Age-associated changes of cytochrome P450 and related phase-2 gene/proteins in livers of rats

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Cytochrome P450s (CYPs) are phase-I metabolic enzymes playing important roles in drug metabolism, dietary chemicals and endogenous molecules. Age is a key factor influencing P450s expression. Thus, age-related changes of CYP 1-4 families and bile acid homeostasis-related CYPs, the corresponding nuclear receptors and a few phase-II genes were examined. Livers from male Sprague-Dawley rats at fetus (-2 d), neonates (1, 7, and 14 d), weanling (21 d), puberty (28 and 35 d), adulthood (60 and 180 d), and aging (540 and 800 d) were collected and subjected to qPCR analysis. Liver proteins from 14, 28, 60, 180, 540 and 800 days of age were also extracted for selected protein analysis by Western-blot. In general, there were three patterns of their expression: Some of the drug-metabolizing enzymes and related nuclear receptors were low in fetal and neonatal stage, increased with liver maturation and decreased quickly at aging (AhR, Cyp1a1, Cyp2b1, Cyp2b2, Cyp3a1, Cyp3a2, Ugt1a2); the majority of P450s (Cyp1a2, Cyp2c6, Cyp2c11, Cyp2d2, Cyp2e1, CAR, PXR, FXR, Cyp7a1, Cyp7b1. Cyp8b1, Cyp27a1, Ugt1a1, Sult1a1, Sult1a2) maintained relatively high levels throughout the adulthood, and decreased at 800 days of age; and some had an early peak between 7 and 14 days (CAR, PXR, PPARα, Cyp4a1, Ugt1a2). The protein expression of CYP1A2, CYP2B1, CYP2E1, CYP3A1, CYP4A1, and CYP7A1 corresponded the trend of mRNA changes. In summary, this study characterized three expression patterns of 16 CYPs, 5 nuclear receptors, and 4 phase-II genes during development and aging in rat liver, adding to our understanding of age-related CYP expression changes and age-related disorders.

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18   **Abbreviations:**

19   AhR, aryl hydrocarbon receptor; BA, Bile acid; CAR, constitutive androstane receptor;

20   CYPs, cytochrome P450s; FXR, Farnesoid X receptor; NRs, nuclear receptors; PPAR,

21   peroxisome proliferator-activated receptor; PXR, pregnane X receptor (PXR); SHP,

22   small heterodimer partner; SULTs, Sulfotransferases; TCDD, tetrachlorodibenzodioxin;

23   UGTs, UDP-glucuronosyltransferases;

25 **Highlights (review only):**

26 • Livers of rats at -2, 1, 7, 14, 21, 28, 35, 60, 180, 540 and 800 days were

27 analyzed.

28 • A total of 16 cytochrome P450s, 5 nuclear receptors, 4 phase-II genes were

29 examined.

30 • Three patterns of age-associated gene expressions were characterized.

31 • Protein of CYP1A2, CYP2B1, CYP2E1, CYP3A1, CYP3A4, CYP4A1, and

32 CYP7A1 verified PCR.

33 • Age-associated P450 gene expressions in relation to diseases were discussed.

35   **ABSTRACT**

36   Cytochrome P450s (CYPs) are phase-I metabolic enzymes playing important roles in

37   drug metabolism, dietary chemicals and endogenous molecules. Age is a key factor

38   influencing P450s expression. Thus, age-related changes of CYP 1-4 families and bile

39   acid homeostasis-related CYPs, the corresponding nuclear receptors and a few phase-

40   II genes were examined. Livers from male Sprague-Dawley rats at fetus (-2 d),

41   neonates (1, 7, and 14 d), weanling (21 d), puberty (28 and 35 d), adulthood (60 and

42   180 d), and aging (540 and 800 d) were collected and subjected to qPCR analysis.

43   Liver proteins from 14, 28, 60, 180, 540 and 800 days of age were also extracted for

44   selected protein analysis by Western-blot. In general, there were three patterns of their

45   expression: Some of the drug-metabolizing enzymes and related nuclear receptors

46   were low in fetal and neonatal stage, increased with liver maturation and decreased

47   quickly at aging (AhR, Cyp1a1, Cyp2b1, Cyp2b2, Cyp3a1, Cyp3a2, Ugt1a2); the

48   majority of P450s (Cyp1a2, Cyp2c6, Cyp2c11, Cyp2d2, Cyp2e1, CAR, PXR, FXR,

49   Cyp7a1, Cyp7b1. Cyp8b1, Cyp27a1, Ugt1a1, Sult1a1, Sult1a2) maintained relatively

50   high levels throughout the adulthood, and decreased at 800 days of age; and some had

51   an early peak between 7 and 14 days (CAR, PXR, PPARα, Cyp4a1, Ugt1a2). The

52   protein expression of CYP1A2, CYP2B1, CYP2E1, CYP3A1, CYP4A1, and CYP7A1

53   corresponded the trend of mRNA changes. In summary, this study characterized three

54   expression patterns of 16 CYPs, 5 nuclear receptors, and 4 phase-II genes during

55   development and aging in rat liver, adding to our understanding of age-related CYP

56   expression changes and age-related disorders.

57   **Keywords:** Ontogeny; Aging; Cytochrome P450s; Nuclear receptors; Rat liver,

58   mRNA/protein expression.

59   **Introduction**

60   Cytochrome P450s (CYPs) are phase-I metabolic enzymes playing important roles

61   in drug metabolism, dietary chemicals, as well as endogenous molecules in the liver.

62   CYP1, 2, 3, and 4 families are responsible for the biotransformation of most foreign

63   substances including 70-80% of all drugs in clinical use, CYP 4 families also participate

64   in lipid metabolism.(Cui et al. 2012; Zanger & Schwab 2013) The CYP7 families,

65   together with CYP8 and CYP27 are important for cholesterol and bile acid metabolism

66   and homeostasis.(Cuesta de Juan et al. 2007; Liu et al. 2014)

67   CYPs are regulated by many physiological, genetic, environmental, and pathological

68   factors. For example, CYPs expression can be affected by hormones (Daskalopoulos et

69   al. 2012), cytokines (Kot & Daujat-Chavanieu 2018), pregnancy,(He et al. 2005) sex,

70   (Agrawal & Shapiro 2003; Das et al. 2014) and age. CYPs are subjected to age-

71   dependent changes in cell differentiation(Czekaj et al. 2010) and epigenetic

72   regulation,(Li et al. 2009) and age-related metabolic syndrome,(Bondarenko et al. 2016)

73   kidney diseases,(Velenosi et al. 2012) diabetes,(Park et al. 2016) nonalcoholic

74   steatohepatitis,(Li et al. 2017) virus hepatitis, and cirrhosis.(Kirby et al. 1996)

75   Age of animals greatly affects drug metabolism,(Durnas et al. 1990) alters

76   pharmacokinetics of xenobiotics,(Matalova et al. 2016; Shi & Klotz 2011) and thus alters

77   the sensitivity to drugs and toxicants such as acetaminophen,(Mach et al. 2014)

78   isoniazid,(Mach et al. 2016) aflatoxin B1,(Kirby et al. 1996; Wang et al. 2018) and

79   thioacetamide.(Kang et al. 2008) Age also influences drug-drug interactions.(Jia et al.

