Cytochrome P450 Transcriptional Regulation by Testis-Specific Y-Encoded-Like Protein: Identification of Novel Upstream Transcription Factors

Suganti Shivaram, † Huanyao Gao, † Sisi Qin, Duan Liu, Richard M. Weinshilboum, and Liewei Wang

Division of Clinical Pharmacology, Department of Molecular Pharmacology and Therapeutics, Mayo Clinic, Rochester, Minnesota

Received May 17, 2022; accepted July 5, 2022

ABSTRACT

Cytochrome P450s (CYPs) display significant inter-individual variation in expression, much of which remains unexplained by known CYP single-nucleotide polymorphisms (SNPs). Testis-specific Y-encoded-like proteins (TSPYs) are transcriptional regulators for several drug-metabolizing CYPs including CYP3A4. However, transcription factors (TFs) that might influence CYP expression through an effect on TSPYL expression are unknown. Therefore, we studied regulators of TSPYL expression in hepatic cell lines and their possible SNP-dependent variation. Specifically, we identified candidate TFs that might influence TSPYL expression using the ENCODE ChIPseq database. Subsequently, the expression of TSPYL1/2/4 as well as that of selected CYP targets for TSPYL regulation were assayed in hepatic cell lines before and after knockdown of TFs that might influence CYP expression through TSPYL-dependent mechanisms. Those results were confirmed by studies of TF binding to TSPYL1/2/4 gene promoter regions. In hepatic cell lines, knockdown of the REST and ZBTB7A TFs resulted in decreased TSPYL1 and TSPYL4 expression and increased CYP3A4 expression, changes reversed by TSPYL1/4 overexpression. Potential binding sites for REST and ZBTB7A on the promoters of TSPYL1 and TSPYL4 were confirmed by chromatin immunoprecipitation. Finally, common SNP variants in upstream binding sites on the TSPYL1/4 promoters were identified and luciferase reporter constructs confirmed SNP-dependent modulation of TSPYL1/4 gene transcription. In summary, we identified REST and ZBTB7A as regulators of the expression of TSPYL genes which themselves can contribute to regulation of CYP expression and—potentially—of drug metabolism. SNP-dependent modulation of TSPYL transcription may contribute to individual variation in both CYP expression and—downstream—drug response phenotypes.

SIGNIFICANCE STATEMENT

Testis-specific Y-encoded-like proteins (TSPYs) are transcriptional regulators of cytochrome P450 (CYP) gene expression. Here, we report that variation in TSPYL expression as a result of the effects of genetically regulated TSPYL transcription factors is an additional factor that could result in downstream variation in CYP expression and potentially, as a result, variation in drug biotransformation.

INTRODUCTION

Approximately half of the population of the United States uses prescription drugs every year ((CDC), 2015–2018b). Adverse drug events and toxicity as a result of prescription drug use could potentially be decreased by enhanced understanding of variation in pharmacokinetic (PK) and/or pharmacodynamic (PD) factors that contribute to inter-individual differences in drug exposure or response ((CDC), 2015–2018a). Many studies ranging from candidate gene studies to genome-wide analyses have highlighted the contribution of genomics to individual variation in the occurrence of adverse drug events and/or inter-individual variability in drug response phenotypes (Nebert et al., 2013; Nelson, 2013; Zanger and Schwab, 2013). The cytochrome P450 (CYP) enzymes play an important role in Phase I drug metabolism and, as a result, have the potential to be major contributors to individual variability in PK. The CYP superfamily includes 18 families of protein encoding human CYP genes, including the CYP1, CYP2, and CYP3 families, which include many important drug-metabolizing enzymes (Bush et al., 2016; Kozyn et al., 2017). CYP3A4, CYP2C9, and CYP2C19 are important CYPs with common, functionally significant genetic polymorphisms (Evans and Relling, 1999). These three enzymes have been estimated to contribute to the metabolism of approximately 50%, 20% and 5% of drugs, respectively (Evans and Relling, 1999; Neavin et al., 2019). However, known single-nucleotide polymorphism (SNP) variants that influence the expression or function of CYP3A4, CYP2C9, and CYP2C19 explain only a portion of inter-individual differences in drug biotransformation catalyzed by these CYPs (Daly et al., 2010; Liu et al., 2010; Zi et al., 2010; He et al., 2011; Wang et al., 2011; Mot-singer-Reif et al., 2013; Wright et al., 2018). Most of the early examples of CYP pharmacogenomic variation involved SNPs that resulted in alterations in the amino acid sequence of the encoded protein.
alterations in gene splicing or variation in gene structure (deletions/insertions) but, increasingly, it is becoming apparent that variants which alter gene transcription represent a major source of pharmacogenomic variation—either directly or indirectly (Wang et al., 2022).

