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EXPRESSION OF CYTOCHROMES P450, CONJUGATING ENZYMES and NUCLEAR RECEPTORS IN HUMAN HEPATOMA HepaRG CELLS

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D. Abbreviations

CYP, cytochrome P450; AhR, aryl hydrocarbon receptor; PXR, pregnane X receptor; CAR, constitutive androstane receptor; PPAR α , peroxisome proliferator-activated receptor α ; RXR, 9-cis retinoid X receptor ; UGT, UDP-glucuronosyl transferase ; GST, Glutathione S-transferase; RT-qPCR, reverse transcriptase quantitative polymerase chain reaction ; FCS, fetal calf serum; IC₅₀, inhibitory concentration 50; AFB₁, Aflatoxin B₁; EROD, Ethoxyresorufin-O-deethylase; DMSO, Dimethylsulfoxide; MTT, methylthiazoletetrazolium; GCS, gamma glutamylcysteine synthase.

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ABSTRACT

Most human hepatocyte cell lines lack a substantial set of liver-specific functions, especially major cytochrome P450 (CYP)-related enzyme activities, making them unrepresentative of *in vivo* hepatocytes. We have used the HepaRG cells derived from a human hepatocellular carcinoma, that exhibit a high differentiation pattern after 2 weeks at confluency to determine whether they could mimic human hepatocytes for drug metabolism and toxicity studies. We show that when passaged at low density these cells reversed to an undifferentiated morphology, actively divided and after having reached confluency formed typical hepatocyte-like colonies surrounded by biliary epithelial-like cells. By contrast, when seeded at high density, hepatocyte-like clusters retained their typical differentiated morphology. Transcripts of various nuclear receptors (AhR, PXR, CAR, PPAR α), CYPs (1A2, 2C9, 2D6, 2E1, 3A4), phase 2 enzymes (UGT1A1, GSTA1, GSTA4, GSTM1) and other liver-specific functions were estimated by RT-qPCR and found to be expressed for most of them at comparable levels in both confluent differentiated and high density differentiated HepaRG cells and in cultured primary human hepatocytes. For several transcripts the levels were strongly increased in presence of 2% dimethylsulfoxide. Measurement of basal activities of several CYPs and their response to prototypical inducers as well as analysis of metabolic profiles and cytotoxicity of several compounds confirmed the functional resemblance of HepaRG cells to primary cultured human hepatocytes. In conclusion, HepaRG cells constitute the first human hepatoma cell line expressing high levels of the major CYPs involved in xenobiotic metabolism and represent a reliable surrogate to human hepatocytes for drug metabolism and toxicity studies.

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INTRODUCTION

Human primary hepatocytes and immortalized hepatocytes are widely used for xenobiotic metabolism, toxicity studies and the design of bioartificial liver devices; however, both systems have limitations (Guillouzo et al., 1993; Maurel, 1996; Guillouzo, 1998; LeCluyse, 2001). Primary hepatocytes have scarce and unpredictable availability, limited growth activity and life-span, and undergo early phenotypic alterations. Huge variations in functional activities, especially CYP levels as well as in magnitude of CYP induction after treatment with prototypical inducers have been reported from one human hepatocyte population to another (Guillouzo and Chesne, 1996; Madan et al., 2003). Moreover, all CYPs are not similarly maintained with time in culture. Although various culture conditions, such as the use of sophisticated media, extracellular matrices as supports or sandwich systems, addition of DMSO or co-culturing with other cell types, may improve to some extent maintenance of CYPs and other liver-specific functions, these are usually already markedly and differently decreased early after hepatocyte seeding. Nevertheless, primary hepatocytes have proved to be the most suitable model for investigating induction of CYPs by chemical inducers and metabolic profiles of new drugs (Guillouzo et al., 1993; Maurel, 1996; Guillouzo, 1998). Hepatocyte cell lines, mainly originated from tumors, have indefinite proliferative capacity but they lack a variable and substantial set of liver-specific functions, making them unsuitable as representative of *in vivo* liver parenchymal cells. In particular, CYP expression is usually very low or undetectable in human hepatoma cells. Even the human hepatoma HepG2 cells that have retained several liver-specific functions, contain little CYP with the exception of the isoforms expressed in fetal cells such as CYP1A1 and CYP3A7 (Sassa et al., 1987; Ogino et al., 2002). Stably transfected liver cell lines have been established by using eukaryotic CYP expression vectors under the control of inducible/constitutive promoters (Pfeifer et al., 1993) and reexpression of CYPs has been

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obtained in human hepatoma cells by transfection of liver-specific transcription factors such as c/EBP alpha (Jover et al., 1998). However, these cell lines do not mimic regulation of gene expression observed in normal hepatocytes (e.g. CYP induction by phenobarbital) (Zelko and Negishi, 2000).

Recently, we have obtained a new human hepatoma cell line derived from an hepatocellular carcinoma, named HepaRG, that exhibits extensive differentiation after 2 weeks at confluency and has the unique property to be susceptible to hepatitis B virus infection (Gripon et al., 2002). In the present study we have analyzed expression of the main drug metabolizing enzymes in HepaRG cells under different culture conditions. Our results demonstrate that, in conditions in which cells attain a differentiated hepatocyte-like morphology, they retain a unique set of drug metabolizing enzymes at levels comparable to those measured in normal human hepatocytes in primary culture.

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METHODS

Chemicals

Aflatoxin B₁ (AFB₁), aflatoxin M₁ (AFM₁), aflatoxin P₁ (AFP₁), chlorpromazine, amiodarone hydrochloride, acetaminophen, testosterone, 6 β -hydroxytestosterone, chlorzoxazone, 3-methylcholantrene, chlopropamide, resorufin, 7-ethoxyresorufin, methylthiazoletetrazolium (MTT), dimethylsulfoxide (DMSO), rifampicin, salicylamide, isoniazid, dexamethasone and insulin were purchased from Sigma (St. Quentin Fallavier, France). Metabolites of acetaminophen were kindly provided by Biopredic (Rennes, France). Aflatoxin-glutathione conjugate (AFB₁-GSH) and aflatoxin B₁-dialcohol were kindly supplied by Pr Guengerich. 6-Hydroxychlorzoxazone was from Ultrafine chemicals (Manchester, UK). William's E medium was purchased from Eurobio (Les Ulis, France). Fetal calf serum (FCS) was from Perbio (Brebieres, France). Penicillin, streptomycin, minimum essential medium (MEM) alpha and non essential amino acids were from Invitrogen Corporation (Gibco). Hydrocortisone hemisuccinate was from Upjhon Pharmacia (Guyancourt, France). All other chemicals were of the highest quality available.

Cell cultures

HepaRG cells were obtained from a liver tumor of a female patient suffering from hepatocarcinoma (Gripon et al., 2002). Briefly, small tumor pieces were digested with 0.025% collagenase D diluted in Hepes buffer supplemented with 0.075% CaCl₂. The cell population was suspended in William's E medium added with 10% FCS, 5 μ g/ml insulin and 5 $\times 10^{-7}$ M hydrocortisone hemisuccinate and distributed in several dishes. The most hepatocyte-like populations were selected and passaged by gentle trypsinisation. After three passages cell aliquotes were cryopreserved. Induction of differentiation was obtained by treating confluent

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cells with the culture medium containing 2% DMSO and $5 \times 10^{-5} \text{M}$ hydrocortisone hemisuccinate.

For the present studies, HepaRG¹ cells were detached by gentle trypsinization and seeded at a density of either 2.6×10^4 cells/cm² (low density) or 0.45×10^6 differentiated cells/cm² (high density). Low density cells were first seeded in the growth medium composed of William's E medium supplemented with 10% FCS, 100 units/mL penicillin, 100µg/mL streptomycin, 5µg/mL insulin, 2mM glutamine and $5 \times 10^{-5} \text{M}$ hydrocortisone hemisuccinate. After 2 weeks they were shifted to the same culture medium supplemented with 2% DMSO (differentiation medium) for 2 more weeks (confluent DMSO-treated cells) (Gripon et al., 2002). The medium was renewed every 2-3 days. High density differentiated HepaRG cells were directly seeded in the differentiation medium.