80   2014) Age-associated changes in P450 and corresponding nuclear factors are a major

81   determinant in CYP regulation of drug metabolism, especially during development

82   (children) and in senescence (elderly).(Durnas et al. 1990; Kilanowicz et al. 2015; Shi &

83   Klotz 2011)

84   The expression and maturation of CYPs during development is a major topic of

85   research,(Kilanowicz et al. 2015) and immature rats have been proposed as a potential

86   model for xenobiotics risk evaluation for children.(McPhail et al. 2016) The ontogeny of

87   CYPs greatly affects the drug metabolism especially during the developmental

88   period,(de Zwart et al. 2008) and is the major cause of altered susceptibility to drugs

89   and toxicants in children.(Li et al. 2017; Yun et al. 2010)

90   Aging is a physiological process characterized by progressive functional decline in

91   various organs over time. Aging is an important factor leading to alterations in the

92   biotransformation, either by reduced expression or decreased function. Many

93   cytochrome P450 genes from CYP 1-3 families show decreased expression in the older

94   rats.(Yun et al. 2010) The ability of liver CYPs to metabolize xenobiotics decreases with

95   aging *in vitro* (Salmin et al. 2017) and *in vivo,*(Wauthier et al. 2007) and hepatic CYP

96   mRNA expressions are decreased with aging.(Mori et al. 2007) The ability of CYPs in

97   response to inducers such as phenobarbital is also decreased in old rats.(Agrawal &

98   Shapiro 2003) Age-associated CYP3A expression changes in the liver are more

99   remarkable as compared to that occurred in the intestine and kidney, and are tissue-

100   specific.(Warrington et al. 2004) Since P450 enzymes in humans are regulated in a

101   manner similar to that in animals.(Durnas et al. 1990; Wauthier et al. 2007) Thus, to

102   examine CYP expressions in the old laboratory animals would help evaluation of drug

103   metabolism, efficacy and toxicity in the elderly.

104   In humans, three patterns of drug metabolizing enzymes are proposed.(Hines 2008)

105   The first pattern (e.g.,CYP3A7) is expressed at the highest level at their highest level

106   during the first trimester and either remains at high concentrations or decreases during

107   gestation, but is silenced or reduced within one to two years after birth; the 2nd pattern

108   (e.g.,SULT1A1) is expressed at relatively constant levels throughout gestation and

109   minimal changes are observed postnatally; and the 3rd pattern (e.g.ADH1C) is not

110   expressed or is expressed at low levels in the fetus.(Hines 2008; Hines 2013) Age-

111   associated changes of drug metabolism in humans, especially during stages before

112   birth and during early development (neonate/infant/child), could be studied in laboratory

113   animals.(Hines 2013; Saghir et al. 2012)

114   We have collected liver samples of Sprague Dawley (SD) rats from prenatal (-2 d),

115   neonatal (1, 7, and 14 d), weanling (21 d), puberty (28 and 35 d), adulthood (60 and 180

116   d), and aging (540 and 800 d), and have published several papers related to hepatic

117   uptake Oatp transporters(Hou et al. 2014) and hepatic efflux MRP transporters.(Zhu et

118   al. 2017) We have also used these samples to characterize the Nrf2 antioxidant

119   pathways,(Xu et al. 2018b) glutathione S-transferases,(Xu et al. 2018a) and the

120   antioxidant metallothionein gene expression.(Hou WY 2014)   The goals of the current

121   study were to use these samples to quantify the expression of 16 major CYP isoforms in

122   rat livers, 5 corresponding nuclear receptors (NRs), and 4 phase-II conjugation genes.

123   Protein expressions of selected CYPs were also performed to confirm qPCR results.

124   Similar to three patterns of CYP expression during mouse liver development,(Hart et al.

125   2009) the current study identified three patterns of CYP expression in the liver of rats at

126   11 time points of entire life span to help our understanding the age-associated changes

127   in these important phase-I and phase-II drug metabolism genes, and age-associated

128   disorders.

129

Materials and Methods

Animals. Adult male and female SD rats (250-300 g, 10 males and 30 females) were purchased from the Experimental Animal Center of Third Military Medical University (Chongqing, China; Certificate No: CXK 2007–0005). Rats were kept in a SPF-grade animal Facilities with controlled environment (22 ± 1 °C, 50 ± 2% humidity and a 12 h: 12 h light: dark cycle) at Key Lab for Basic Pharmacology of Ministry of Education. Rats had free access to purified water and standard laboratory chow (Experimental Animal Center, Chongqing, China). All animal care and experimental protocols were complied with the Animal Management Guidelines of China and approved by the Animal Use and Care Committee of Zunyi Medical University (2012−02).

Sample collection. Rats were acclimatized for one week before timely mating overnight and a positive vaginal plug next morning was considered as gestation day 1. Livers of offspring male rats were collected at gestation day 19 (−2 d), at birth (1 d), at the neonatal stage (7 and 14 d), at weanling (21 d), at puberty (28 and 35 d), at the adulthood (60 and 180 d), and at aging (540 and 800 d). Six samples per time point were collected, however, n=4-5 was used to for a 96-well qPCR plate to hold all time points. Rats were anesthetized by chloral hydrate (10%, 5 mL/kg, ip), followed by decapitation to minimize potential pain and distress. Liver tissues were stored at −80 °C prior to analysis.

Real-time RT-PCR analysis. Liver total RNA was extracted by using RNAiso Plus kit (TaKaRa Biotechnology Co., Ltd., Dalian, China). The quality and quantity of total RNA were determined by nanodrop and the 260/280 nm ratio > 1.8. The total RNA

153 was reverse transcribed to cDNA (Applied Biosystems, Foster City, CA) and real-time

154 RT-PCR analysis (Bio-Rad Laboratories, Hercules, CA) was conducted as described

155 (Xu et al. 2018b). Relative expression of genes was calculated by the $2^{-\Delta\Delta Ct}$ method and

156 normalized to the house-keeping gene β-actin or GAPDH (results were similar, data not

157 shown), and expressed as relative transcript levels, setting controls as 100%. The

158 primer sequences used in this study were shown in the Supplemental Table 1.

159   **Western-blot analysis.** Liver tissues (50-100 mg) were homogenized in RIPA

160 lysis buffer (Beyotime Institute of Biotechnology, Shanghai, China) containing 1 mM

161 phenylmethanesulfonyl fluoride (PMSF) and freshly prepared proteinase inhibitors.

162 Protein concentrations were quantified by the BCA assay (Beyotime Institute of

163 Biotechnology, Shanghai, China) and denatured (90 °C, 10 min with Nupage Loading

164 buffer). Aliquoted proteins (30 µg) were separated on NUPAGE 10% BT gels (Thermo

165 Fisher Scientific, Waltham, MA) and transferred to PVDF membranes. After blocking

166 with 5% nonfat milk at room temperature for two hours, membranes were incubated with

167 primary mouse antibody against β-actin, rabbit polyclonal antibodies against rat

168 CYP1A2 (bs-2589R), CYP2B1 (bs-14177R), CYP2E1 (bs-4562R), CYP3A1 (bs-

169 20586R), CYP4A1 (bs-5054R) and CYP7A1 (bs-21429R) (1:1000) (Biosynthesis

170 Biotechnology Co., LTD. Beijing, China) overnight at 4 °C. After washes with TBST,

171 membranes were incubated with horseradish peroxidase conjugated anti-rabbit, anti-

172 mouse IgG secondary antibodies (1:5000) for 1 h at room temperature. Protein antibody

173 complexes were visualized using an Enhanced Chemiluminescent reagent and a

174 ChemiDoc XRS system (Bio Rad Laboratories, Inc., USA). Band intensities were semi-

175 quantified by densitometry using Quantity One® software (version 4.6.2, Bio Rad

176   Laboratories, Inc., USA) (Xu et al. 2018a).

177   **Statistical analysis.** The software SPSS version 16.0 (SPSS, Inc., Chicago, IL,

178   USA) was used for statistical analysis. Data were expressed as the mean ± SEM (n= 4-

179   5 per time point). Age associated differences were analyzed by one-way analysis of

180   variance, followed by the least significant difference post hoc test, $p < 0.05$ was

181   considered to indicate a statistically significant difference from the levels of birth.