Previous studies from our group reported that testis-specific Y-encoded-like proteins (specifically TSPYL1, 2, and 4) are transcriptional regulators that can influence the expression of CYP3A4, CYP2C9, and CYP2C19 (Qin et al., 2018). Elevated expression of these TSPYLs can suppress the expression of CYP3A4, CYP2C9, and CYP2C19 (Qin et al., 2018). The TSPYL gene family consists of six genes, TSPYL1 to TSPYL6, with TSPYL3 being a pseudogene. The Genotype-Tissue Expression database (https://gtexportal.org/) reports that the TSPYLs are expressed in most human tissues, with isoform-specific variation in their tissue distribution. TSPYLs have multiple cellular functions (de Andrade et al., 2006; Epping et al., 2015), and genetic polymorphisms and/or variation in the methylation status of these genes have been related to disease states (Kim et al., 2006; Guo et al., 2012; Le Gallo et al., 2012). In addition, as stated above, functionally significant polymorphisms in TSPYL genes have been reported to alter their ability to regulate transcription and, as a result, the expression of CYPs, resulting in inter-individual variation in drug biotransformation (Qin et al., 2018; Qin et al., 2020). Specifically, and of importance for the studies described subsequently, we reported previously that knock-down (KD) of TSPYL1, 2 and 4 in HepaRG cells can result in increased expression of CYP2C9, 2C19, and 3A4, while overexpression (OE) of these same TSPYL genes can result in decreased expression of the same CYPs, with the most striking effects for CYP3A4 (Qin et al., 2018; Qin et al., 2020). Given our increasing recognition of the role of the TSPYLs in drug metabolism, it is important to understand the possible role of upstream regulators of TSPYL gene expression, specifically, transcription factors (TFs) that influence TSPYL gene expression, to help us achieve a more comprehensive understanding of downstream variability in CYP expression and drug response phenotypes. In the present study, we set out systematically to identify TFs that might be involved in the regulation of TSPYL1, 2, and 4 expression in human hepatic cell lines as a step toward a more comprehensive understanding of the potential contribution of the TSPYLs to individual variation in CYP expression and function.

Materials and Methods

**ENCODE Chromatin Immunoprecipitation (ChIP)-Seq Data.** The ENCODE UCSC genome browser includes ChIP-seq data for HepG2 cells that lists TFs that bind to the promoter regions of TSPYL1, TSPYL2, and TSPYL4, 1 kbp upstream or downstream of the transcription starting site. We used that information as a starting point for this series of studies of possible transcriptional regulatory factors that might contribute to variation in the expression of human TSPYLs.

**Hepatic Expression Quantitative Trait Loci (eQTL) Database Association Analysis.** We next determined associations between TFs that bind to TSPYL gene promoters and TSPYL1, TSPYL2, and TSPYL4 expression in an hepatic eQTL database (Innocenti et al., 2011) using Pearson correlation analyses and identified TFs that might bind near TSPYL1, TSPYL2 or TSPYL4 and, as a result, might influence the expression of genes influenced by TSPYL expression with P values <0.05.

