were no age-differences due to age for the expression of bile acid metabolism genes. Compared to Caucasians, Hispanics had higher expression of *SHP* and *BSEP*.

Insert Figure 2

3.1.3 Transporter genes

Figure 3 shows sex-, age- and race/ethnicity-dependent expression of transporter genes. Males had lower expression of *OATP1B1 (SLCO1A2)*, *OAT2 (SLC22A7)*, *OCTN2 (SLC22A5)*, *MRP4 (ABCC4)*, *MDR1 (ABCB1)*, *MDR2/3 (ABCB4)*, *ABCG8*, *ABCA1*, *MATE1 (SLC47A1)*, and *ENT1 (SLC29A1)* than females; There were no

differences in the expression of *OATP1B3* (*SLCO1B3*), *OATP2B1* (*SLCO2B1*), *OCT1* (*SLC22A1*), *MRP2* (*ABCC2*), *MRP3* (*ABCC3*), *MRP6* (*ABCC6*), *ABCG5*, *ATP8B1*, and *BCRP* (*ABCG2*) between the sexes. There were no differences between sexes in expression of transporter genes except elderly had higher expression of *MRP3*. Compared to Caucasians, both African Americans and Hispanics had lower expression of *OAT2*.

Insert Figure 3

3.1.4 NRF2 targeted genes

Figure 4 shows a heatmap of the relative transcript levels of the 21 NRF2-regulated genes examined by the QuantiGene multiplex suspension array and normalized with *GAPDH* on the plate. The lowest expression was *NQO1*, and the highest expression was *PRDX1*. The data was sorted by age: adult (21-59 years old), elderly (>60 years old) for females (upper panel) and males (lower panel). Expression levels in females appeared to be greater compared to males. Females had higher expression of *KEAP1*, *GSR*, *GCLC*, *GPX1*, *NQO2*, *CAT*, *EH1*, *GLRX*, *H6PD*, *HO-1*, *OGG1*, *PRDX1*, *SLC3A1*, *SLC3A9*, *CRCC2*, *TXNRD1*, and *TXN* (asterisk label by ANOVA $p < 0.05$), and there were no differences in expression between sexes for *GCLM* and *NQO1*. Males had higher expression of *NRF2*. There were no age differences in NRF2 genes, as determined by one-way ANOVA. The expressions of some of the genes were subsequently verified using RT-qPCR.

Insert Figure 4

3.2 Real-time RT-PCR analyses of NRF2 genes

3.2.1 One-way ANOVA comparisons

Sex-differences in the expression of NRF2 relevant genes via qPCR are shown in Figure 5A. Similar to QuantiGene multiplex suspension array (Figure 4), females had higher expression of 6 of 14 genes examined than males: *KEAP1* (18.5 vs 15.8), *GCLC* (54.4 vs 41.5), *HO-1* (68.8 vs 50.0), *CAT* (133 vs 90.6), *SOD1* (301 vs 125), and

TXNRD1 (133 vs 86.2). There were no statistical differences in expression between sexes for *NRF2*, *GCLM*, *MT-1A*, *MT-2A*, *MTF-1*, and *GSTP1*.

Age differences in NRF2-regulated gene expression via qPCR are shown in Figure 5B. Similar to QuantiGene multiplex suspension array (Figure 4), there were no differences among age groups, except for the slightly higher *GCLM* in children as compared to adult levels (34.1 vs 24.8 of housekeeping genes), while no significant differences were observed in the expression of other genes.

Race/ethnic differences in NRF2 regulated gene expression via qPCR are shown in Figure 5C. There were no differences in NRF2-regulated gene expression noted among race/ethnic groups, except a slightly higher expression of *HO-1* (82 vs 57) in African Americans as compared to Caucasians.

Insert Figure 5

3.2.2. Principle Component Analysis

The 247 human samples were then analyzed by Principle Component Analysis (PCA) (Figure 6). The PCA value is 51.26%, with PC1 = 27.56%, PC2 = 13.80%, and PC3 = 9.91%. Distribution by sex, age, race/ethnicity is shown in Fig. 6A, 6B, and 6C, respectively. There were more outliers in the female group. There was no clear separation between any of the groups.