Human hepatocytes from adult donors undergoing resection for primary and secondary tumors were obtained by perfusion of histologically-normal liver fragments (Guguen-Guillouzo et al., 1982). Briefly, hepatocytes were seeded at a density of 110,000 cells/cm² in 24-well plates in William's E medium supplemented with 10% FCS, 100 units/mL penicillin, 100µg/mL streptomycin, 1µg/mL insulin, 2mM glutamine and 1µg/mL bovine serum albumin. The medium was discarded 12 hours after seeding and cells were thereafter maintained in serum-free medium supplemented with 10^{-7}M dexamethasone. The medium was renewed every day. Human hepatocytes were used either freshly isolated or 3 to 5 days after seeding. HepG2 cells were seeded at a density of 100,000 cells/cm² in 24-well plates and were used at the time they reached confluency. The growth medium was composed of MEM alpha supplemented with 10% FCS, non essential amino acids, 100 units/mL penicillin and 100µg/mL streptomycin.

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Isolation of RNA and RT-qPCR analysis.

Total RNA was extracted from 10^6 HepaRG cells, 10^6 HepG2 cells or 10^6 human hepatocytes with the SV total RNA isolation system (Promega, Madison, WI, USA) which directly included a DNAase treatment step. RNAs were reversed-transcribed into cDNA using High-Capacity cDNA Archive kit (Applied Biosystems, Foster City, CA, USA). Real-time quantitative PCR for all genes except for PPAR α was performed by the fluorescent dye SYBR Green methodology using the SYBR $^{\circledR}$ Green PCR Master Mix (Applied Biosystems) and the ABI Prism 7000 (Applied Biosystems). Table 1 shows primer pairs for each transcript chosen with Primers 3 (http://frodo.wi.mit.edu/cgi-bin/primer3/primer3_www.cgi), except for PPAR α (Assay-on-demand, Applied Biosystems) and CYP2D6 (gift from Biopredic, Rennes, France). For PPAR α , we detected FAM fluorescence of the Taqman probe using the TaqMan $^{\circledR}$ Universal PCR Master Mix kit (Applied Biosystem). The amplification curves were read with the ABI Prism 7000 SDS Software using the comparative Cycle threshold method. The relative quantification of the steady-state mRNA levels was calculated after normalization of the total amount of cDNA tested by an active reference, 18S RNA. Furthermore, a dissociation curve was performed after the PCR reaction to verify the specificity of the amplification. Results were expressed as a percentage of mRNA levels measured in freshly isolated hepatocytes arbitrarily set at 100%.

Determination of drug metabolizing enzyme activities and metabolic profiles

For the determination of CYP-related activities, HepaRG cells and primary human hepatocytes were incubated with specific substrates in phenol red-free medium deprived of either both FCS and 2% DMSO or only FCS. The substrate concentrations were 200 μ M testosterone, 300 μ M chlorzoxazone, 0.2mM tolbutamide and 5 μ M ethoxyresofurin. For induction studies, HepaRG cells were first exposed to either 25 or 50 μ M rifampicin or 50 μ M

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isoniazid for 72h, or to 5 μ M 3-methylcholantrene for 24h before incubation with the specific substrate. These concentrations of substrates and inducers are those usually used with primary human hepatocyte cultures (Langouet et al, 1995, Guillouzo and Chesne, 1996; Madan et al, 2003). 6 β -Hydroxylation of testosterone, tolbutamide 4-hydroxylation and chorzoxazone 6-hydroxylation were estimated by HPLC analysis (Guillouzo and Chesne, 1996). Resorufin formation by 7-ethoxyresorufin O-deethylation (EROD) was quantified by fluorimetry with a fluorescence plate reader (SpectraMAX Gemini; Molecular Devices®) after a 30min incubation with ethoxyresorufin in the presence of 3 μ M salicylamide in order to inhibit phase II enzyme activities (Burke and Mayer, 1983). Fluorescence was determined at λ_{ex} 544 nm and λ_{em} 584 nm.

Acetaminophen and AFB₁ metabolites were analysed by HPLC. Metabolites of acetaminophen were determined as previously described (Guillouzo and Chesne, 1996). Acetaminophen was incubated at 2mM for 10 hours before medium harvesting. AFB₁ metabolism was analysed as follows: after a 8 hours incubation with the mycotoxin at 5 μ M (Langouet et al., 1995), aliquots of media were collected and centrifugated 2 minutes at 10,000 rpm. 90 μ L of sample were injected in the HPLC system. An Interchrom C₁₈ column (250 \times 4.6mm, 5 μ m) was used for the chromatographic separation. The mobile phase consisted of two solvents, A (ammonium acetate 0.01M pH 6.5) and B (acetonitrile) with the following gradient : 0 min 15 % B – 23 min 23% B – 43 min 53%B – 45 min 100% B – 47 min 100% B – 47.5 min 15%B – 52 min 15% B. All the gradients were linear and the flow rate was set at 1 mL/min. Fluorescence detection was monitored at excitation and emission wavelengths of 430 nm and 370 nm respectively.

The HPLC apparatus consisted of an Agilent 1100 series HPLC equipped with an autosampler and Agilent 1100 Series fluorescence and UV detectors. A computer running Agilent 1100 software (ChemStation®) was used to integrate and calculate the separated peak

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areas and to plot metabolite patterns. Metabolites tested were identified by comparison of retention times and quantifications were estimated from calibration curves.

Evaluation of drug cytotoxicity

The effects of four reference hepatotoxic compounds, namely acetaminophen, chlorpromazine, amiodarone and AFB₁, were evaluated on HepaRG and HepG2 cells after either 24 or 72 hours of exposure. Incubations were performed with medium deprived of 2% DMSO and FCS. At the end of the incubation time, cultures were observed by phase-contrast microscopy using an Olympus 1X70. Then the medium was discarded and replaced with FCS-free medium containing 1mg MTT/mL. After 2 hours formozan crystals were dissolved in DMSO and the intensity of color was determined at 540 nm using a microplate reader (iEMS Reader MF, Labs systems®).

Statistical analysis

Data are presented as means +/- SD. Each value corresponded to a different cell culture. Student's t test was applied to samples for statistical analysis. Data were considered significantly different when $p < 0.05$.

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RESULTS

Behavior of HepaRG cells in culture (Figure 1).

When seeded at low density onto plastic, HepaRG cells took a morphology of elongated undifferentiated cells characterized by a clear cytoplasm and actively divided until they reached confluency, i.e. around day 10. Then they progressively formed typical colonies of granular epithelial cells surrounding by more flattened and clearer epithelial cells. Addition of DMSO was followed by appearance of a denser cytoplasm and a morphology resembling that of typical normal hepatocytes in primary culture with the formation of bile canaliculus-like structures. At this stage, hepatocyte-like cells represent 30 to 40% of the population. When seeded at high density after differentiation, HepaRG cells retained their hepatocyte-like morphology. This particular condition allowed to concentrate the hepatocyte-like population.

Expression of specific genes analyzed by RT-qPCR

Transcripts of 6 CYPs (1A2, 2B6, 2C9, 2D6, 2E1, 3A4), 4 nuclear receptors (AhR, PXR, CAR, PPAR α), 4 phase 2 enzymes (UGT1A1, GSTA1, GSTA4, GSTM1), 3 liver-specific proteins (albumin, haptoglobin, aldolase B) as well as alpha-fetoprotein (AFP), glutathione-related enzymes (GCS regulatory subunit, GCS catalytic subunit, glutathione synthase, glutathione reductase) and thioredoxin were analyzed by RT-qPCR in HepaRG cells at different times after seeding and in the different culture conditions described in Figure 2. For comparison, the same transcripts were analyzed in HepG2 cells, in freshly isolated human hepatocytes and in addition for several major genes in primary human hepatocytes at various times of culture. As shown in Tables 2 and 3, all the mRNAs analysed, including CYP ones, were expressed in HepaRG cells. However, transcripts of CYPs and the CAR nuclear receptor were detectable in low density seeded cells only after 8 days. mRNA levels were usually