**Transfection of HepaRG Cells and HepG2 Cells.** Specific short interfering RNAs (siRNAs) targeting the 30 candidate TFs that we had identified in the ENCODE database were then used to knock down the expression of those TFs in HepaRG and HepG2 cells using specific siRNAs, with non-targeting siRNAs as a control (see Supplemental Table 1). The cells were harvested 48 hours after transfection, and RNA was extracted for the performance of reverse transcription polymerase chain reaction (RT-PCR).

**Gene Expression Quantification.** Total RNA from HepG2 and HepaRG cells was extracted and was used to perform real-time quantitative PCR to assay expression levels of TSPYL1, TSPYL2, TSPYL4, CYP3A4, CYP2C9, and CYP2C19, as well as after the after KD of TFs using the primers listed in Supplemental Table 2. Alterations in the expression of those genes were expressed as fold change from baseline.

**ChIP for HepaRG Cells.** HepaRG cells were used to perform ChIP assays to validate TF binding to promoter regions of the TSPYL1 and TSPYL4 genes, and the results were analyzed using real-time quantitative PCR. TSPYL1 and TSPYL4 were selected for study because they map in relatively close proximity in the genome and because our previous experiments had demonstrated that those two TSPYL genes appeared to have significant impact on variation in the expression of CYP3A4 (Qin et al., 2018).

![Fig. 1. Transcription factors that might transcriptionally regulate TSPYL1/2/4 expression. The table lists the 30 TFs identified as binding to the promoter regions of TSPYL 1/2/4 as well as those that also displayed significant correlations with TSPYL expression in human liver tissue (Storey et al., 2011). The three TFs that were studied in detail here, ZBTB7A, REST, and MAFK, are highlighted in red type in the TF gene list.](image-url)
Luciferase Reporter Assay. The luciferase reporter vector, pGL4.23 (Cat#: E8411), was obtained from Promega with inserts encoding either 2 Kbp of the TSPYL1 or 2 kbp of the TSPYL4 promoter regions and were used to create TSPYL1 wild-type promoter, TSPYL1 variant promoter, TSPYL4 wild-type promoter or TSPYL4 variant promoter constructs (Supplemental Table 4). Those vectors were then used to transfect HepaRG cells. The cells were harvested 48 hours after transfection to assay relative luciferase and Renilla activities.

Additional methodological details have been provided as Supplemental Methods.

Results

The series of studies described subsequently was designed to pursue our previous observation of the potential importance of members of the TSPYL gene family in regulation of the expression of drug metabolizing CYPs (Qin et al., 2018; Qin et al. 2020). Specifically:

1. As a first step in the present studies, the ENCODE database was consulted to identify TFs that might bind to the promoters of the TSPYL1/2 and 4 genes in HepG2 cells. Thirty potential candidate TFs were identified.

2. Those 30 candidate TSPYL TFs were then knocked down in HepaRG cells, and the effect of KD on the expression of CYP3A4, CYP2C9, and CYP2C19 was determined and compared with our previous results after the KD of TSPYL1, 2, and 4 in this same cell line. The most striking similarities observed related to CYP3A4 and the putative TSPYL TFs REST and ZBTB7A. Therefore, the final series of studies focused on SNPs in the promoters of TSPYL1 and TSPYL4—two genes that map in close proximity to each other in the genome—as well as the effect of REST and ZBTB7A on their transcription.

3. The final series of experiments addressed the possible binding of REST and ZBTB7A to the promoters of TSPYL1 and TSPYL4 and the influence of SNPs in those genes on that binding and the expression of those two TSPYLs. Neither REST nor ZBTB7A appeared to bind to the promoter of TSPYL1, so TSPYL2 was not included in this series of experiments.