Insert Figure 6

3.3. Nrf2 regulated gene expression in diseased liver samples

Diseased liver samples were examined using RT-qPCR for the expression of 7 Nrf2-related genes (Figure 7). In steatosis liver samples, a lower expression of *GCLC* (50%), *GCLM* (15%), and *HO-1* (5%) was observed. In 8 HCC samples, there was a higher expression of *NQO1* (2.8-fold), and *KEAP1* (1.2-fold), and a lower expression of *HO-1* (20%). In liver fibrosis samples, a higher expression of *NRF2* (3.5-fold), *NQO1* (5.2-fold), *GCLC* (4.3-fold) and *KEAP1* (11-fold) was observed; while the expression of *PRDX1* was lower (27%) compared to 10 normal liver samples.

Insert Figure 7

Discussion

The present study utilized 247 normal human liver samples to profile drug-processing genes and NRF2-regulated genes to identify differences in expression with regard to sex, age, and race/ethnicity. Sex differences were found in the expression of about half of the genes. There were no apparent differences due to age, except children had higher *GCLM* and elderly had higher *MRP3*. African Americans had lower expression of *FXR* but higher expression of *HO-1*, Caucasians had higher expression of *OAT2*, and Hispanics had higher expression of *FXR*, *SULT2A1*, *SHP*, and *BSEP*. The study on 34 disease-related human liver samples showed alterations in NRF2 gene expression with disease: fibrotic livers had higher *NQO1*, *GCLC*, *GCLM* and *NRF2*; HCC had higher *NQO1* and *KEAP1*; and steatotic livers had lower *GCLC*, *GCLM* and *HO-1*. The information obtained, though descriptive, adds to our understanding of individual variation.

Sex-differences in drug-processing and NRF2 genes

In the present study, sex-differences in drug processing genes and NRF2 genes were major findings. Sex-differences in pharmacokinetics and pharmacodynamics of many drugs contribute to individual differences in drug efficacy and toxicity (Waxman and Holloway, 2009). The sex-dependent variations in humans are much less as compared to rodents (rats and mice) (Waxman and O'Connor, 2006).

Males had higher expression of *AHR*, *CYP1A2*, *CAR*, *FXR*, *PPAR α* , *LRH1*, *LXR α* , *RXR α* , *HNF1 α* , *HNF4 α* , and *CPT1A*, while females had higher expression of *CREBBP* and *ME1* (Fig. 1). *RXR α* is an obligate partner for many nuclear receptors and considered a master regulator of hepatic gene expression. *RXR α* binding shows more unique genes in males than in females, with sex-dimorphism, for example, *Cyp7b1* is male-dominant, while *Me1* is female-dominant (Kosters et al., 2013). In human liver microsomes, there were no significant differences in 10 CYP activities between sexes

except a higher CYP1A2 in males, however, in cytopreserved human hepatocytes, higher CYP3A4 mRNA was observed (Parkinson et al., 2004). Sex dimorphism in CYP2B6 activity was not evident, but CYP2B6 polymorphisms are associated with CYP2B6 activity (Zanger et al., 2005; Ilic et al., 2013). In human liver tissues, males also had higher expression of *CYP1A2*, *HNF4a* and *START5b* (Waxman and Holloway, 2009).

In bile acid homeostasis genes, males had higher expression of *CYP27A1*, *CYP7B1*, *CYP39A1*, *FXR*, *SHP*, and *FGF19* (Fig 2). Some of these sex-dimorphism is in agreement with the literature, e.g., males had higher expression of *CYP7B1* (Leuenberger et al., 2009), while some are in contradiction with the literature, e.g., females had higher, not lower expression of *CYP27A1* and *CYP39A1* (Yang et al., 2012); the discrepancy requires further studies.

In transporters, females had higher *OATP1B1*, *OAT2*, *OCTN2*, *MRP4*, *MDR1*, *MDR2/3*, *ABCG8*, *ABCA1*, *MATE1*, and *ENT* (Fig. 3). In one study, *OATP1B1* expression was higher in females (Yang et al., 2012), but in another study, there were no sex differences in *OATP1B1*, *OATP1B3*, and *OATP2B1* proteins (Badée et al., 2015). Female rats have higher expression of *Mrp3* (Fusco et al., 2020). In the liver of *Oatp1a4*-null mice, females had higher expression of *Mrp4*, *Mdr1a*, *Mdr1b*, and *Abcg5* (Zhang et al., 2013). In a review on sex-differences in transporters, female mice have higher hepatic expression of *Oatp1a4*, *Oatp2b1*, *Mrp3*, and *Mate1* (Klaassen and Aleksunes, 2010). Overall, women and female rodents appeared to have higher transporter gene expression than males.