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slightly higher in HepaRG cells seeded at high density than in those seeded at low density and attaining differentiation after 2 weeks at confluency, probably due to a greater proportion of differentiated hepatocyte-like cells in the former. Furthermore, the highest values were frequently observed in differentiated cells exposed to 2% DMSO. However, some differences were evidenced: mRNA levels of CYP2B6, CYP2E1, CYP3A4 and to a lower extent CAR, UGT1A1, GSTA4, GSTM1 and GSTA1/A2, were markedly increased in the presence of DMSO while those of CYP1A2, CYP2C9, CYP2D6, PXR, PPAR α , AhR, albumin, aldolase B and haptoglobin were only slightly modulated. Compared to those measured in primary human hepatocytes (Table 4), with the exception of CYP2D6 that remained low whatever the culture conditions, a trend towards either close or higher (CYP2B6 and CYP3A4) levels of other transcripts was observed in HepaRG cells. As expected, the greatest values found in human hepatocytes were obtained after 3-5 days of culture. Compared to HepG2 cells major differences were noticed: indeed some transcripts were not detected in these cells (CYP2C9, CYP2E1, CYP3A4, aldolase B) while the levels of others, with the exception of CYP2D6 and especially alpha-fetoprotein, showed a trend towards a decrease (CYP1A2, CYP2B6, CAR, UGT1A1, GSTA1/2, GSTA4, GSTM1, haptoglobin and albumin) or were close (AhR, PXR, PPAR α) compared to HepaRG cells. Whatever the cell type and the culture conditions, no variations were observed in thioredoxin mRNAs as well as in transcripts of glutathione-related enzymes involved in glutathione metabolism (data not shown).

Drug metabolizing enzyme activities

Four enzyme activities, namely 7-ethoxyresorufin O-deethylation, 6 β -hydroxylation of testosterone, tolbutamide 4-hydroxylation and chorzoxazone 6-hydroxylation, were analysed in HepaRG cells cultured in five different experimental conditions (Table 5). Incubations with specific inducers were performed in media free of FCS and in the presence or absence of

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DMSO for either 24h (ethoxyresorufin \pm 3-methylcholantrene) or 72h (other substrates \pm inducers). With the four substrates the lowest values were obtained with 15 days cultures from low density cell seeding. Whatever the culture condition only traces of 7-ethoxyresorufin O-deethylation was detected in the absence of inducer. By contrast after a 24h treatment with 5 μ M 3-methylcholantrene, a strong induction of this activity was observed. Furthermore, the highest values were found in DMSO-exposed cultures (more than a 2-fold increase) compared to corresponding DMSO-free cultures. Tolbutamide 4-hydroxylase activity (CYP2C9) was detected in all culture conditions. However, in basal conditions, this activity was increased around 6-10 fold in differentiated HepaRG cells whether seeded at low or high density and exposed or not to DMSO compared with 15 days cultures. A 72h treatment with 25 μ M rifampicin resulted in a non significant increase in 15 days cultures and no more than around 2-fold increase in differentiated cells exposed or not to DMSO. Chlorzoxazone 6-hydroxylase activity (CYP2E1) was also much greater in differentiated than in 15 days HepaRG cell cultures. The highest values were obtained with cells seeded at high density. A 3 days exposure to 50 μ M isoniazid had limited effects if any. As tolbutamide 4-hydroxylase and chlorzoxazone 6-hydroxylase activities, 6 β -hydroxytestosterone formation (CYP3A4) was augmented in DMSO-free differentiated HepaRG cell cultures compared with 15 days cultures (3.5 -5.0 fold) and was further strongly increased in differentiated cells when maintained in the presence of DMSO (around 14-fold more) whether the cells were seeded at low or high density. These activities represented around 10 and 500-800 pmoles/mg/min in 15 days HepaRG cells and DMSO-treated differentiated HepaRG cells respectively. A 72h rifampicin treatment also resulted in a huge significant increase both in 15 days cells and in differentiated cells seeded at low and high density and exposed in the absence of DMSO (11.8, 5.3 and 10-fold respectively). By contrast, when differentiated cells seeded at high

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density were treated with rifampicin in the presence of DMSO no significant increase of testosterone 6 β -hydroxylase activity was evidenced

Metabolic profiles

AFB₁ is the most powerful hepatocarcinogen compound in human. Its action is mediated by the formation of AFB₁-8,9-epoxide which can bind covalently DNA to form AFB₁-DNA adducts. CYP1A2 and CYP3A4 are involved in its biotransformation (Langouet et al., 1996). Metabolism of AFB₁ leads to the formation of several metabolites : AFM₁ and AFP₁ which are hydroxylated products of AFB₁ and aflatoxin B₁-dialcohol and AFB₁-GSH which are detoxified products of AFB₁-8,9-epoxyde. The metabolite profiles of AFB₁ after incubation with differentiated HepaRG cells and 3 days primary human hepatocytes are displayed in Figure 3.A. AFM₁, AFP₁ and aflatoxin B₁-dialcohol were identified and the same range of values was obtained in both cell cultures (AFM₁: 0.27 and 0.4 ; AFP₁: 66 and 92 and AFB₁-diol: 0.3 and 0.3 pmol/mg/min in HepaRG cells and human hepatocytes respectively). AFB₁-GSH conjugates were detected only after a 3-methylcholantrene induction in HepaR cells and were found in higher amounts in human hepatocyte cultures (<0.1 and 0.32 pmol/mg/min respectively).

Acetaminophen is one of the most highly used non-prescription analgesic and antipyretic drugs. At therapeutic doses, this compound is detoxified through the formation of glucuronides and sulfoconjugates that are rapidly excreted in urine. At toxic doses, a depletion in glutathione occurred and an electrophilic metabolite, the N-acetyl-p-benzoquinone imine, is formed by CYP2E1, CYP3A4 and CYP1A2. Figure 3.B shows that differentiated HepaRG cells seeded at low density were able to metabolize acetaminophen in sulfate and glucuronide metabolites. The same profile was observed when acetaminophen was incubated with human hepatocytes after 5 days in primary culture. The values were 280.2 \pm 37.0 and 347.9 \pm 70.2

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pmol/mg/min for glucuronides and 51.5 ± 6.4 and 132.6 ± 11.7 pmol/mg/min for sulfoconjugates in HepaRG cells and human hepatocytes respectively.

Evaluation of xenobiotic cytotoxicity

Toxicity of four compounds, namely acetaminophen, AFB₁, amiodarone and chlorpromazine, was estimated in differentiated HepaRG cells from low or high density cultures and in HepG2 cells using the MTT test (Figure 4). Whatever the compound similar data were obtained with differentiated HepaRG cells whether they were seeded at low or high density and differences between HepaRG and HepG2 cells were observed only for the two compounds, acetaminophen and AFB₁, which toxicity is mediated by formation of toxic metabolites by CYPs. Indeed, as expected, their toxicity, especially that of the most toxic one, AFB₁, was much greater in HepaRG than in HepG2 cells after either 24 or 72h of treatment. No toxicity of AFB₁ was even observed in HepG2 cells after a 24 hours exposure to the highest dose tested (100 μ M) while the IC₅₀ was around 5 μ M in HepaRG cell cultures at the same time. At 72h, no viable HepaRG cells were observed with AFB₁ concentrations greater than 5 μ M while around 50% of HepG2 cells were still alive with a 100 μ M concentration. Similar but much less marked differences were observed with acetaminophen. The slightly more intense toxicity observed in HepaRG cells seeded at high density than in HepaRG cells seeded at low density after a 24 or 72h incubation with AFB₁ or acetaminophen was probably due to a higher proportion of hepatocyte-like cells after seeding at high density.

For the two other compounds, amiodarone and chlorpromazine, that do not require metabolism to exhibit toxic effects, the dose-curve responses were quite similar in the two cell lines. Amiodarone, an antiarrhythmic drug, induced phospholipidosis characterized by cytoplasmic accumulation of vesicles in hepatocytes (Poucell et al., 1984). Such vesicles were easily observed in HepaRG cells after a 24h treatment by phase-contrast microscopy (Figure

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5); they also appeared in HepG2 cells (not shown). Similar dose-curves responses were observed in HepaRG and HepG2 cells. IC_{50} were around $50\mu M$ and $20\mu M$ after respectively 24 and 72h of treatment. Chlorpromazine, a cholestatic agent, exhibited IC_{50} close to those calculated in amiodarone-treated HepaRG and HepG2 cell cultures.