Candidate Transcriptional Regulators of TSPYL1, TSPYL2, and TSPYL4. The initial list of candidate TFs that might participate in regulation of the expression of TSPYL1, TSPYL2, and TSPYL4 was assembled based on their ability to bind to promoter regions of the genes encoding these three TSPYLs based on ENCODE data for HepG2 cells. Specifically, using HepG2 cell ChIP-seq data, we identified TFs that bound to 2 Kbp regions extending 1 Kbp on either side of the transcription start sites for TSPYL1, TSPYL2, or TSPYL4. As the next step, significant correlations between expression levels of these candidate TFs and the expression of TSPYL1, TSPYL2, and TSPYL4 were determined by Pearson correlation analysis of hepatic eQTL expression data obtained from the Genotype-Tissue Expression database—with the full understanding that hepatic tissue expression might differ significantly from that for either HepG2 or HepaRG cells, the two cell lines used in our experiments. TFs with correlation coefficients >0.2 were then advanced to the next step of the analysis. By applying this step-wise narrowing-down process, we identified the 30 candidate TFs that are listed in Fig. 1. Those 30 candidate TFs were then knocked down in HepaRG cells using siRNAs with KD efficiencies as shown graphically in Supplemental Fig. 1. We used HepaRG rather than HepG2 cells in these experiments because they have been reported to better reflect the biology of hepatocytes than do HepG2 cells (Ramboer et al., 2015). The mRNA expression levels of TSPYL1, TSPYL2, and TSPYL4 and of CYP3A4, CYP2C9, and CYP2C19 were then assayed in HepaRG cells by qRT-PCR as shown in Fig. 2 for CYP3A4. Panels (a), (b), and (c) in Fig. 2 display data for the expression of CYP3A4 versus those of TSPYL1, TSPYL2, and TSPYL4, respectively, after KD of the candidate TFs, with each black or red circle representing one of the 30 TFs studied and with error bars showing the impact of KD of the indicated TSPYL as a vertical line and the impact on the expression of CYP3A4 as a horizontal line. We have highlighted points in Fig. 2 in red in which the relationship of the expression of those TFs mapped to the lower right quadrant of the four quadrant graphical representations of the data—i.e., these were TFs that were associated with increased expression of CYP3A4 in the setting of decreased TSPYL expression—a relationship that we had reported previously in our KD and OE studies of TSPYL genes in HepaRG cells (Qin et al., 2018). After excluding TFs already known to be involved in the regulation of CYP3A4 expression (Martinez-Jimenez et al., 2007; Jover et al., 2009) as well as TFs known to bind to the promoter region of CYP3A4 based on ENCODE data, 18 TFs were found to significantly influence the mRNA expression of CYP3A4 and at least one of the TSPYLs in HepaRG cells (fold change ≥2). However, only the KD of REST, MAFA, and ZBTB7A resulted in the downregulation of TSPYL expression coupled with the
up regulation of CYP3A4 expression (see Fig. 2 panel c), consistent with our previous findings. KD of these three TFs resulted in striking upregulation of CYP3A4 expression coupled with the downregulation of TSPYL4 expression. Supplemental Fig. 1A through (i) shows similar data for CYP2C9 and CYP2C19. However, for CYP2C9 and 2C19, as shown in the figure, there was a noticeable absence of points in the lower right quadrants of the figures. As a result, REST, MAFK, and ZBTB7A were selected for further study after a rescue experiment designed to verify our initial results and to help determine the mechanism of regulation of CYP3A4 expression by TSPY1s—in this case focusing on TSPYL4.

Transcriptional Regulation of CYPs by TFs by Regulation of TSPYL Expression. As the next step in this series of experiments, a candidate TF KD and TSPYL4 OE rescue study was performed for REST, MAFK, and ZBTB7A, the three TFs that displayed the most striking upregulation of CYP3A4 expression after the downregulation of TSPYL4 (see Fig. 2C). The results of that experiment, as shown in Fig. 3, demonstrated that KD of ZBTB7A, REST, and MAFK consistently resulted in increased expression of CYP3A4, while OE of TSPYL4 decreased CYP3A4 expression. However, TSPYL4 OE was able to reverse the upregulation of CYP3A4 expression (Fig. 3, B and E) only after ZBTB7A or REST KD, but not after MAFK KD (Fig. 3H).

