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Expression and tissue distribution of the mRNA’s encoding the human thromboxane A₂ receptor (TP) α and β isoforms.

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Keywords: Thromboxane A₂, receptor, TPₐ, TPₜ, isoforms, gene expression.

Abbreviations: TXA₂, thromboxane A₂; thromboxane A₂ receptor is abbreviated to TP, and its splice variants are designated by the greek letters α and β, as recommended by the IUPHAR classification on prostanoid receptors; VSM, vascular smooth muscle, SMC, smooth muscle cell; depc, diethyl pyrocarbonate; RT-PCR, reverse-transcriptase polymerase chain reaction; HEL, human erythroleukemia cells; HUVEC, human umbilical vein endothelial cell; FBS, foetal bovine serum.

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Summary

The human (h) TXA$_2$ receptor (TP), a G protein-coupled receptor, exists as two isoforms, TP$_a$ and TP$_b$, which arise by alternative mRNA splicing and differ exclusively in their carboxyl terminal cytoplasmic regions. In this study, a reverse transcriptase - polymerase chain reaction (RT-PCR) based strategy was developed to examine the expression of the TPs in tissues of physiologic relevance to TXA$_2$. Although most of the 17 different cell / tissue types examined expressed both TP isoforms, the liver hepatoblastoma HepG2 cell line was found to exclusively express TP$_a$ mRNA. In most cell types, TP$_a$ mRNA predominated over TP$_b$ mRNA. Moreover, although the levels of TP$_a$ mRNA expression were similar in most of the cell / tissue types examined, extensive differences in the levels of TP$_b$ mRNA were observed. Consequently, the relative expression of TP$_a$ : TP$_b$ mRNA varied considerably due to extensive differences in TP$_b$ mRNA expression. Most strikingly, primary HUVEC’s were found to express: (i) low levels of TP$_b$ and (ii) approximately 6-fold greater levels of TP$_a$ than TP$_b$. These data were confirmed in the spontaneously transformed HUVEC derived ECV304 cell line. Expression of TP mRNAs in the various tissue / cells correlated with protein expression, as assessed by radioligand binding using the selective TP antagonist $[^3]$H SQ29,548.
Introduction

The prostanoid thromboxane A$_2$ (TXA$_2$), mainly synthesised in platelets, induces a variety of cellular responses including platelet shape change and aggregation, constriction of bronchial and vascular smooth muscle (VSM) cells, stimulation of mitogenesis and/or hypertrophic responses in VSM (1-5). TXA$_2$ mediates its actions through interaction with the shared endoperoxide prostaglandin (PG)H$_2$/TXA$_2$ receptor (termed TP; 6), a member of the rhodopsin like G protein coupled receptor (GPCR) family. Imbalances in the levels of TXA$_2$ or in its specific TXA$_2$ synthase or its receptor (TP) have been implicated as mediators in a number of disease states including myocardial infarction (7-9), atherosclerosis (10), angina (9, 7), pregnancy induced hypertension (11), ureteral obstruction (12), lupus nephritis (13), dysmenorrhea and uterine ischemia (14), endometrial cancer (15) and bronchial asthma (16). In addition, U46619, a TP agonist has been reported to induce apoptotic cell death of immature thymocytes (17) implying that TXA$_2$ may play a role in modulation of immune responses (18).

Early pharmacological and biochemical evidence indicated both inter and intra-species variations of TPs (19-22). Moreover, the selective TP antagonist GR32191 could distinguish between two forms of the receptor in human platelets; one linked to phospholipase C activation, resulting in platelet aggregation and granule secretion and a second linked to calcium mobilization, mediating platelet shape change (2). The cDNA for the human TP was initially cloned from placenta and the platelet like MEG-01 cell line (23) and since then cDNAs for TP receptors from a number of species have been cloned including TPs from mouse (24), rat (25,26) and bovine (27) sources. All TPs are predicted to share similar 7 transmembrane, $\alpha$ helical domain arrangements typical of members of the GPCR superfamily. Despite the evidence for receptor heterogeneity, genomic cloning of the human TP gene confirmed the existence of a single gene, located on chromosome 19p13.3 (28). The gene consists of 3 exons and 2 introns and has 2 putative promoters; DNA sequence analysis indicates polymorphism, including polymorphism within the putative promoter 2 (29). In 1994, Raychowdhury et al., (30) isolated a cDNA encoding a second isoform of the TP from a human umbilical vein endothelial cell (HUVEC) cDNA library. The endothelial receptor, termed TP$_b$, and the platelet/placental TP, termed TP$_a$, are encoded by the same gene but arise by a novel differential splicing event. The two receptors are identical for the first 328 amino acids but differ in their C-terminal terminal cytoplasmic tails. Polymerase chain reaction (PCR) experiments indicated that HUVECs express TP$_b$ only (30) whereas platelets were reported to express both TP$_a$ and TP$_b$ isoforms (31).