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DISCUSSION

Primary human hepatocytes represent the most pertinent model for *in vitro* drug metabolism and toxicity studies. However, they are not functionally stable with time in culture. Indeed, in agreement with previous observations (Morel et al., 1990; Abdel-Razzak et al., 1993; Morel et al., 1993) and as shown in this study, compared to those expressed in freshly human hepatocytes, a rapid and marked decrease of transcripts was observed for some genes, especially those encoding CYPs, after cell plating although significant levels of various phase 1 and phase 2 xenobiotic metabolizing enzyme activities were still observed for at least a few days in standard culture conditions. Transcript levels expressed in freshly human hepatocytes are comparable to those found in human liver tissue (Rodriguez-Antona et al., 2000) and a pool of three cell populations was used to reduce interindividual variations. Several approaches have been reported to improve preservation of liver-specific functions in primary hepatocyte cultures, e.g. co-culture with rat liver biliary epithelial cells (Guguen-Guillouzo et al., 1983), plating cells at different densities and using sandwich configuration by additional layer of extracellular matrix (Hamilton et al., 2001); however in all cases marked phenotypic changes have been observed resulting particularly in reduced expression of several major CYPs. By contrast, most human and animal hepatoma cell lines have retained little drug metabolism capacity. We show here that HepaRG cells exhibited a unique behavior in culture characterized by their ability to express various liver-specific functions after having reached confluency.

Six CYPs were analysed : three of them, CYP2C9, CYP3A4 and CYP2D6 are responsible for the metabolism of around 90% of the drugs presently in use while the three others, CYP1A2, CYP2B6 and CYP2E1 also metabolize various drugs and other chemicals including a number of carcinogens. When comparison was performed with human

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hepatocytes in primary culture maintained 3 to 5 days without DMSO, transcript levels of these CYPs were in the same range as those found in differentiated HepaRG cells except for CYP3A4 which is particularly enhanced in DMSO-treated HepaRG cells. Furthermore, levels of CYP activities in differentiated HepaRG cells were also comparable to those usually found in primary human hepatocyte cultures (Guillouzo and Chesne, 1996; Gomez-Lechon et al., 2001). By contrast, the levels of CYPs expressed in HepG2 cells (Sassa et al., 1987; Sumida et al., 2000; Ogino et al., 2002) and other transformed hepatocytes of tumoral origin (Iwahori et al., 2003) or obtained by oncogenic immortalization (Pfeifer et al., 1993; Mills et al., 2004) are quite low if detectable. Recently, Mills et al. (Mills et al., 2004) measured conversion of testosterone to 6 β -hydroxytestosterone catalysed by CYP3A4 in an immortalized human hepatocyte cell line and found that, although responsive to the prototypical inducer rifampicin, this activity was several hundred fold lower than that estimated in HepaRG cells. Even when compared to the levels of CYP activities determined in human hepatoma B16A2 cells (Gomez-Lechon et al., 2001), another cell line obtained in our laboratory and found to express various liver-specific functions, those found in HepaRG cells were much higher (formation of the 6 β -hydroxytestosterone was around 60 pmol/mg/min in B16A2 cells and around 500 pmol/mg/min in differentiated HepaRG cells in presence of 2% DMSO).

Most of the genes belonging to CYP1-4 families can be transcriptionally induced by xenobiotics and specific receptor proteins are playing a key role in gene induction stimulated by each of the four mechanistically distinct classes of P450-inducing xenochemicals (Rushmore and Kong, 2002; Dickins, 2004). The first identified, the Ah receptor, belongs to the bHLH/PAS (basic helix-loop-helix/Per-Arnt-Sim) family of transcription factors and stimulates transcription of CYP1A genes and various other genes by a well understood mechanism. This receptor, which is expressed in various cell types, including undifferentiated ones (van Grevenynghe et al., 2005), was found at comparable levels in HepaRG cells

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whatever their stage of differentiation and in primary human hepatocytes. The three other known xenobiotic induction mechanisms include three distinct orphan receptors, CAR, PXR and PPAR α , that are members of hormone nuclear receptor family. They form heterodimers with RXR and for CAR and PXR regulate expression of CYP 2 and 3 families and several GSTs and UGT enzymes; they also interact with nuclear receptors controlling various pathways of endogenous metabolism. PPAR α regulates expression of CYP4A in rodents and plays a role in the regulation of lipid and carbohydrate metabolism. These receptors that are most highly expressed in the liver were also found in high levels in differentiated HepaRG cells. Interestingly, a high expression of CAR has never been reported before in any hepatoma cell line (Zelko and Negishi, 2000). Accordingly, CYPs 1A2, 2C9 and 3A4 known to be transcriptionally increased by prototypical inducers in normal hepatocytes were similarly induced in HepaRG cells.

For some functions, the highest values were found in HepaRG cells maintained in the presence of DMSO. This agent is recognized as a differentiation inducing compound in many tumor cell lines. DMSO also increases albumin production in immortalized hepatocytes (Higgins and Borenfreund, 1980) and favors cell survival and maintenance of differentiated functions, such as production of plasma proteins, in primary rat hepatocytes (Isom et al., 1985; Mitaka et al., 1993). The mechanism(s) by which DMSO induces cellular differentiation is still poorly understood; it has been shown to act as a reactive oxygen species scavenger and an antiapoptotic agent (Villa et al., 1991; Gilot et al., 2002). The results reported here clearly show that DMSO induced a more differentiated state and enhanced expression of several metabolizing enzymes in HepaRG cells. However, it was ineffective on some CYPs and the liver-specific proteins studied, including albumin. Interestingly, certain CYP inducers were ineffective in DMSO-exposed HepaRG cells, especially when cells were seeding at high density. Indeed, the levels of activities reached in the presence of DMSO was

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comparable to those observed in DMSO-free cells treated with the prototypical inducer. It may be postulated that by enhancing expression of certain nuclear receptors and liver transcription factors, DMSO allowed certain CYP genes to reach maximum transcription activity as already observed by others (Nishimura et al., 2003; Su and Waxman, 2004).

In agreement with the active expression of phase 1 and phase 2 xenobiotic metabolizing enzymes the suitability of HepaRG cells for the determination of chemical metabolism profiles was supported by analyzing metabolic profiles of acetaminophen and AFB₁ and the cytotoxicity effects of several hepatotoxicants. The same metabolites as those obtained with primary human hepatocyte cultures were observed with the two compounds indicating that HepaRG cells expressed the different enzymes involved in their biotransformation at suitable levels. This conclusion is supported by the toxicity of reference hepatotoxicants. Their cytotoxicity was dependent on the compound, dose and duration of exposure. As expected, AFB₁ and acetaminophen that are hepatotoxic via the formation of electrophilic metabolites by CYP-dependent reactions were more cytotoxic to HepaRG than to HepG2 cells. By contrast, amiodarone and chlorpromazine induced similar toxicity in both cells. Characteristic accumulation of cytoplasmic vesicles corresponding to secondary lysosomes loaded with phospholipids (Poucell et al., 1984) was observed under light microscopy after treatment with amiodarone in both types of HepaRG cells and in HepG2 cells.

Why are HepaRG cells much more differentiated than any other human hepatocyte cell line already described ? It may be noticed that they are derived from an hepatocarcinoma and not, like HepG2 cells, from an hepatoblastoma. Second, they show only limited chromosomal rearrangements (Gripon et al., 2002; Parent et al., 2004). Third, and certainly the most original feature, when passaged at low density, they recover characteristic features of

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progenitor cells able to differentiate in both hepatocytes and biliary epithelial cells (Parent et al., 2004) and to form a co-culture system that strongly resembles that we have a long time ago described by associating primary normal hepatocytes with rat liver epithelial cells and resulting in long-term maintenance of liver-specific functions at high levels (Guguen-Guillouzo et al., 1983). Indeed, several studies have demonstrated that various functions, including phase 1 and phase 2 xenobiotic enzyme activities were better and longer preserved in cocultures versus pure cultures of human and animal hepatocytes (Begue et al., 1983; Fraslin et al., 1985; Niemann et al., 1991). Such a model should represent a unique tool to distinguish the liver epithelial cell type target of hepatotoxicants.