182

183   **Results**

184

185   ***Age-related expression of CYP-1 family***

186   The expression of CYP-1 family is shown in Figure 1. Aryl hydrocarbon receptor

187   (AhR) mainly mediates the expression of CYP1A1 and CYP1A2 proteins. 2,3,7,8-

188   Tetrachlorodibenzodioxin (TCDD) is a typical CYP1A1 inducer. When TCDD is

189   combined with AhR, AhR is dissociated from the complex and transferred to the nucleus.

190   It forms heteromeric dimers with AhR nuclear transport protein, and then induces the

191   expression of target genes. In this way, TCDD and other AhR activators significantly

192   induce the expression of CYP1A genes.(Aleksunes & Klaassen 2012) AhR was low in

193   fetal livers (-2d), and gradually increase after birth, and reached the highest levels at 35

194   days of age (6.7-fold of birth), and gradually declined, and at 800 days of age, it

195   remained 4.2-fold higher than at birth (Figure 1A). Cyp1a1 was low at -2 days of age

196   through 14 days of age, and begin to increase at 21 days of age, rapidly increased 48-

197   fold at 28-60 days of age, and decline rapidly after 60 days of age, and returned to 2.4-

198   fold of the birth level at 800 days of age (Figure 1B). In contrast, Cyp1a2 followed the

199 similar pattern as AhR. Cyp1a2 increased dramatically after birth, reached 250-fold at

200 weanling (21 day), and peaked on 35 days of age (1100 fold). It was gradually declined

201 afterwards. Similar to AhR, Cyp1a2 still remained at the high level at 800 days of age

202 (880 fold of birth). CYP1A2 protein expression followed the similar pattern (Figure 1C).

203

Age-related expression of CYP-2 family

205 The expression of CYP-2 family is shown in Figure 2. Constitutive androstane

206 receptor (CAR) is a nuclear receptor of steroid hormones. It regulates the metabolizing

207 enzymes and transporters in liver and small intestine. CAR mediates endogenous

208 hormone or exogenous drug reactions, such as phenobarbital, and transcriptionally

209 regulates CYP2 expression.(Aleksunes & Klaassen 2012) CAR was low in fetal livers (-

210 2d), and gradually increase after birth, first peaked at 7 days of age, and reached the

211 highest levels at 60 days of age (6-fold of birth), and gradually declined, and at 800

212 days of age, it remained 2.3-fold higher than at birth (Figure 2A). Cyp2b2 was low in

213 fetal livers (-2 d), and begin to increase after birth, and rapidly increased at weaning (21

214 d), reaching the peak at 35 days of age (7-fold of birth) and decreased afterwards, and

215 returned to birth level after 540 days of age (Figure 2B). The expression of Cyp2b1

216 followed the similar pattern as Cyp2b2, and the expression of CYP2B1 protein followed

217 the similar pattern (Figure 2C). Cyp2c6 increased after weanling, reached the peak of

218 liver maturation (350 fold) at 60 days of age, and remained high till 540 days of age, and

219 decreased to 250-fold over birth levels at 800 days of age (Figure 2D). Cyp2c11

220 increased 800-fold at puberty (35 days of age), but dramatically increased with liver

221 maturation (60000-fold at 60 days, 98000-fold at 180 days, and 110000-fold at 540 days

222   of age), and rapidly decreased at aging of 800 days of age, but it was still 40000-fold

223   over the birth level. (Figure 2E). Cyp2d2 increased gradually after birth, reached the

224   peak (9-fold) of liver maturation at 35 -180 days of age, and decreased to 6-fold of birth

225   at 540 and 800 days of age (Figure 2F). The expression pattern of Cyp2e1 was

226   relatively stable: Cyp2e1 increased rapidly after birth, reached 30-fold of the birth levels

227   at weanling (21 days of age), and peaked on 35 days of age (35 fold). It was gradually

228   declined but remained at the high level at the age of 800 days (22 fold of the birth level).

229   CYP2E1 protein expression followed the similar pattern (Figure 2G).

230

231   ***Age-related mRNA expression of CYP-3 family***

232   The expression of CYP-3 family is shown in Figure 3. Pregnane X receptor (PXR)

233   is a highly conserved ligand-dependent transcription factor. It is mainly expressed in the

234   liver and partly expressed in the colon and small intestine. The regulation of CYP3A by

235   PXR-mediated signaling pathway is an important pathway of drug

236   metabolism.(Aleksunes & Klaassen 2012) The expression of PXR was relatively stable

237   throughout the life with approximately 2-fold variations (Figure 3A). The expression of

238   Cyp3a2 markedly increased 4 fold at 7 days of age, and rapidly increased after

239   weanling (21 days of age), reached the peak at 28 days of age (25-fold of birth) and

240   decreased gradually afterwards, and the level was still 5.4-fold of the birth level at 800

241   days of age (Figure 3B). Cyp3a1 follows similar pattern as Cyp3a2. It was markedly

242   increased after weanling, reached the peak at 28 days of age (13-fold of the birth level)

243   and decreased gradually afterwards, and the level was still 3.4-fold of the birth level at

244 800 days of age. The expression of Cyp3a1protein followed the similar patter (Figure

245 3C).

246

Age-related expression of CYP-4 family

248   The expression of CYP-4 family is shown in Figure 4. Peroxisome proliferator-

249 activated receptors (PPARs) nuclear receptor family regulates the expression of genes

250 that control fatty acid synthesis, storage, and catabolism. PPARs mainly include PPARα,

251 PPARβ and PPARγ. The activation of PPAR can improve insulin resistance, slow down

252 atherosclerosis, and promote the metabolism of cholesterol. PPARα regulates induction

253 of CYP4A gene.(Aleksunes & Klaassen 2012) The expression of PPARα was relatively

254 stable throughout the life, except for 7 and 14 days of age (2-fold of the birth level), and

255 at 800 days of age, its levels returned to the birth level (Figure 4A). Cyp4a1 started to

256 increase after birth, with the first peak at 7 days (3.5-fold) and decreased after 14 days

257 of age, and again gradually increased after weanling and remained high throughout 540

258 days of age. At 800 days of age, it was still 1.8-fold of the birth level. The expression of

259 CYP4A1 protein followed the similar pattern (Figure 4B).

260

Age-related mRNA expression of CYPs involved in bile acids homeostasis

262   The expression of CYPs involved in cholesterol and bile acids homeostasis is

263 shown in Figure 5. Bile acids (BAs) are the endogenous ligands of farnesoid X receptor

264 (FXR), so FXR is also called the BA receptor. Cholesterol 7α hydroxylase (Cyp7a1) is

265 important for BA synthesis. When BA overloads in the liver, toxicity to liver cells occurs,

266 including oxidative stress, inflammation, necrosis and even cirrhosis.(Cuesta de Juan et

267   al. 2007; Liu et al. 2014) The expression of FXR increased at 14 days of age (5 fold),

268   and gradually increased afterwards with age, reached peak at 180 days (13 fold), and

269   still high at 800 days (6.8 fold) (Figure 5A). Cyp7a1 started to increase at 14 days of

270   age, reached the peak at 28 days (37 fold of birth), and remained high throughout the

271   adulthood, and was still 11-fold higher than the birth level at 800 days of age. The

272   expression of CYP7A1 protein followed similar pattern (Figure 5B). The expression of

273   Cyp7b1 started to increase after birth, reached the peak at 28 days of age, and

274   decreased at 800 days of age (Figure 5C). Cyp8b1 increased at birth and decreased at

275   7 days of age. Cyp8b1 started to increase again after weanling, reached the peak at

276   adulthoods at 180 days of age, and gradually decreased thereafter. It was still higher at

277   800 days of age (Figure 5D). The expression of Cyp27a1 held a similar pattern,

278   reached the peak on 35 days of age (5.8-fold over the birth level), and remained the

279   high levels throughout 540 days of age, and decreased at 800 days of age with 3-fold

280   higher over the birth level (Figure 5E).