In the present study, females had higher expression of most of NRF2-regulated genes (*KEAP1*, *GSR*, *GCLC*, *GPX1*, *NQO2*, *CAT*, *EH1*, *GLRX*, *G6PD*, *HO-1*, *MT-1A*, *OGG1*, *PROX1*, *SLC3A1*, *SLC7A9*, *CRCC2*, *SOD*, *TXNRD1* and *TXN*) (Fig. 4 and 5). In a large mouse microarray compendium (86) analysis, the livers of female mice exhibited higher NRF2 activation than males under basal and chemical-treated conditions (Rooney et al., 2018). The cysteine transporter SLC3A1, important for glutathione synthesis, is also female-dominant in mice and humans (Yang et al., 2012; Uno et al.,

2017; Wu et al., 2020). Deficiency in NRF2 renders female NRF2-null mice to lower antioxidative and detoxifying enzyme genes than males (Pellegrini et al., 2017).

Age-differences in drug-processing and NRF2 genes

The ontogeny of drug-processing and NRF2 genes is important for adequate interpretation of the findings during development (de Zwart et al., 2008; Wu et al., 2019), that impacts drug efficacy and the risk of adverse events in the neonate and young child (Hines, 2013). In the present study, the QuantiGene multiplex suspension array, did not include children, and only the qPCR on NRF2 gene study included a children group (13 sample), and a higher expression of HO-1 was found in the children group. HO-1 is important in pediatric nonalcoholic fatty liver disease (NAFLD), and obese children with longer allelic frequencies of (GT)_n repeats of HO-1 are more susceptible to NAFLD (Chang et al., 2015).

Elderly are more susceptible to therapeutic failure and adverse drug reactions (Cardelli et al., 2012). However, the aging liver appears to preserve its function relatively well (Anantharaju et al., 2002). In the present study, no apparent differences in drug-processing and NRF2 genes between adults and elderly were evident, except a slightly higher expression of GCLM in the elderly. GCLM expression is reported to be 20-80% higher with liver diseases (Cheng et al., 2015).

Race/ethnicity-differences in drug-processing and NRF2 genes

PXR variants greatly affect drug metabolism and protein-protein interactions (Brewer and Chen, 2016). The HIV protease inhibitor atazanavir clearance is 35% slower in African Americans due to polymorphisms of PXR and CYP3A5 (Kile et al., 2012). coinciding with lower PXR in African Americans (Fig. 1). SULT 2A1 catalyzes DHEA sulfation in the adrenal cortex. Polymorphisms in SULT2A1 in African Americans (AA) are associated with decreased activity and expression (Wilborn et al., 2006), but little is known about Hispanics.

Mutations in SHP are associated with mild obesity in childhood and increased susceptibility of Japanese to type 2 diabetes later in life (Enya et al., 2008). In

Caucasians, BSEP and MDR3 genetic variations play a role in the pathogenesis of primary biliary cirrhosis (PBC) and primary sclerosing cholangitis (PSC) (Pauli-Magnus et al., 2004). The significance of higher expression of SHP and BSEP in the Hispanic group in the present study needs further investigation.

OAT2 mRNA is highly expressed in the liver to transport organic anions and is reregulated by HNF1 α and HNF4 α , as well as by CAR, PXR and NRF2 activators (Burckhardt, 2012). In the present study, Caucasians had higher expression of OAT2 than African American and Hispanics. A microsatellite polymorphism in the HO-1 promoter in Austrians is associated with a risk for melanoma (Okamoto et al., 2006). In the present study, African Americans had higher expression of HO-1. The significance for these race differences requires further investigation.

It is known that NRF2 polymorphisms can affect the susceptibility of humans to various diseases. For example, lower expression of NRF2 was found to be associated with ulcerative colitis in a Japanese population (Arisawa et al., 2008). A lower expression of NRF2 is associated with vitiligo in a Chinese Han population (Guan et al., 2008), which could be associated with oxidative stress. Compared to Caucasians, Asians have lower NQO1 activity in the liver, and overweight children have higher NQO1 (Rougée et al., 2016), suggesting obesity may increase NQO1. Genetic variations in NRF2, NQO1, HO-1, and MT are associated with the severity of coronary artery disease (Sarutipai boon et al., 2020).