Based on the results of the rescue experiment, we concluded that ZBTB7A and REST clearly enhanced TSPYL4 expression which, in turn, downregulated the expression of CYP3A4. Similar results were observed when we used NCI-H2405 human lung adenocarcinoma cells to perform similar studies (see Supplemental Fig 2, B and C). Therefore,
REST and ZBTB7A appeared to be negative regulators of CYP3A4 expression as a result, at least in part, of an effect on TSPYL4 expression. As the next step in the analysis, ChIP-qPCR experiments were performed using HepaRG cells to validate specific TF binding sites in the promoter regions of the TSPYL4 and TSPYL6 genes (Fig. 4). Specifically, primers were designed to target the promoter regions of TSPYL4 and TSPYL6 based on ZBTB7A ChIPseq performed with HepG2 cells (ENCODE experiment ENCSR000BQA) and REST ChIPseq performed with hepatic tissue (ENCODE experiments ENCSR867WPH and ENCSR893QWP) (see Supplemental Table 3). We chose to study TSPYL1 and TSPYL4 together because those two genes map only 20 kbp away from each other. The results of ChIP-qPCR, as shown in Fig. 4, demonstrated significant enrichment of the binding of ZBTB7A or REST antibody to the promoter regions of both TSPYL1 and TSPYL4 as compared with IgG, indicating that both ZBTB7A and REST could bind directly to the promoter regions of these two TSPYLs.

SNP-Dependent Modulation of Transcriptional Regulatory Activity for TSPYL Expression by REST and ZBTB7A.

We next identified six common SNPs, rs9400898(G/C), rs3828743(G/A), rs3749895(C/G), rs910391(T/G), rs17524614(G/T), and rs2232470(C/A) that mapped within the ChIPseq peaks for REST (ENCODE experiments ENCSR867WPH and ENCSR893QWP) and ZBTB7A (ENCODE experiment ENCSR000BQA) on the TSPYL1 and TSPYL4 gene promoter regions. Specifically, the first three SNPs mapped to the TSPYL1 promoter region and were in tight linkage disequilibrium, with minor allele frequencies (MAFs) that ranged from 0.26 to 0.30 for the group near the transcription start site for TSPYL1 based on 1000 Genomes Project data (https://www.genome.gov/27528684/1000-genomes-project) (Supplemental Table 5), while the latter three SNPs mapped to the TSPYL4 promoter region with MAF values that ranged from 0.16 to 0.53, as depicted graphically in Fig. 5A and Supplemental Table 6. Luciferase reporter constructs were then designed that incorporated wild-type and variant SNP TSPYL promoter region SNPs, as shown schematically in Fig. 5, B and C to study possible SNP-dependent modulation of regulatory activity. Specifically, after transfecting HepaRG cells with a series of luciferase reporter constructs, we found that the TSPYL1 variant promoter displayed reduced luciferase activity (Fig. 5B) as compared with the TSPYL1 wild-type promoter, while the TSPYL4 variant promoter resulted in increased luciferase activity (see Fig. 5C) as compared with the TSPYL4 wild-type promoter, thus revealing SNP-dependent regulatory differences in their effect on TSPYL gene expression. Very similar results were observed when we transfected luciferase reporter constructs into Caco2 and HepG2 cells, using the same constructs that had been employed in a previous TSPYL study (Qin et al., 2020) (See Supplemental Fig. 4, A–D).

Discussion

Our previous studies showed that TSPYLs are transcriptional regulators of several CYPs and that downregulation of the expression of TSPYLs can result in the upregulation of CYP3A4, CYP2C9, and CYP2C19 gene expression (Qin et al., 2018; Qin et al., 2020). Furthermore, genetic polymorphisms present in both the TSPYLs and CYPs are known to be associated with variation in drug response phenotypes, but those polymorphisms only explain a portion of the population variability that has been observed in CYP expression. The present study of upstream regulators of TSPYL expression has revealed additional factors that could contribute to individual variation in CYP-dependent drug metabolism pathways. The results of the series of experiments described here may help us better understand molecular factors that contribute to that variation.