281

282   ***Age-related mRNA expression of UGT and SULT families***

283   The expression of UGT and SULT families is shown in Figure 6. UDP-

284   glucuronosyltransferases (UGTs) and sulfotransferases (SULTs) are the two most

285   important phase-2 conjugation enzymes to conjugate the CYP catalyzed metabolites

286   and drugs contain functional groups such as hydroxyls and carboxylic acids.(Coughtrie

287   2015) Glucuronidation involves the reaction of uridine 5′-diphosphoglucuronic acid with

288   a number of functional groups generated from CYP metabolism and is a major

289   mechanism for the formation of water-soluble substrates for their elimination in bile or in

290 urine, especially for the clearance of a number of drugs in children.(Krekels et al. 2012)

291 SULTs transfer the sulfuryl moiety from the universal donor PAPS (3'-

292 phosphoadenosine 5'-phosphosulfate) to a wide variety of substrates with hydroxyl- or

293 amino-groups after CYP metabolism.(Coughtrie 2016) Ugt1a1 was low in fetal livers (-2

294 d), and gradually increase after birth, marked increase after weanling (21 days), and

295 reached the highest levels at 28 days of age (7.8-fold of birth), and gradually declined,

296 and at 800 days of age, it remained 4-fold higher than the level of birth (Figure 6A). The

297 expression of Ugt1a2 was relatively stable throughout the life, except for a small peak at

298 day 28 and 35 days of age (2.5-fold higher than the birth level) (Figure 6B). The

299 expression of Sult1a1 started to increase at 14 days of age, reached the peak at 180

300 days of age (20-fold), remained 14-fold higher than the birth levels (Figure 6C). The

301 expression of Sult1a2 started to increase at 14 days of age, reached the first peak at

302 weanling (15 fold), but dramatically increased after 35 days of age, reached 110-fold at

303 60 days of age, and 190-fold at 540 days of age. It remained 70-fold higher than the

304 levels of birth (Figure 6D). The expression pattern of Sult1a1 was quite similar to the

305 expression pattern of Cyp2c11.

306

307

Discussion

The present study characterized age-related expression of 16 CYPs, 5 NRs, and 4
phase-II genes in livers of rats across 11 time points from fetus (-2 d), neonates (1, 7,
14 and 21 d), puberty (28 and 35 d), adulthood (60 and 180 d), to aging (540 and 800 d).
In general, there are three patterns of their expression: (1) The expressions of AhR,
Cyp1a1, Cyp2b1, Cyp2b2, Cyp3a1, Cyp3a2, and Ugt1a2 were low in fetal and neonatal
stage, increased with liver maturation and decreased extensively after 180 days; (2) the
majority of CYPs and other genes maintained relatively high levels throughout the
adulthood and decreased at aging of 540 and/or 800 days; (3) the expression of CAR
PXR, PPARα, Cyp4a1, Ugt1a2 had a first peak between 7-14 days of age. The protein
expression of CYP1A2, CYP2B1, CYP2E1, CYP3A1, CYP4A1, and CYP7A1 followed
the trend of mRNA changes. Characterization of CYPs in rat entire life span provides
fundamental information for drug metabolism and pharmacology studies in children and
elderly.

There are three unique features of the current study: (1) Most of the studies on age-
related changes in hepatic CYPs are performed in mice,(Cui et al. 2012; Hart et al. 2009;
Li et al. 2009) this study characterized CYPs and NRs in rats, another commonly-used
laboratory animals; (2) Most of the age-related changes in hepatic P450 are focused on
the developmental stages to maturation,(Asaoka et al. 2010; Bondarenko et al. 2016;
Cui et al. 2012; de Zwart et al. 2008; Kilanowicz et al. 2015; Park et al. 2016) and this
study covered the whole life span, and (3) this study extended our efforts to
characterize age- and sex-related changes in hepatic drug transporters(Hou et al. 2014;
Zhu et al. 2017) and defense mechanisms. (Hou WY 2014; Xu et al. 2018a; Xu et al.

331   2018b)

332

333   *P450-1 family*

334   CYP1 family is responsible for activation of toxicants and drugs. Cyp1a1 is

335   expressed very early in rodents and involved in developmental toxicity of

336   hexachloronaphthalene,(Kilanowicz et al. 2015) and immature rats has been proposed

337   as a potential model for chemical risks in children.(McPhail et al. 2016) Ontogeny of

338   hepatic CYP1A2 showed it rapidly increased after weanling, followed by significant

339   decrease during adulthood,(Elbarbry et al. 2007) However, CYP1A1/2 activity did not

340   change when fed Zuker diabetic fatty rats with high fat diet at 5 week (insulin resistant

341   stage) and 11-week (diabetic stage).(Park et al. 2016) Glycyrrhetinic acid potentiation

342   of clozapine hepatotoxicity is associated with CYP1A2 induction and suppression of

343   CYP2C11 and 2C13.(Jia et al. 2014)   CYP1A1 and CYP1A2 are regulated differently,

344   CYP1A1 decreased rapidly after maturation, while CYP1A2 remained the high

345   expression levels till 104 weeks.(Yun et al. 2010) The present results agreed with the

346   literature.

347

348   *P450-2 family*

349   Hepatic CYP2C2 and CYP2C11 decreased with age, along with CYP3A enzyme

350   genes.(Mori et al. 2007) In diethyl nitrosamine-induced liver insufficiency, the altered

351   expression of cytokines might contribute to CYP2C and CYP3A isoform regulation. (Kot

352   & Daujat-Chavanieu 2018) The expression of CYP2C11 is under the regulation of

353   growth hormones,(Das et al. 2014) as well as the dopaminergic

354   receptors.(Daskalopoulos et al. 2012) The expressions of CYP2C, CYP2E1, and

355   CYP3A are influenced by metabolic syndrome.(Bondarenko et al. 2016) CYP2C11 is a

356   male-specific CYP, its expression began to increase after weanling, and at puberty

357   reached 830-fold over the birth, and further dramatically increased over 100000-fold

358   over the birth level throughout the adulthood, but rapidly decreased at aging, consistent

359   with the literature.(Agrawal & Shapiro 2003; Das et al. 2014; Yun et al. 2010)

360   Age-associated CYP2E1 expression has important implications in pharmacology

361   and toxicology. Old rats have decreased CYP2E1, altered acetaminophen

362   pharmacokinetics, resulting in less sensitive to acetaminophen toxicity.(Mach et al. 2014)

363   On the other hand, higher CYP2E1 in young rats might be a reason of increased

364   sensitivity to isoniazid toxicity.(Mach et al. 2016) The observed expression pattern for

365   CYP2B1 (marked decreases at 800 days of age) and CYP2E1 (slight decreases at 800

366   days of age) are in agreement of the literature.(Yun et al. 2010) CYP2E1 plays roles in

367   thioacetamide hepatotoxicity, as Cyp2e1-/- mice are less sensitive to liver injury.(Kang

368   et al. 2008) Age-related differences in CYP2E1 levels can have important implications

369   for the toxic and carcinogenic actions of some hydrocarbons (e.g., benzene, hexane)

370   and short-chain halocarbons, such as carbon tetrachloride.(McPhail et al. 2016)

371

372

373   ***P450-3 family***

374   CYP3 families are responsible for most drug metabolism.(Zanger & Schwab

375   2013) In rats with chronic kidney diseases, CYP3A and CYP2C mediated metabolism

376   are decreased.(Velenosi et al. 2012) Using liver microsomes (S9) from young and old

377   rats, severe metabolism impairment with aging for CYP3A and CYP2D substrates are

378   observed.(Salmin et al. 2017) CYP3A1 is higher in cells from young rats than in old

379   rats.(Czekaj et al. 2010) CYP3A in the liver are sensitive to aging with 50-70%

380   decreases, while CYP3A in the intestine is unchanged and in the kidney

381   increased.(Warrington et al. 2004) Generally speaking, hepatic CYP3A enzymes are

382   decreased with age.(Mori et al. 2007) In the present study, age-associated changes of

383   CYP3A1 and CYP3A2 followed "Pattern 1", while the expression of PXR, Cyp3a11

384   (mouse), and CYP3A4 protein followed "Pattern 2", a phenomenon in agreement of the

385   literature.(Mori et al. 2007; Yun et al. 2010)

386

387   ***3.4. P450-4 family***

388   PPARα activation induces CYP4A1, together with acyl-CoA oxidase and SREBPs,

389   that play important roles in regulating lipid metabolism, especially in rats fed with high-

390   fat-diet.(Chang et al. 2011) The herbicide propaquizafop dose-dependently activates

391   PPARα and CYP4A, leading to increased liver weight and hypertrophy as a mode of

392   action in hepato-carcinogenesis.(Strupp et al. 2018) In addition to PPARα activation, the

393   induction of CYP4A by K^+PFOS also involves CAR and PXR activation,(Elcombe et al.