Human hepatoma cell lines have also been used for the design of bioartificial livers although their detoxifying capacity was limited even when cultured in a 3-dimensional perfusion system that led to an increased expression of CYP3A4 and inducibility by rifampicin (Iwahori et al., 2003). HepaRG cells could represent a very good alternative to either primary hepatocytes or other human hepatoma cell lines; not only they exhibit a large set of liver-specific functions but in addition, although they derive from an hepatitis C virus-infected liver they do not express viral markers.

In conclusion, for the first time we report that a human hepatoma cell line is able to express the major CYP-related activities as well as other liver-specific functions. The fact that when seeded at high density hepatocyte-like clusters retain their differentiated state and can immediately be used after seeding makes them suitable for high throughput screening as well as studies on metabolism and hepatotoxicity of chemicals.

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- ¹ Availability of HepaRG cells: contact christiane.guillouzo@rennes.inserm.fr (academic laboratories) or christophe.chesne@biopredic.com (industrial laboratories)

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LEGENDS FOR FIGURES

Figure 1. Phase-contrast micrographs of HepaRG cells. Cells seeded at low density and cultured for either 10 days without DMSO (the cells exhibited variable shapes) (A), 30 days without DMSO (B) or 15 days without DMSO then exposed to 2% DMSO for 15 days (C), differentiated HepaRG cells seeded at high density and maintained in culture for 72h in a medium deprived of 2% DMSO (D), or supplemented with 2% DMSO (E). Hepatocyte-like (H) and epithelial-like (EP) cells ; bile canaliculus (BC). (Original magnification x 150)

Figure 2. mRNA analysis by RT-qPCR (A) HepaRG cells seeded at low density and cultured for 5, 8, 15 and 30 days in the absence or presence of 2% DMSO between days 15 and 30. (B) HepaRG cells cultured for 35 or 37 days. At day 15, 2% DMSO was added to the culture medium until day 34. Then the cells were cultured the last 24h (day 35) or 72h (day 37) without 2% DMSO. (C) HepaRG cells seeded at high density and cultured for 24h or 72h with or without 2% DMSO.

Figure 3. HPLC metabolic profiles of AFB₁ and acetaminophen in primary human hepatocyte cultures and 30 days differentiated DMSO-treated HepaRG cells. (A-1) aflatoxin B₁-dialcohol (A-2) Aflatoxin M₁ (AFM₁), (A-3) Aflatoxin P₁ (AFP₁) and (A-4) AFB₁, (B-1) glucuronide acetaminophen, (B-2) sulfate acetaminophen and (B-3) acetaminophen. Incubations lasted 8h with 5 μ M AFB₁ and 10h with 2mM acetaminophen; human hepatocyte primary cultures were used 5 and 3 days after seeding respectively. Detection was performed at $\lambda=250$ nm for acetaminophen and by fluorescence (λ_{ex} 430nm and λ_{em} 370nm) for AFB₁.

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Figure 4. Comparative cytotoxic effects of chlorpromazine, amiodarone, AFB₁ and acetaminophen on HepaRG and HepG2 cells. Differentiated HepaRG cells from low density seeding (●) and high density seeding (□) and confluent HepG2 cells (▲) were exposed to the chemicals for 24h (A) or 72h (B). Cell viability was assayed using a standard MTT test. The results were normalized to control cells and expressed as means ± S.D. (n=3 cultures).

Figure 5 – Effects of amiodarone on HepaRG cells. Phase-contrast micrographs of confluent DMSO-treated HepaRG cells cultured for 24h in a FCS-free medium containing either only the vehicle (0.2% DMSO) (A) or 50μM amiodarone (B). Numerous intracytoplasmic vesicles are visible in amiodarone-treated HepaRG cells (arrow). (Original magnification x 300).

Table 1. Primer sequences used for RT-qPCR

<i>Accession number</i>	<i>Genes</i>	<i>Foward Primer</i>	<i>Reverse Primer</i>
A06977	Albumin	TGCTTGAATGTGCTGATGACA GG	AAGGCAA GTCA GCA GGCATCTCATC
X02747	Aldolase B	GCATCTGTCA GCA GAATGGA	TAGA CA GCA GCCA GGA CCTT
V01514	Alpha-fetoprotein	TGCA GCCAAAGTGAA GA GGGAA GA	CATA GCGA GCA GCCCAA GA A GAA
X00637	Haptoglobin	CGGTT CGCTACCA GTGTAA GAAC	CCACTGCTTCTTATCATTAA GGTGTA
L19872	AhR	ACATCA CCTACGCCA GTCGC	TCTATGCCGCTTGGA A GGAT
BC069626	CAR	TGATCA GCTGCAA GA GGAGA	AGGCCTA GCAACTTCGCA TA
BC017304	PXR	CCA GGA CATA CA CCCCTTTG	CTACCTGTGATGCCGAA CAA
Z00036	CYP 1A2	TGGA GA CCTCCGA CA CTCTCT	CGTTGTGTCCCTTGTGTGC
M29874	CYP 2B6	TTCCTA CTGCTCCGTCTATCAAA	GTGCA GAATCCCACA GCTCA
S46963	CYP 2C9	GGACA GA GA CGA CA A GCACA	AATGGA CATGAA CAACCCTCA
J02625	CYP 2E1	TTGAA GCCTCTCGTTGA CCC	CGTGGTGGGATACA GCCAA
X12387	CYP 3A4	CTTCATCCAATGGACTGCATAAAT	TCCCAA GTATAACTCTA CACA GA CAA
M16594	GSTA1/2	TGCAACAATTAAGTGCTTTACCTAA GTG	TTAACTAA GTGGGTGAATA GGA GTTGTATT
Y13047	GSTA4	GGATGGTAA CCACCTGCTG	TGCCAAA GA GATTGTGCTT
X08020	GSTM1	ATGGTTGTCCA GGTCTGG	CGCCATCTTGTGCTACATT
M57899	UDP-glucuronosyl transferase 1 A1	TGACGCCCTCGTTGTACATCAG	CCTCCCTTTGGAATGGCA C

Table 2 – Comparative expression of CYPs and nuclear receptors mRNA in HepaRG cells, freshly isolated human hepatocytes and HepG2 cells. Results are expressed as percentage compared to freshly isolated hepatocytes (FIH) arbitrarily set at 100%. FIH correspond to a pool of 3 different cell populations. Results are the mean of two independent experiments in duplicate.

	CYP1A2	CYP2B6	CYP2C9	CYP2D6	CYP2E1	CYP3A4	PXR	CAR	PPARα	AhR
FIH	100	100	100	100	100	100	100	100	100	100
HepG2 cells	0.3	0.5	0	2.3	0	0	49.5	2.4	208.5	35.5
HepaRG cells seeded at low density (days)										
5	0.1	0	0	1	0	0	6.8	0	56.5	94.5
8	0.1	0.1	0.1	1.2	0	0	8	0.1	126.8	134.3
15	0.3	3.2	3.3	0.9	0.1	4.5	51.3	4.1	175.6	121.7
30	2.3	3.5	9.5	1.2	0.2	8.1	95.7	9.1	187.2	64.2
30 (DMSO)	9.1	34.6	34.7	0.8	3.5	176	142.9	22.2	346.5	169.7
35 (-DMSO 24h)	5.5	3.5	26.5	1	0.8	1.6	99.9	8.3	136.7	98.8
37 (-DMSO 72h)	3.9	1.6	16.7	0.9	0.8	2.3	122.6	7.1	135.1	47.5
HepaRG cells seeded at high density after differentiation										
+ DMSO 24h	17.8	72.4	38.1	1.1	13.3	243	176.8	26.4	330.1	92.5
- DMSO 24h	7.5	4.9	22.1	0.8	0.7	6.8	106.4	5.3	173.1	72.9
+ DMSO 72h	3.7	73.1	43.8	1	7	255.6	175.3	30.2	561.1	66.4
- DMSO 72h	5.4	11.9	22	0.8	1	2.8	151.1	6.4	222.9	73.4

Table 3 – Comparative expression of phase 2 enzymes and liver specific-proteins mRNA in HepaRG cells, freshly isolated human hepatocytes and HepG2 cells. Results are expressed as percentage compared to freshly isolated human hepatocytes (FIH) arbitrarily set at 100%. FIH correspond to a pool of 3 different cell populations. Results are the mean of two independent experiments in duplicate.