We used the HepaRG cell line for most of our studies since those cells have been reported to be more similar biologically to human hepatocytes than are many other widely used hepatic cell model systems such as HepG2, Huh7 or the Hep3B (Zeiling er et al., 2016), especially in terms of basal CYP expression and/or induction (Ramboer et al., 2015). Our mRNA expression results for TSPYLs and CYP3A4 after the silencing of REST and ZBTB7A reflect known eQTL relationships that have been reported between TSPYLs and CYPs in HepaRG cells (Qin et al., 2018; Qin et al., 2020), and they made it possible for us to identify REST and ZBTB7A as upstream regulators of TSPYL expression. Our studies of the expression of TSPYLs and CYPs after silencing these TFs as well as rescue experiments performed with TSPYL overexpression vectors further supported the apparent regulation of TSPYL gene expression by REST and ZBTB7A. Future proteomic analysis (Graves and Haystead, 2002) of HepaRG cells might provide insight into additional transcriptional cofactors involved in the sequential, stepwise regulation of the expression of TSPYLs and, downstream, of CYPs.

In one of our previous reports, 4 missense variants in TSPYL genes were studied, with the identification of one missense SNP, rs3828743(G/A) (Pro62Ser), in the TSPYL1 gene promoter regions. Furthermore, genetic polymorphisms present in both the TSPYLs and CYPs are known to be associated with variation in drug response phenotypes, but those polymorphisms only explain a portion of the population variability that has been observed in CYP expression. The present study of upstream regulators of TSPYL expression has revealed additional factors that could contribute to individual variation in CYP-dependent drug metabolism pathways. The results of the series of experiments described here may help us better understand molecular factors that contribute to that variation.

We used the HepaRG cell line for most of our studies since those cells have been reported to be more similar biologically to human hepatocytes than are many other widely used hepatic cell model systems such as HepG2, Huh7 or the Hep3B (Zeiling er et al., 2016), especially in terms of basal CYP expression and/or induction (Ramboer et al., 2015). Our mRNA expression results for TSPYLs and CYP3A4 after the silencing of REST and ZBTB7A reflect known eQTL relationships that have been reported between TSPYLs and CYPs in HepaRG cells (Qin et al., 2018; Qin et al., 2020), and they made it possible for us to identify REST and ZBTB7A as upstream regulators of TSPYL expression. Our studies of the expression of TSPYLs and CYPs after silencing these TFs as well as rescue experiments performed with TSPYL overexpression vectors further supported the apparent regulation of TSPYL gene expression by REST and ZBTB7A. Future proteomic analysis (Graves and Haystead, 2002) of HepaRG cells might provide insight into additional transcriptional cofactors involved in the sequential, stepwise regulation of the expression of TSPYLs and, downstream, of CYPs.

In one of our previous reports, 4 missense variants in TSPYL genes were studied, with the identification of one missense SNP, rs3828743(G/A) (Pro62Ser), in the TSPYL1 gene promoter regions. Furthermore, genetic polymorphisms present in both the TSPYLs and CYPs are known to be associated with variation in drug response phenotypes, but those polymorphisms only explain a portion of the population variability that has been observed in CYP expression. The present study of upstream regulators of TSPYL expression has revealed additional factors that could contribute to individual variation in CYP-dependent drug metabolism pathways. The results of the series of experiments described here may help us better understand molecular factors that contribute to that variation.