NRF2 gene expression in liver diseases

Compared to disease-free liver samples, we observed a higher expression of *NRF2*, *NQO1*, *GCLC* and *KEAP1* and a lower expression of *PRDX1* in fibrotic liver samples, a higher expression of *NQO1* and *KEAP1* in HCC samples, but a lower expression of *GCLC*, *GCLM* and *HO-1* was evident in steatotic liver samples. These results are largely in agreement with the findings in end stage human disease samples, in that *NQO1* and *KEAP1* were increased in the end-stage liver diseases, and *GCLC*, *HO-1* and *PRDX1* were lower in HCC compared to surrounding liver tissue (Cheng et al., 2015). In end-stage human liver diseases, the ratio of Nrf2/Keap1 is decreased

(Kurzawski et al., 2012), consistent with the increased *KEAP1* expression in the present observations. In HCC specimens, expression of *KEAP1* can be increased (55%) or decreased (45%) that are often associated with *NRF2* levels (Chen et al., 2016). *KEAP1* can also act as a therapeutic target, its inactivation could lead to activation of the *NRF2* pathways to reduce oxidative stress during chemotherapy (Zheng et al., 2019), but sustained *NRF2* overexpression, especially *NQO1* overexpression, is associated with poor prognosis of HCC (Eichenmüller et al., 2014). The downregulation of *GCLC*, except for liver fibrosis, is also in agreement with end-stage liver diseases (Kurzawski et al., 2012), and in HCC (Cheng et al., 2015). The Keap1/Nrf2 is a cellular protective system, thus it not only protects normal cells, but also facilitates HCC progression and aggressiveness (Raghunath et al., 2018). Thus, upregulation of *NQO1* and *KEAP1*, and decreases in *GCLC* might be associated with liver diseases, but their changes are dependent on the type and the stage of the liver diseases. Liver fibrosis seems to be associated with more *NRF2*-dependent gene expression changes.

In summary, this study profiled the expression of drug-processing and *NRF2*-regulated genes, based on the sex, age, and race/ethnicity differences. Diseased human liver samples exhibited changes in *NRF2*-regulated gene expression; these data provide additional information that adds to our understanding of individual variation in drug-processing genes and the *NRF2*/ARE antioxidant pathway.

Author Contributions

Participated in research design: Klaassen C.D, Liu J.,

Conducted experiments: Liu J, Lu YF

Contributed new reagents or analytic tools: Klaassen CD

Performed data analysis: Liu J., Cui JY, Corton JC

Wrote or contributed to the writing of the manuscript: Liu J, Cui JY, Corton JC, Klaassen CD

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Footnotes

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Legends for Figures

Figure 1. Sex-, age-, and race/ethnicity-differences in nuclear receptor and drug metabolism genes. Total liver RNA was isolated from 226 human livers and subjected to QuantiGene multiplex suspension arrays. The results were normalized with *GAPDH* on the plate. A, Sex; B, Age and C, Race/ethnicity differences. The values of *#CREBBP* and *#ME1* were multiplied 10 to allow the expression to be visible. Data are mean \pm SEM, *Significantly different from Male, Adult, and Caucasians, respectively by one-way ANOVA at $p < 0.05$.

Figure 2. Sex-, age-, and race/ethnicity-differences in bile acid metabolism genes. Total liver RNA was isolated from 226 human livers and subjected to QuantiGene multiplex suspension arrays. The results were normalized with *GAPDH* on the plate. A, Sex; B, Age and C, Race/ethnicity differences. The values of *#CYP7A1*, *#FGF19*, and *#TAUT* were multiplied 10 to allow the expression to be visible. Data are mean \pm SEM, *Significantly different from Male, Adult, and Caucasians, respectively by one-way ANOVA at $p < 0.05$.

Figure 3. Sex-, age-, and race/ethnicity-differences in transporter genes. Total liver RNA was isolated from 226 human livers and subjected to QuantiGene multiplex suspension arrays. The results were normalized with *GAPDH* on the plate. A, Sex; B, Age and C, Race/ethnicity differences. The values of *#OATP1B1* and *#MRP4* were multiplied 10 to allow the expression to be visible. Data are mean \pm SEM, *Significantly different from Male, Adult, and Caucasians, respectively by one-way ANOVA at $p < 0.05$.

Figure 4. NRF2-regulated gene expression in human livers. Total RNA was extracted from 226 human livers (no children samples) and subjected to QuantiGene multiplex suspension array for 21 NRF2-regulated genes. The 1-100 scale indicates that the more abundant the transcript level the deeper the color. The values of *#KEAP1*, *#NQO1*, *#OGG1*, *#SLC3A1*, *#SLC7A9* and *#XRCC2* were multiplied 10-fold to allow the expression to be comparable to the other genes. Data are mean \pm SEM, *Significantly different from Male by one-way ANOVA at $p < 0.05$.