	GSTA1/2	GSTA4	GSTM1	UGT1A1	Aldolase B	Haptoglobin	Albumin	AFP	Thioredoxin
FIH	100	100	100	100	100	100	100	100	100
HepG2 cells	0.2	2.1	2.4	5.2	0	5.1	12.3	89011	115.8
HepaRG cells seeded at low density (days)									
5	0.4	6.7	8.5	7.4	0	5.1	1.8	0.6	1250.6
8	8	5.9	7.6	9	0.2	76.4	14.1	21	877
15	37.3	9	9.8	10.5	7.8	199.9	85.6	75.6	422
30	36.8	13.1	15.5	17.1	20.9	256.6	82.9	79.4	303.4
30 (DMSO)	108.6	22.6	26.3	186.3	13.5	216.4	70.7	45.8	304.4
35 (-DMSO 24h)	35.7	3.9	5	43	8.7	294.1	63.1	71.3	610.2
37 (-DMSO 72h)	18.3	5.8	6.8	35.4	9.6	344.7	77.9	64.8	479.7
HepaRG cells seeded at high density after differentiation									
+ DMSO 24h	258.2	26.4	33.6	240.6	16.3	197.5	57.1	40.2	429.8
- DMSO 24h	50	4.2	5.8	82.4	7.3	344.8	47.2	54	790.9
+ DMSO 72h	160.3	36.7	45.1	221.1	14.9	196.6	60.4	36.9	280.9
- DMSO 72h	31.3	9.7	7.5	47.3	9.4	479.8	65.2	114	460.9

Table 4 – Expression of CYPs and nuclear receptors mRNA in primary human hepatocytes. RT-qPCR analysis of hepatocyte RNA samples prepared from primary hepatocytes from day 0 (Freshly isolated hepatocytes (FIH)) to day 5 of culture in absence of DMSO. Experiment was performed on one cell population. Results are expressed as % compared to freshly isolated hepatocytes.arbitrarily set at 100%.

Days	CYP1A2	CYP2B6	CYP2C9	CYP2D6	CYP2E1	CYP3A4	PXR	CAR
0	100	100	100	100	100	100	100	100
1	15	29	18	20	14	22	95	7
3	2	8	48	9	2	6	160	14
5	12	4	58	60	11	30	121	29

Table 5 – Drug metabolizing enzyme activities in HepaRG cells. Determinations of testosterone 6 β -hydroxylation (CYP3A4), O-dealkylation of 7-ethoxyresorufin (CYP1A2), chlorzoxazone 6-hydroxylation (CYP2E1) and tolbutamide 4-hydroxylation (CYP2C9) activities were performed on HepaRG cells seeded at low density and cultured for either 15 days or 30 days with addition of 2% DMSO between days 15 and 30, and on differentiated HepaRG cells seeded at high density. Pretreatment with inducers or their vehicle was performed using FCS-free medium added or not with 2% DMSO. The cultures were exposed either 24h (3-methylcholantrene : 3-MC) or 72h (rifampicin : RIF, isoniazid : ISO) to the inducers or their vehicle (UT). Results are expressed as pmoles/mg/min. Student's t test was applied between UT cells and cells treated with inducer for statistical analysis : * p< 0.05, ** p<0.01 and *** p<0.001 (GraphPad Prism software).

	DMSO	EROD (CYP1A1/2)		Tolbutamide 4-hydroxylase activity (CYP2C9)		Chlorzoxazone 6-hydroxylase activity (CYP2E1)		Testosterone 6 β -hydroxylase activity (CYP3A4)	
		UT	3MC (5 μ M)	UT	RIF (25 μ M)	UT	ISO (50 μ M)	UT	RIF (50 μ M)
15 days culture HepaRG cells seeded at low density	-	Traces	48.2 \pm 3 (n=4)	1.0 \pm 0.6 (n=5)	4.5 \pm 3.8 (n=6)	31.9 \pm 13.2 (n=6)	33.4 \pm 11.9 (n=6)	10.9 \pm 4.7 (n=5)	129.3 \pm 22*** (n=6)
Differentiated HepaRG cells seeded at low density	-	Traces	68 \pm 5.2 (n=6)	6 \pm 1.4 (n=3)	7.8 \pm 1.8 (n=3)	131.3 \pm 11.2 (n=3)	96 \pm 12 * (n=3)	39.7 \pm 15 (n=3)	212.9 \pm 48 ** (n=3)
	+	Traces	154.6 \pm 13.7 (n=6)	7.5 \pm 0.3 (n=3)	10.15 \pm 0.5** (n=3)	140.9 \pm 56.5 (n=3)	221.5 \pm 10 (n=3)	576 \pm 3 (n=3)	806.8 \pm 104 (n=3)
Differentiated HepaRG cells seeded at high density	-	Traces	63.1 \pm 0.7 (n=6)	6.2 \pm 1.6 (n=3)	13.1 \pm 2.6* (n=3)	278 \pm 8.4 (n=3)	197.8 \pm 103 (n=3)	54.4 \pm 10 (n=3)	540.1 \pm 68 *** (n=3)
	+	Traces	129 \pm 16.3 (n=6)	9.8 \pm 1.5 (n=3)	11.5 \pm 3.5 (n=3)	483.1 \pm 30.3 (n=3)	455.2 \pm 65 (n=3)	781.8 \pm 85 (n=3)	820.5 \pm 210 (n=3)