394   2012) leading to hepatomegaly. In the present study, the expression of PPARα,

395   CYP4A1, CAR, and PXR followed "Pattern 3". That is the first expression peak

396   appeared at 7-14 days of age, similar to that observed in mice.(Hart et al. 2009)

397

398   ***P450-7 family and BA homeostasis***

399   Bile acid (BA) homeostasis is tightly regulated via a feedback loop operated by the

400   nuclear receptors FXR and small heterodimer partner (SHP). Loss of either FXR or SHP

401   alone, or Fxr-/-Shp-/- double knock out mice resulted in cholestasis and liver injury as

402   early as 3 weeks of age, and this dysfunction is linked to the dysregulation of bile acid

403   homeostatic key genes, particularly Cyp7a1.(Anakk et al. 2011) Hepatic CYP7A1 is a

404   rate-limiting enzyme that catabolizes cholesterol to bile acids, together with CYP8B1 as

405   the classic BA synthesis pathway, while CYP27A1 and CYP7B1 contribute to the

406   alternative pathway of BA biosynthesis.(Cuesta de Juan et al. 2007; Liu et al. 2014)

407   CYP27A1 is sensitive to inhibition by many xenobiotics.(Lam et al. 2018) In the present

408   study, the CYPs responsible for cholesterol metabolism and bile acid homeostasis

409   followed "Pattern 2", that was low at the neonatal stage, remained relative high levels

410   throughout the adulthood, and decreased at 800 days of age.

411   Taken together, CYPs are crucial enzymes in drug metabolism and

412   disposition.(Zanger & Schwab 2013) Induction or inhibition of CYPs have been

413   implicated in therapeutic efficacy and toxicity,(Jia et al. 2014; Mach et al. 2014; Mach et

414   al. 2016) and age-associated diseases.(Bondarenko et al. 2016; Velenosi et al. 2012)

415   especially in children(Kilanowicz et al. 2015; Li et al. 2017; McPhail et al. 2016) and in

416   elderly(McPhail et al. 2016; Salmin et al. 2017; Wauthier et al. 2007) Thus, a better

417   understanding of age-associated changes of CYPs is of significance for pharmacology,

418   toxicology, and therapeutics.

419

420   **_UGT and SULT_**

421   Glucuronidation and sulfation are two most important phase-II reactions to conjugate

422   the CYP-catalyzed metabolites for biliary or urinary elimination. Age has significant

423 impact on hepatic activities of glucuronidation and sulfation. For example, porcine

424 hepatic glucuronidation and sulfation activities were low at birth, peaked at 5-10 weeks,

425 and then declined at 20 weeks,(Hu 2017) similar to the observations in the present

426 study.

427   In childhood and adolescence, UGT expression can be affected by hormones and is

428 a reason of individual variation to medication.(Neumann et al. 2016) Compared to adults,

429 glucuronidation is reduced in children.(Krekels et al. 2012) UGT1A1 and UGT1A6 are

430 subjected to CAR and PPARα regulation,(Osabe et al. 2008) and age-associated

431 UGT1A1 changes are paralleled with CYP3A expression alterations in rats fed high-fat

432 diet.(Kawase et al. 2015; Osabe et al. 2008)

433   Sulfation is the most highly developed pathway during fetal development where

434 glucuronidation in particular is lacking.(Coughtrie 2015) Sulfation is normally a

435 detoxification reaction to facilitate the elimination of xenobiotics, although for some

436 molecules sulfation could be bioactivation.(Coughtrie 2016) The decreased Sult1a1

437 paralleled with major CYP metabolism genes in 600-day old rats,(Mori et al. 2007)

438 similar to current observations.

439

440 ***Conclusions***

441   Overall, the present study characterized age-related changes in a total of 25 CYP

442 isoforms and relevant genes in rat livers from development to aging. In general, these

443 genes are low in neonatal stages, increase with age, but decreased in aged animals,

444 and three expression patterns are characterized. These data could help our better

445 understanding of the effects of CYPs on drug metabolism, pharmacology, and

446 toxicology in the context of maturation and aging.

447

448 **Supplementary materials:** Supplemental Table 1 of qPCR primers can be found at

449 http://www.aspet/dmd.com

450 **Author Contributions:**

451 *Participate in research design:* Xu, Wu, Liu

452 *Conducted experiments:* Xu, Hu, Xie, Liu

453 *Performed data analysis:* Xu, Hu, Xie, Liu, Liu

454 *Wrote or contributed to the writing of the manuscript:* Xu, Hu, Xie, Wu, Liu

457 **Conflicts of Interest:** The authors declare no conflict of interest.

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461   **Figure Legends:**

462   **Figure 1. Age-related expression of CYP-1 family gene/proteins in livers of male**

463   **rats.**   Livers from male SD rats at the fetus (-2 d before birth), the neonatal stage (1, 7,

464   and 14 d), and at weanling (21 d), at puberty (28 and 35 d), at adult (60 and 180 d), and

465   at aging (540 and 800 d), were collected to extract RNA, followed by qPCR analysis

466   (n=4-5 for each time point). *Significantly different from at birth, $p < 0.05$. For Western-

467   blot insert, the neonatal (14 d), at weanling (21 d), at puberty (28 d), at adult (60 and

468   180 d), and at aging (540 and 800 d) were collected to extract protein. Aliquoted

469   proteins (30 μg) were separated on NUPAGE 10% BT gels and the representative

470   western-blot was inserted into the figure (n=3). The molecular weight for CYP1A1 was

471   55 kD, and β-actin 43 kD.

472

473   **Figure 2. Age-related expression of CYP-2 family gene/proteins in livers of male**

474   **rats.**   Livers from male SD rats at the fetus (-2 d before birth), the neonatal stage (1, 7,

475   and 14 d), and at weanling (21 d), at puberty (28 and 35 d), at adult (60 and 180 d), and

476   at aging (540 and 800 d), were collected to extract RNA, followed by qPCR analysis

477   (n=4-5 for each time point). *Significantly different from at birth, $p < 0.05$. For Western-

478   blot insert, the neonatal (14 d), at weanling (21 d), at puberty (28 d), at adult (60 and

479   180 d), and at aging (540 and 800 d) were collected to extract protein. Aliquoted

480   proteins (30 μg) were separated on NUPAGE 10% BT gels and the representative

481   western-blot was inserted into the figure (n=3). The molecular weight for CYP2B1 was

482   56 kD, CYP2E1 57 kD, and β-actin 43 kD.

483

484

485 **Figure 3. Age-related expression of CYP-3 family gene/proteins in livers of male**

486 **rats.**   Livers from male SD rats at the fetus (-2 d before birth), the neonatal stage (1, 7,

487 and 14 d), and at weanling (21 d), at puberty (28 and 35 d), at adult (60 and 180 d), and

488 at aging (540 and 800 d), were collected to extract RNA, followed by qPCR analysis

489 (n=4-5 for each time point). *Significantly different from at birth, $p < 0.05$. For Western-

490 blot insert, the neonatal (14 d), at weanling (21 d), at puberty (28 d), at adult (60 and

491 180 d), and at aging (540 and 800 d) were collected to extract protein. Aliquoted

492 proteins (30 μg) were separated on NUPAGE 10% BT gels and the representative

493 western-blot was inserted into the figure (n=3). The molecular weight for CYP3A1 was

494 57 kD, and β-actin 43 kD.