We used the HepaRG cell line for most of our studies since those cells have been reported to be more similar biologically to human hepatocytes than are many other widely used hepatic cell model systems such as HepG2, Huh7 or the Hep3B (Zeiling er et al., 2016), especially in terms of basal CYP expression and/or induction (Ramboer et al., 2015). Our mRNA expression results for TSPYLs and CYP3A4 after the silencing of REST and ZBTB7A reflect known eQTL relationships that have been reported between TSPYLs and CYPs in HepaRG cells (Qin et al., 2018; Qin et al., 2020), and they made it possible for us to identify REST and ZBTB7A as upstream regulators of TSPYL expression. Our studies of the expression of TSPYLs and CYPs after silencing these TFs as well as rescue experiments performed with TSPYL overexpression vectors further supported the apparent regulation of TSPYL gene expression by REST and ZBTB7A. Future proteomic analysis (Graves and Haystead, 2002) of HepaRG cells might provide insight into additional transcriptional cofactors involved in the sequential, stepwise regulation of the expression of TSPYLs and, downstream, of CYPs.

In one of our previous reports, 4 missense variants in TSPYL genes were studied, with the identification of one missense SNP, rs3828743(G/A) (Pro62Ser), in the TSPYL1 gene promoter regions. Furthermore, genetic polymorphisms present in both the TSPYLs and CYPs are known to be associated with variation in drug response phenotypes, but those polymorphisms only explain a portion of the population variability that has been observed in CYP expression. The present study of upstream regulators of TSPYL expression has revealed additional factors that could contribute to individual variation in CYP-dependent drug metabolism pathways. The results of the series of experiments described here may help us better understand molecular factors that contribute to that variation.

We used the HepaRG cell line for most of our studies since those cells have been reported to be more similar biologically to human hepatocytes than are many other widely used hepatic cell model systems such as HepG2, Huh7 or the Hep3B (Zeiling er et al., 2016), especially in terms of basal CYP expression and/or induction (Ramboer et al., 2015). Our mRNA expression results for TSPYLs and CYP3A4 after the silencing of REST and ZBTB7A reflect known eQTL relationships that have been reported between TSPYLs and CYPs in HepaRG cells (Qin et al., 2018; Qin et al., 2020), and they made it possible for us to identify REST and ZBTB7A as upstream regulators of TSPYL expression. Our studies of the expression of TSPYLs and CYPs after silencing these TFs as well as rescue experiments performed with TSPYL overexpression vectors further supported the apparent regulation of TSPYL gene expression by REST and ZBTB7A. Future proteomic analysis (Graves and Haystead, 2002) of HepaRG cells might provide insight into additional transcriptional cofactors involved in the sequential, stepwise regulation of the expression of TSPYLs and, downstream, of CYPs.
enzymes and of genetic polymorphisms associated with variability in drug response.

In summary, the novel transcription factors REST and ZBTB7A appear to be transcriptional regulators of TSPYL gene expression resulting in variation in expression which then plays a role downstream in CYP expression and CYP-mediated variation in drug metabolism. This series of events represents a novel upstream source of variation in downstream CYP expression that may mechanistically help us to better understand variation in CYP expression. Ultimately, this novel SNP-dependent modulation of transcription regulating TSPYL expression and activity may contribute to variability in both CYP expression and, as a result, variation in drug response phenotypes.

**Authorship Contributions**

Participated in research design: Shivaram, Gao, Qin, Liu, Weinshilboum, Wang.

Conducted experiments: Shivaram, Qin.

Performed data analysis: Shivaram, Gao, Qin, Liu.

Wrote or contributed to the writing of the manuscript: Shivaram, Gao, Liu, Weinshilboum, Wang.

**References**


Address correspondence to: Dr. Liewei Wang, Department of Molecular Pharmacology & Experimental Therapeutics, Mayo Clinic, 200 First Street Southwest, Rochester, MN 55905. E-mail: Wang.Liewei@mayo.edu; Dr. Richard M. Weinshilboum, Department of Molecular Pharmacology & Experimental Therapeutics, Mayo Clinic, 200 First Street SW, Rochester, MN 55905. E-mail: Weinshilboum.Richard@mayo.edu