Figure 5. Sex-, age- and race/ethnicity-differences in NRF2-regulated gene expression. Total liver RNA was isolated and purified from 247 normal human livers, and the expression of specific genes of interest was examined with specific primers via RT-qPCR compared to housekeeping genes (*GAPDH* and *β -actin*). A, Sex; B, Age and C, Race/ethnicity differences. The values of *#NQO1* and *#MTF-1* were multiplied 10 to allow the expression to be visible. Data are mean \pm SEM, *Significantly different from Male, Adult, and Caucasians, respectively by one-way ANOVA at $p < 0.05$.

Figure 6. The Principal Component Analysis of the distribution of 247 human liver samples labeled by (A) Sex (Female, Male), (B) Age (Children, Adult, Elderly), and (C) Race (African Americans, Asia American, Caucasian, Hispanic).

Figure 7. Expression of NRF2-regulated genes in diseased liver samples. Sample sizes were steatosis (n = 8), fibrosis (n = 8), and HCC (n = 8). The expression of specific genes of interest was examined with specific primers via RT-qPCR, compared to housekeeping genes. *Significantly different from normal liver samples (n=10), $p < 0.05$ via one-way ANOVA analysis followed by Dunn's multiple range test.

Table 1. Sample demographics

Sex	Male	n = 142
	Female	n = 105

Age	Children (0-18)	n = 13
	Adult (19-59)	n = 170
	Elderly (60 and over)	n = 63

Race/ Ethnicity	African American	n = 20
	Asian American	n = 4
	Caucasian	n = 205
	Hispanic	n = 18