495

496

497 **Figure 4. Age-related expression of CYP-4 family gene/proteins in livers of male**

498 **rats.**   Livers from male SD rats at the fetus (-2 d before birth), the neonatal stage (1, 7,

499 and 14 d), and at weanling (21 d), at puberty (28 and 35 d), at adult (60 and 180 d), and

500 at aging (540 and 800 d), were collected to extract RNA, followed by qPCR analysis

501 (n=4-5 for each time point). For Western-blot insert, the neonatal (14 d), at weanling

502 (21 d), at puberty (28 d), at adult (60 and 180 d), and at aging (540 and 800 d) were

503 collected to extract protein. Aliquoted proteins (30 μg) were separated on NUPAGE 10%

504 BT gels and the representative western-blot was inserted into the figure (n=3). The

505 molecular weight for CYP4A1 was 59 kD, and β-actin 43 kD.

506

507

Figure 5. Age-related expression of CYP-7 family gene/proteins in livers of male rats. Livers from male SD rats at the fetus (-2 d before birth), the neonatal stage (1, 7, and 14 d), and at weanling (21 d), at puberty (28 and 35 d), at adult (60 and 180 d), and at aging (540 and 800 d), were collected to extract RNA, followed by qPCR analysis (n=4-5 for each time point). *Significantly different from at birth, $p < 0.05$. For Western-blot insert, the neonatal (14 d), at weanling (21 d), at puberty (28 d), at adult (60 and 180 d), and at aging (540 and 800 d) were collected to extract protein. Aliquoted proteins (30 µg) were separated on NUPAGE 10% BT gels and the representative western-blot was inserted into the figure (n=3). The molecular weight for CYP7A1 was 55 kD, and β-actin 43 kD.

518

519

Figure 6. Age-related mRNA expression of UGT and SULT family genes in livers of male rats. Livers from male SD rats at the fetus (-2 d before birth), the neonatal stage (1, 7, and 14 d), and at weanling (21 d), at puberty (28 and 35 d), at adult (60 and 180 d), and at aging (540 and 800 d), were collected to extract RNA, followed by real-time RT-PCR analysis (n=4-5 for each time point). *Significantly different from at birth, $p < 0.05$.

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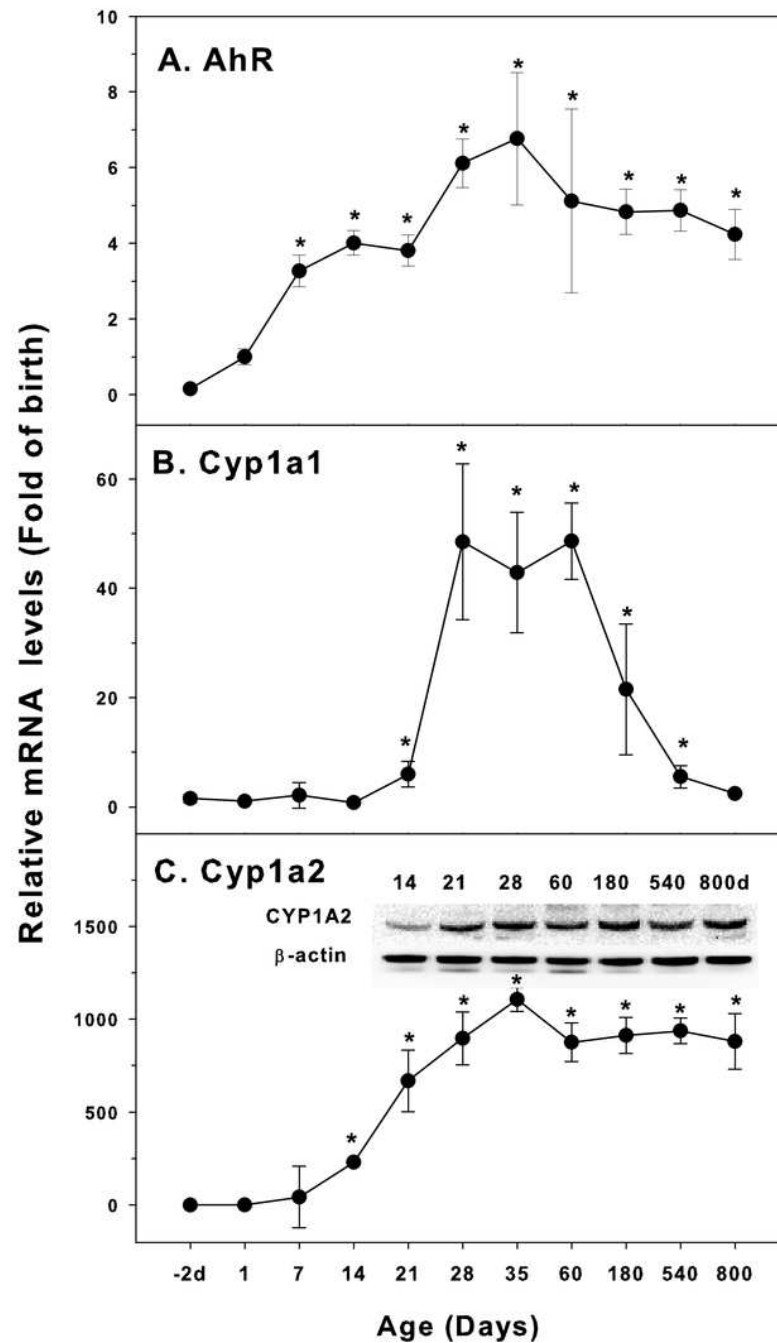
685

Figure 1

Figure 1. Age-related expression of CYP-1 family gene/proteins in livers of male rats.

Livers from male SD rats at the fetus (-2 d before birth), the neonatal stage (1, 7, and 14 d), and at weanling (21 d), at puberty (28 and 35 d), at adult (60 and 180 d), and at aging (540 and 800 d), were collected to extract RNA, followed by qPCR analysis (n=4-5 for each time point). *Significantly different from at birth, $p < 0.05$. For Western-blot insert, the neonatal (14 d), at weanling (21 d), at puberty (28 d), at adult (60 and 180 d), and at aging (540 and 800 d) were collected to extract protein. Aliquoted proteins (30 μg) were separated on NUPAGE 10% BT gels and the representative western-blot was inserted into the figure (n=3). The molecular weight for CYP1A1 was 55 kD, and β-actin 43 kD.

Figure 2

Figure 2. Age-related expression of CYP-2 family gene/proteins in livers of male rats.