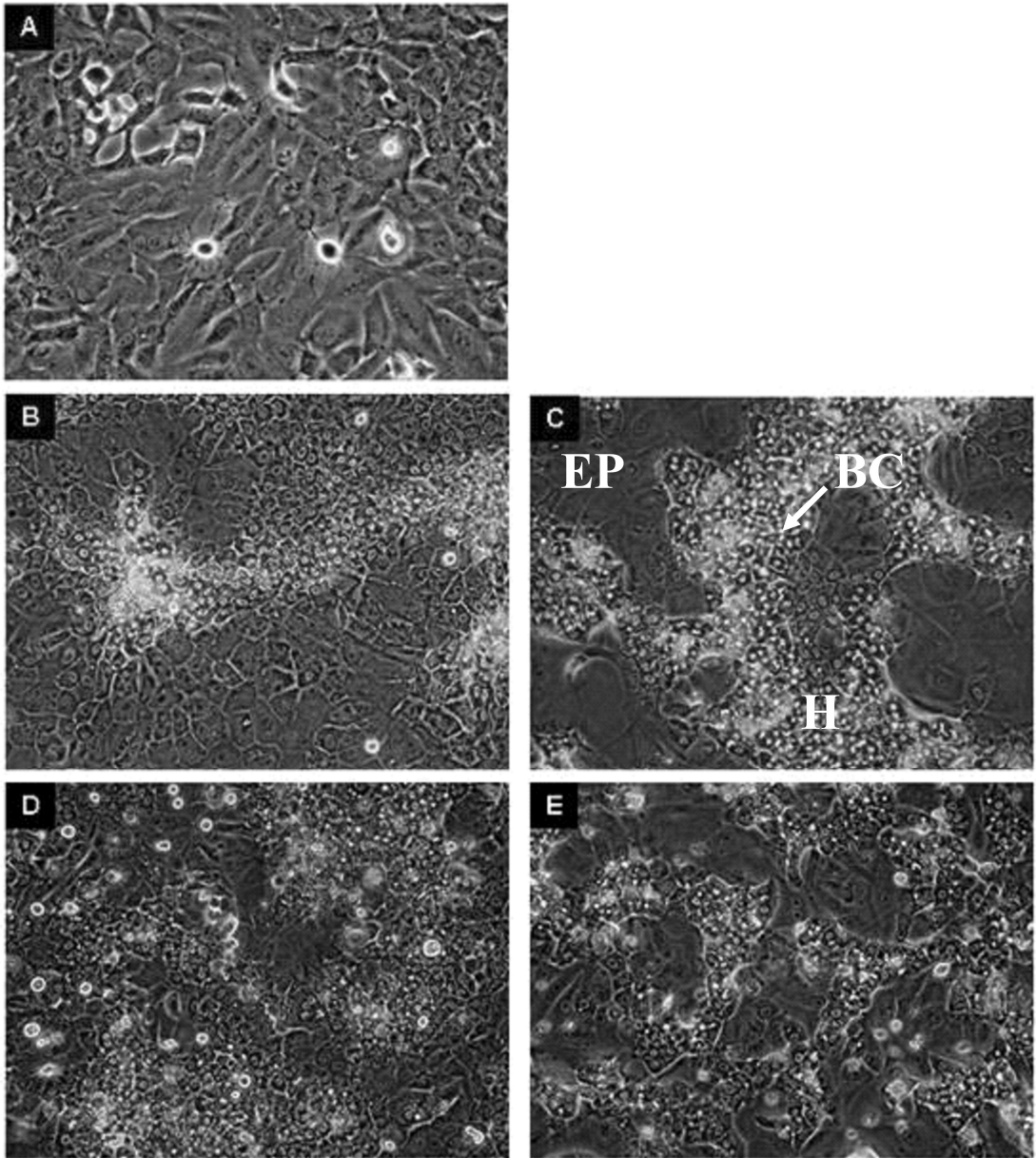
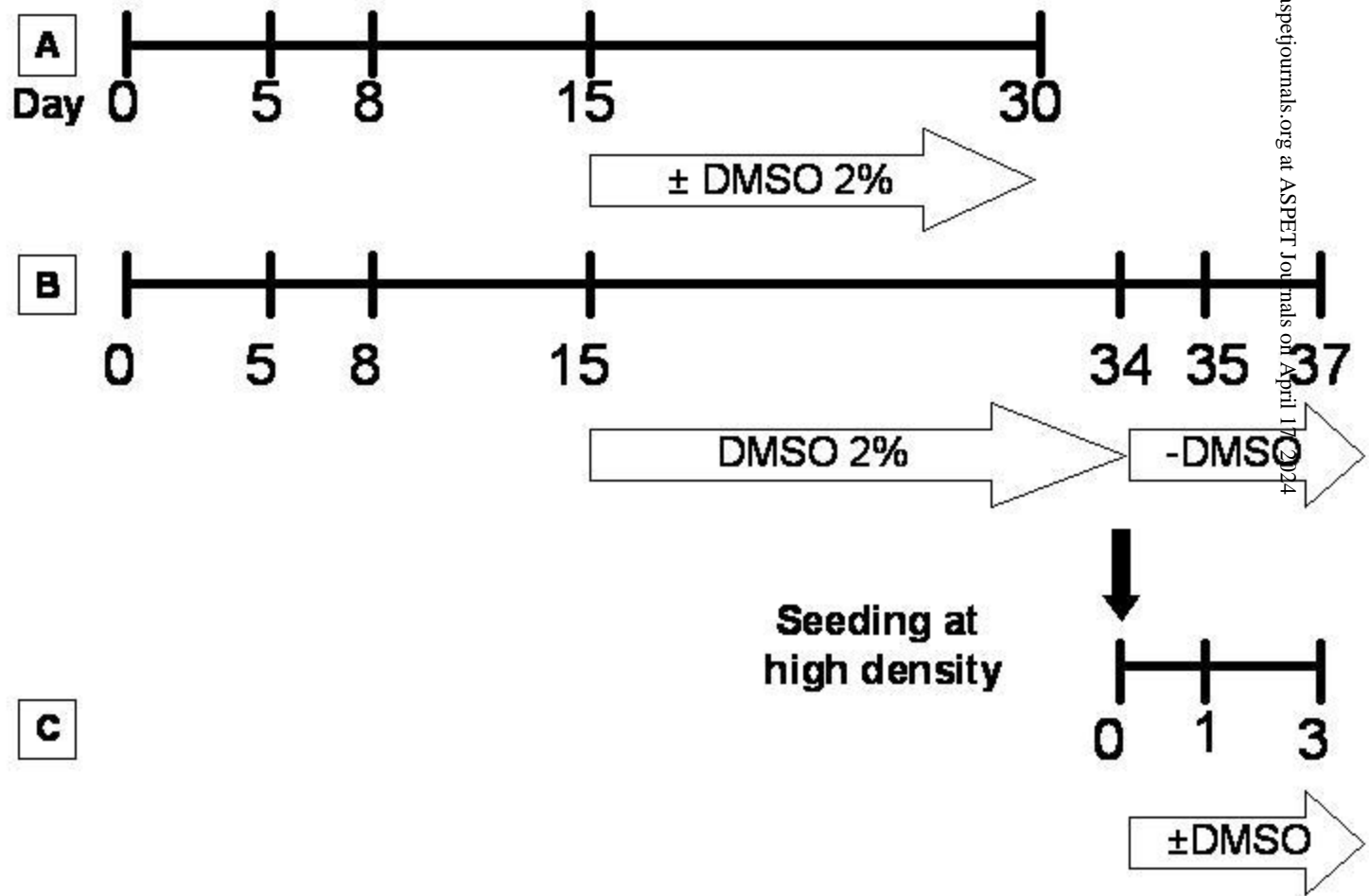


Figure 1



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Figure 2

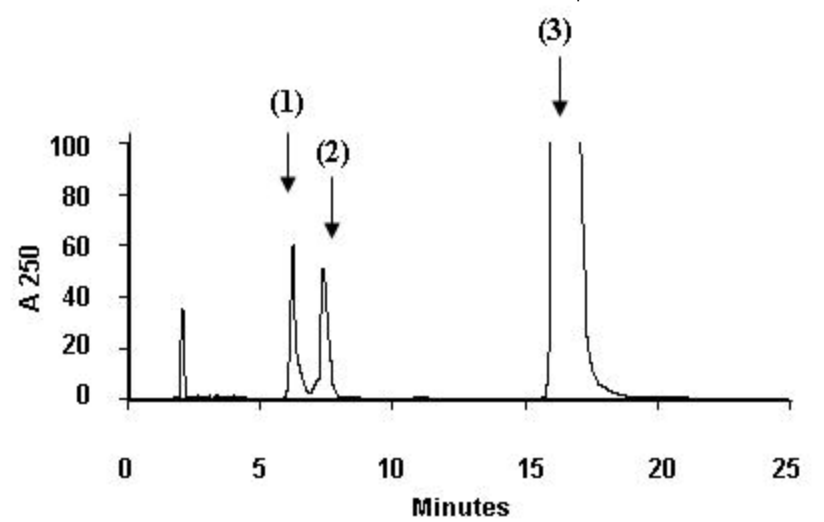
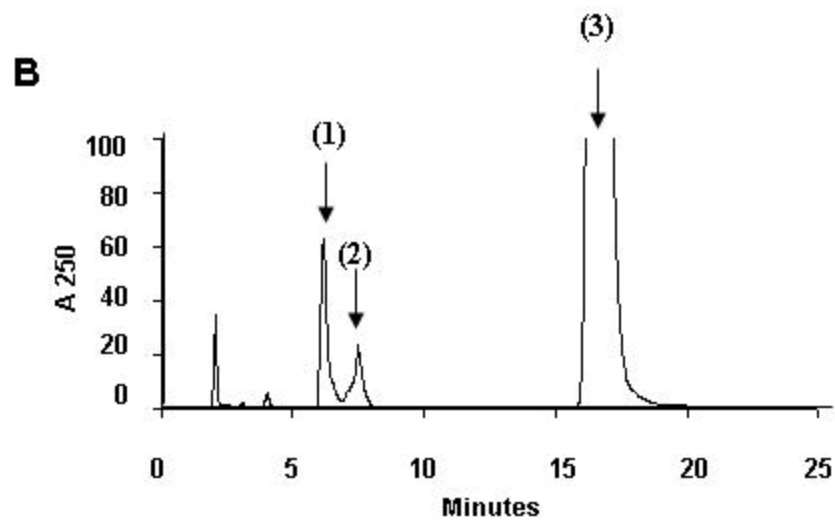
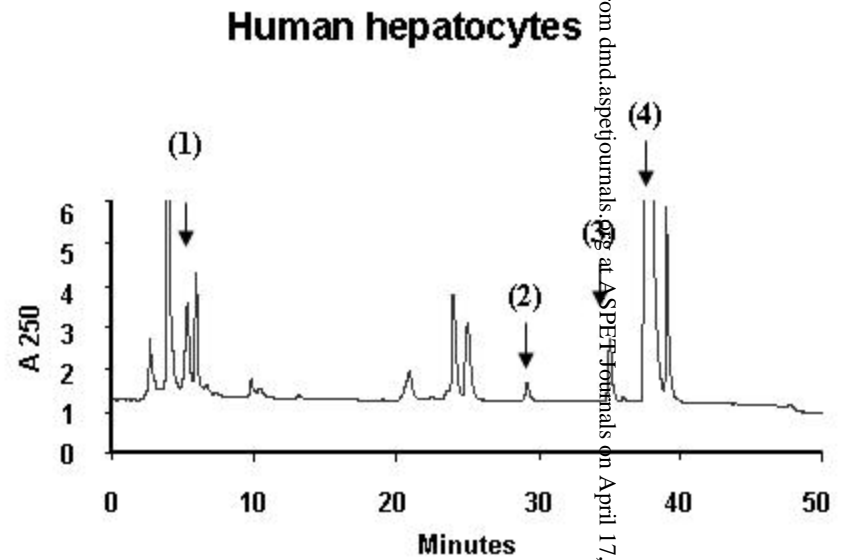
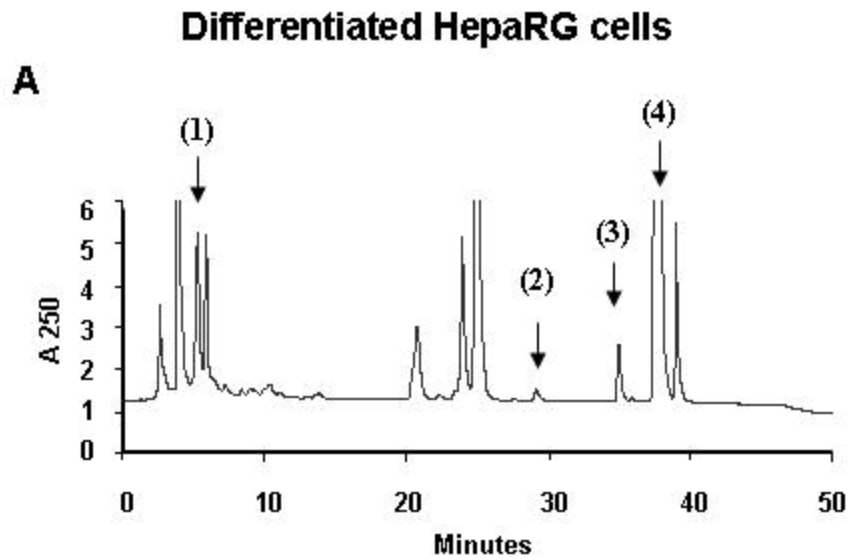