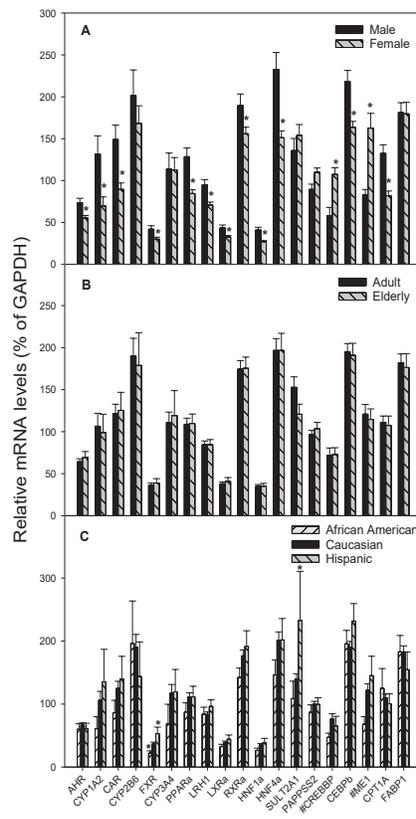


Figure 1

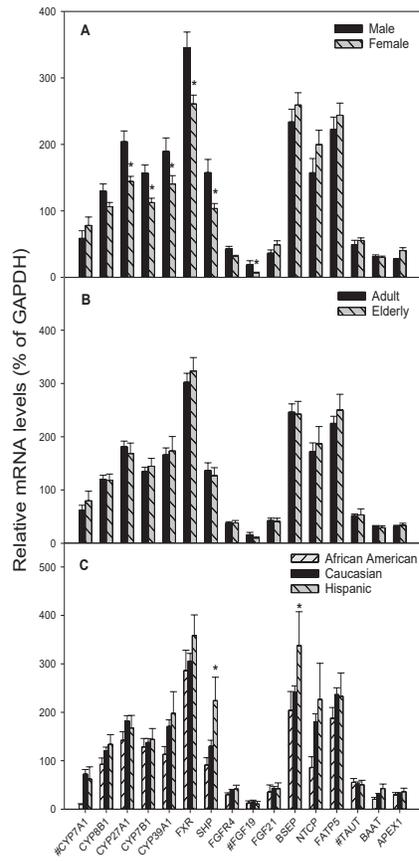


Figure 2

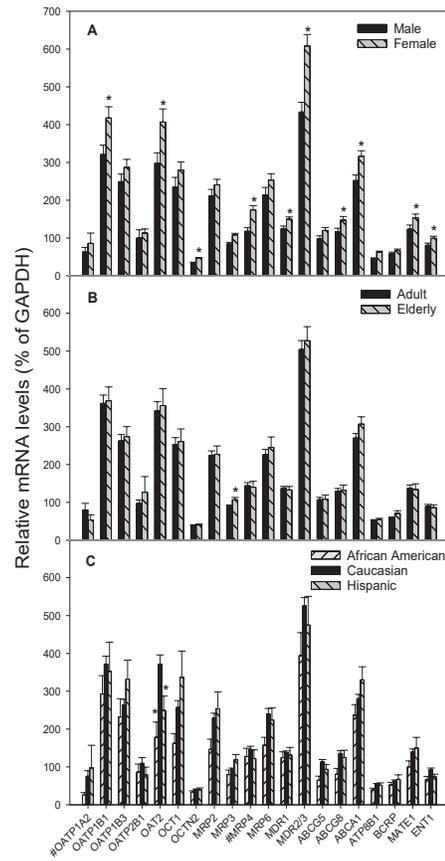


Figure 3

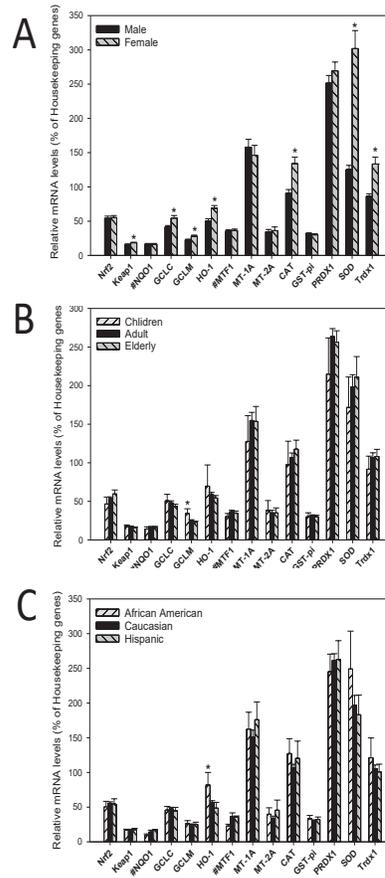


Figure 5

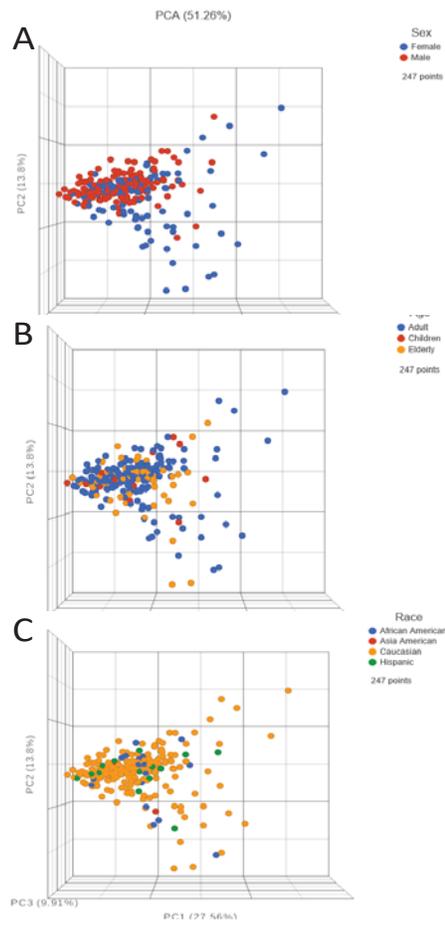


Figure 6

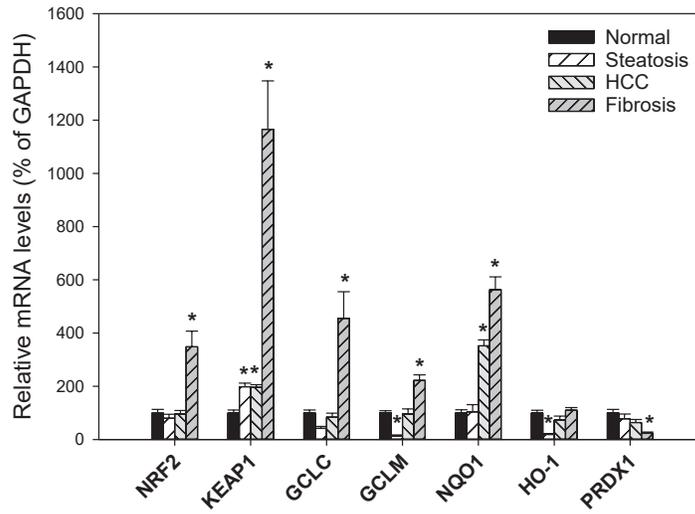


Figure 7