Livers from male SD rats at the fetus (-2 d before birth), the neonatal stage (1, 7, and 14 d), and at weanling (21 d), at puberty (28 and 35 d), at adult (60 and 180 d), and at aging (540 and 800 d), were collected to extract RNA, followed by qPCR analysis (n=4-5 for each time point). *Significantly different from at birth, $p < 0.05$. For Western-blot insert, the neonatal (14 d), at weanling (21 d), at puberty (28 d), at adult (60 and 180 d), and at aging (540 and 800 d) were collected to extract protein. Aliquoted proteins (30 µg) were separated on NUPAGE 10% BT gels and the representative western-blot was inserted into the figure (n=3). The molecular weight for CYP2B1 was 56 kD, CYP2E1 57 kD, and β-actin 43 kD.
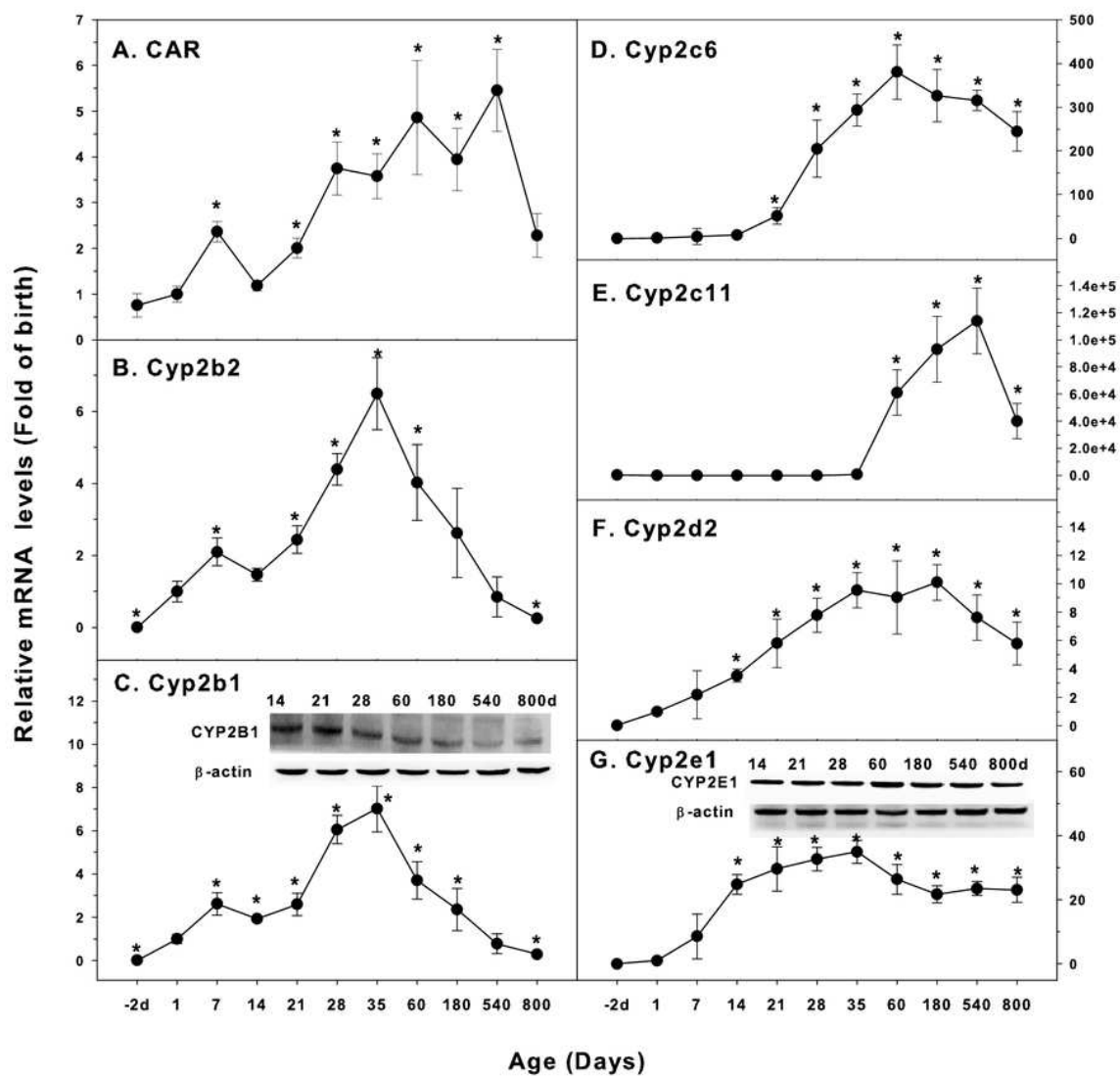
Figure 3

Figure 3. Age-related expression of CYP-3 family gene/proteins in livers of male rats.

Livers from male SD rats at the fetus (-2 d before birth), the neonatal stage (1, 7, and 14 d), and at weanling (21 d), at puberty (28 and 35 d), at adult (60 and 180 d), and at aging (540 and 800 d), were collected to extract RNA, followed by qPCR analysis (n=4-5 for each time point). *Significantly different from at birth, $p < 0.05$. For Western-blot insert, the neonatal (14 d), at weanling (21 d), at puberty (28 d), at adult (60 and 180 d), and at aging (540 and 800 d) were collected to extract protein. Aliquoted proteins (30 µg) were separated on NUPAGE 10% BT gels and the representative western-blot was inserted into the figure (n=3). The molecular weight for CYP3A1 was 57 kD, and β-actin 43 kD.
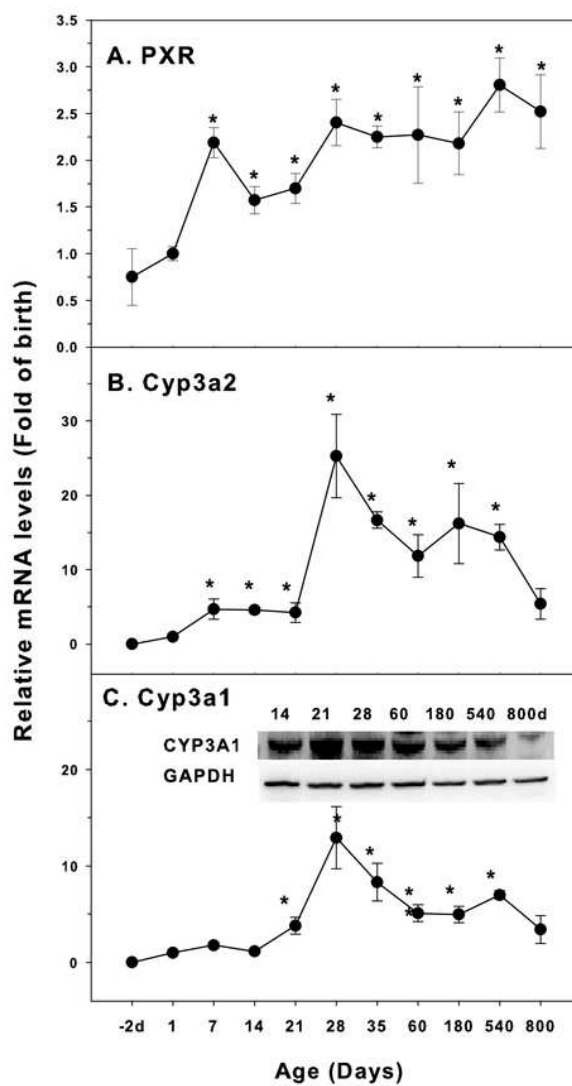
Figure 4

Figure 4. Age-related expression of CYP-4 family gene/proteins in livers of male rats.