Figure 3

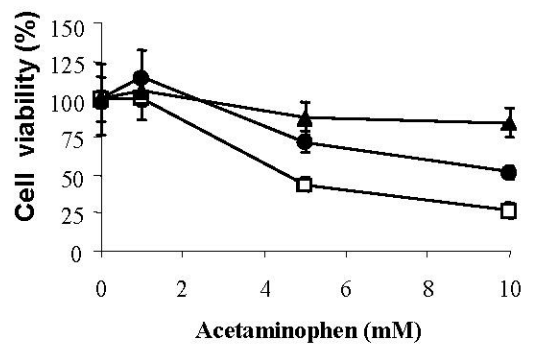
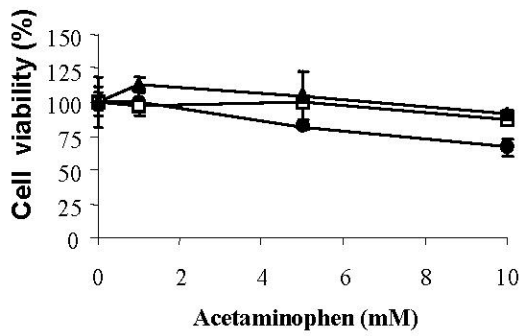
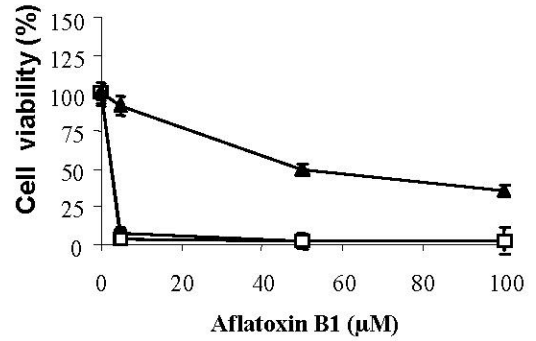
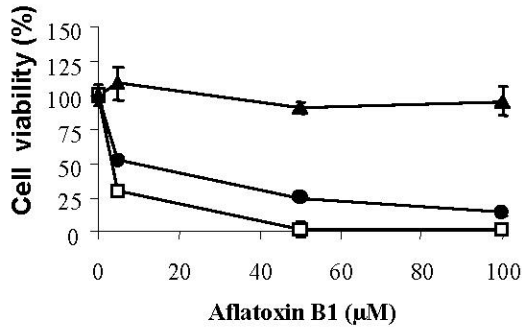
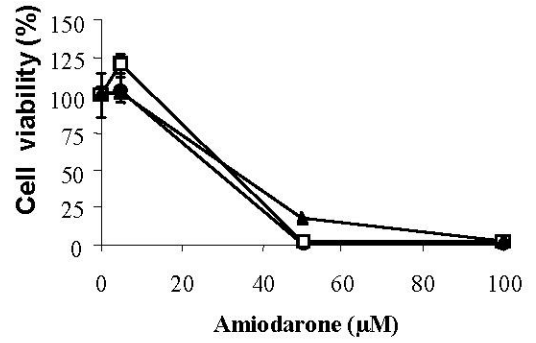
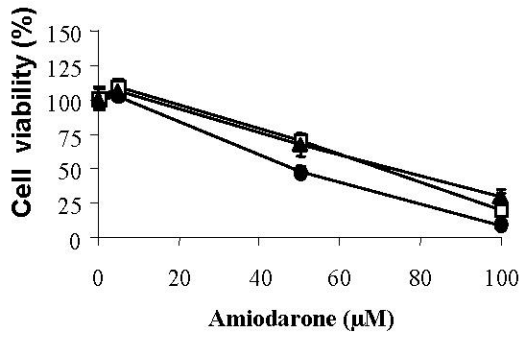
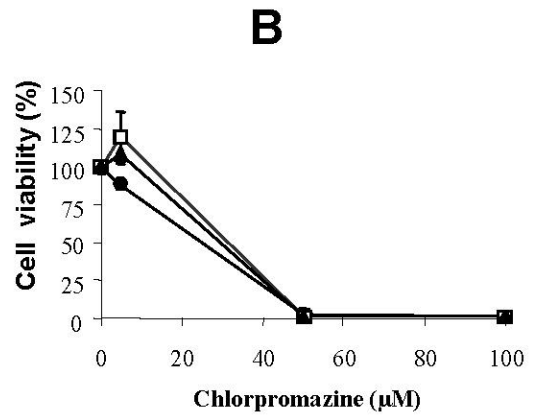
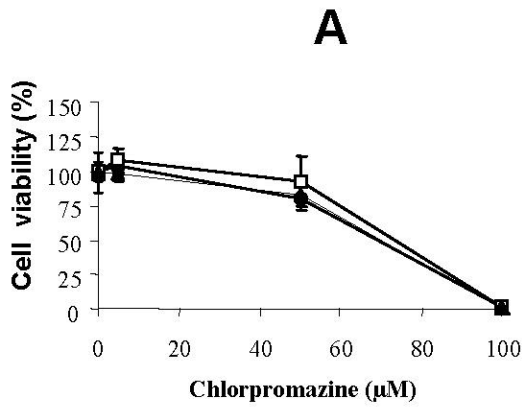


Figure 4

Figure 5