Livers from male SD rats at the fetus (-2 d before birth), the neonatal stage (1, 7, and 14 d), and at weanling (21 d), at puberty (28 and 35 d), at adult (60 and 180 d), and at aging (540 and 800 d), were collected to extract RNA, followed by qPCR analysis (n=4-5 for each time point). For Western-blot insert, the neonatal (14 d), at weanling (21 d), at puberty (28 d), at adult (60 and 180 d), and at aging (540 and 800 d) were collected to extract protein. Aliquoted proteins (30 μg) were separated on NUPAGE 10% BT gels and the representative western-blot was inserted into the figure (n=3). The molecular weight for CYP4A1 was 59 kD, and β-actin 43 kD.
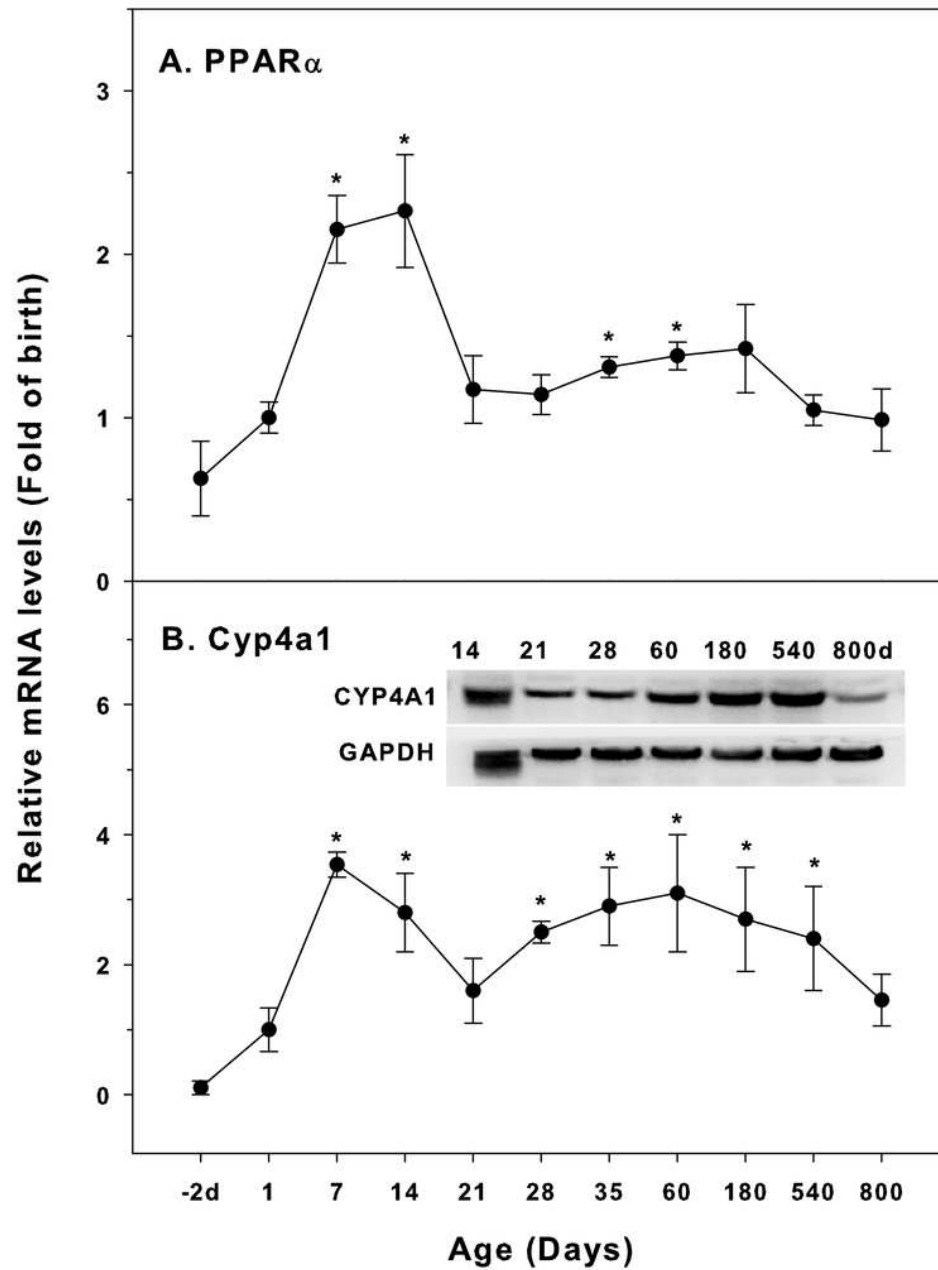
Figure 5

Figure 5. Age-related expression of CYP-7 family gene/proteins in livers of male rats.

Livers from male SD rats at the fetus (-2 d before birth), the neonatal stage (1, 7, and 14 d), and at weanling (21 d), at puberty (28 and 35 d), at adult (60 and 180 d), and at aging (540 and 800 d), were collected to extract RNA, followed by qPCR analysis (n=4-5 for each time point). *Significantly different from at birth, $p < 0.05$. For Western-blot insert, the neonatal (14 d), at weanling (21 d), at puberty (28 d), at adult (60 and 180 d), and at aging (540 and 800 d) were collected to extract protein. Aliquoted proteins (30 µg) were separated on NUPAGE 10% BT gels and the representative western-blot was inserted into the figure (n=3). The molecular weight for CYP7A1 was 55 kD, and β-actin 43 kD.
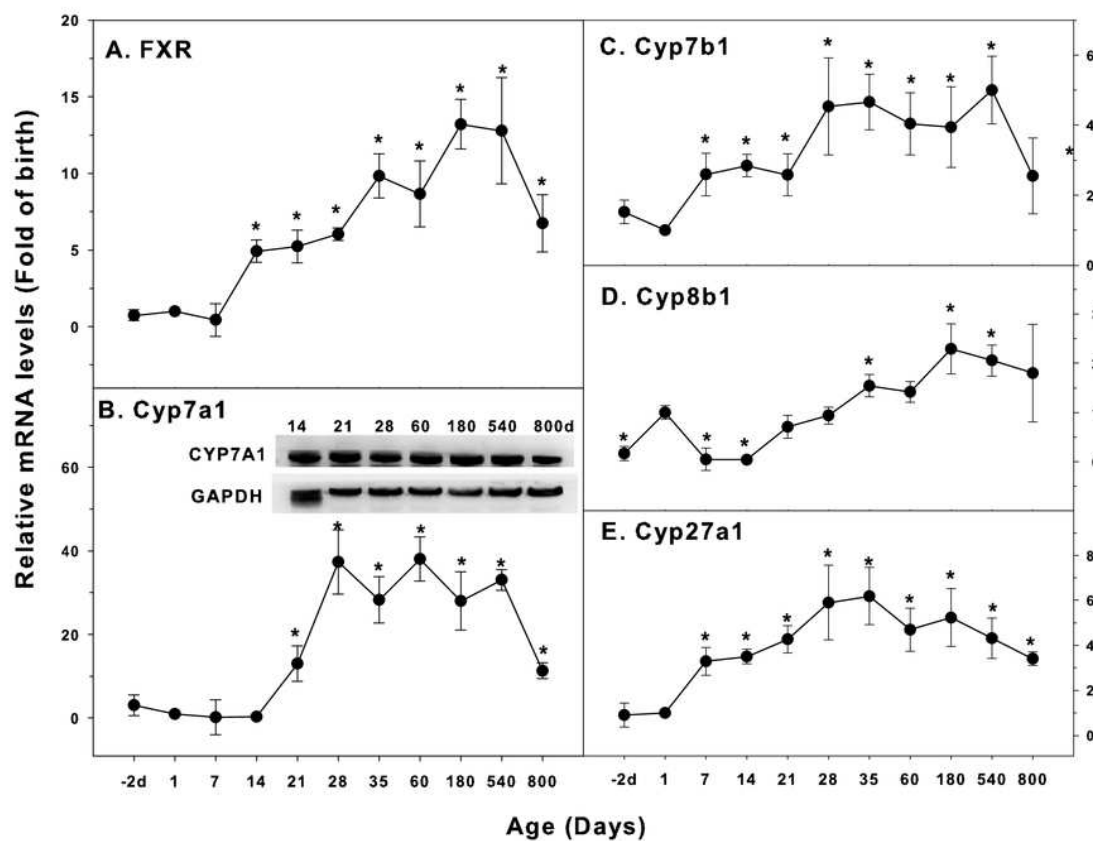
Figure 6

Figure 6. Age-related mRNA expression of UGT and SULT family genes in livers of male rats.

Livers from male SD rats at the fetus (-2 d before birth), the neonatal stage (1, 7, and 14 d), and at weanling (21 d), at puberty (28 and 35 d), at adult (60 and 180 d), and at aging (540 and 800 d), were collected to extract RNA, followed by real-time RT-PCR analysis (n=4-5 for each time point). *Significantly different from at birth, $p < 0.05$.