Both receptor isoforms have been shown to be regulated both in vitro and in vivo by phosphorylation (32,33). Direct functional coupling of TP$_a$ to Gq and G11 in response to the TXA$_2$ mimetic U46619 and the isoprostane 8-epi prostaglandin F$_{2\alpha}$ has been demonstrated in vivo (34). Moreover, in stably transfected Chinese hamster ovary cells, Hirata et al., (31) reported that the individual receptors may activate different intracellular signalling pathways. Whilst showing similar phospholipase C activation, each receptor oppositely regulate adenylyl cyclase activity, with TP$_a$ activating it and TP$_b$ inhibiting it. None the less, despite these studies, the physiologic significance of the existence of 2 receptors for TXA$_2$ is presently unclear but it is possible that each receptor isoform may be involved in mediating specific functions among the diversity of those attributed to the autocoid TXA$_2$. To date, no detailed study has been undertaken to analyse the relative expression of the TP$_a$ or TP$_b$ isoforms in cells or tissues of relevance to TXA$_2$ biology. Whereas Northern blot analyses have confirmed the existence of TP mRNA in human MEG-01 cells, placental and lung tissue (23), in human erythroleukemic (HEL) cells (35,29) and in mouse thymus, lung, spleen, ileum brain and kidney (36), the probes utilised in these studies did not discriminate between
expression of the $\alpha$ or $\beta$ isoforms. Similarly, at the protein level, TP selective radioligands currently available, such as $[^3]H$SQ29,549 (30,37) or $[^3]H$S-145 (31) do not discriminate between either receptor isoform and sufficiently sensitive receptor specific antibodies that will allow for detection of low amounts of TP expressed on cell membranes are not currently available. As a necessary prelude to studies which may elucidate the possible differential physiologic roles of the TPs, it is necessary to establish the expression and tissue distribution of the individual TP isoforms. Hence, in this study, a semi quantitative reverse-transcriptase PCR (RT-PCR) approach has been developed that allows for the identification of and the assessment of relative expression and abundance of the mRNAs for the $\text{TP}_\alpha$ and $\text{TP}_\beta$ isoforms from different tissue and cell types. Where possible, TP receptor expression was validated by radioligand binding studies using the highly selective TP antagonist SQ29,548. This study will provide a starting foundation for elucidating the roles of TP isoforms in physiologic and pathophysiologic states.
Materials and Methods

Materials. Ultraspec™ total RNA isolation system was purchased from Biotecx Laboratories (Houston, TX). All oligonucleotides were synthesised by Genosys Biotechnologies (Cambridgeshire, UK). Mouse moloney leukemia virus (MMLV) reverse transcriptase (RT), ribonuclease inhibitor RNasin®, Klenow fragment, RQ DNase I and deoxynucleotides were purchased from Promega. Random hexamers were purchased from Life Technologies Inc. Taq DNA polymerase, T4 DNA ligase, calf intestinal alkaline phosphatase and restriction endonucleases were purchased from Boehringer Mannheim. Sequenase Version 2.0 DNA sequencing kit was purchased from U.S. Biochemical Corp. Foetal bovine serum (FBS) was purchased from PAA laboratories Ltd., (Kingston Upon Thames, UK.). Dulbecco’s minimal essential medium, RPMI 1640 and minimal essential medium were purchased from HyClone Europe (Northumberland, UK). Endothelial growth medium (EGM) and supplements were purchased from BioWhittaker Inc., (Walkerville, MD, U.S.A.). All human tissue RNA samples were purchased from Clontech. The Escherichia coli (E.coli) cloning vector pBluescript II SK(-) was purchased from Stratagene.

Culture of Primary and Immortalised Cells:
Primary (1º) human umbilical vein endothelial (HUVEC) cells and first trimester trophoblast cell lines, namely ED-27, ED-31, ED-77 and Tm-1, derived from 4 individual donors were obtained from Professor Desmond Fitzgerald, Royal College of Surgeons, Dublin, Ireland. The following immortalised human cell lines were purchased from the American Type Culture Collection (ATCC): Human erythroleukemia (HEL) 92.1.7 cells; hepatoblastoma (Hep) G2 cells; ECV304 cells. The foetal and adult aortic vascular smooth muscle (VSM) cell lines VLTR and ALTR and the uterine smooth muscle cell (SMC) line ULTR, described by Perez-Reyes et al., (38), were obtained from J. K. McDougall, Dept. Pathology, University of Washington, Seattle, USA.
All cells were maintained at 5% CO₂ in an incubator at 37°C and were cultured using standard conditions, essentially as recommended by the suppliers. Briefly, the megakaryocytic HEL cell line were routinely cultured in RPMI 1640, 10% FBS. Immortalised VSM cell lines, VLTR, ALTR; the uterine SMC cells, ULTR; the 1º trophoblast cell lines ED-27, ED-31, ED-77 and Tm-1, were routinely grown in Dulbecco’s minimal essential medium, 10% FBS. The liver-derived cell line, HepG2 cells were cultured in Eagle’s minimal essential medium, 10% FBS. The spontaneously transformed HUVEC-derived cell line, ECV304 was cultured in medium 199, 10% FBS whereas the 1º HUVEC cells was grown in EGM supplemented with 10 ng ml⁻¹ human epidermal growth factor, 0.5 µg ml⁻¹ hydrocortisone, 50 µg ml⁻¹ gentamicin sulphate, 50 µg ml⁻¹ amphotericin B, 12 µg ml⁻¹ bovine brain extract, 2% FBS.

RNA Preparation.
Total RNA from foetal and adult brain tissue, thymus, small intestine and liver were purchased from Clontech. Total RNA was isolated from placental tissue and all cell lines using the Ultraspec® RNA isolation procedure, essentially as described by the supplier. RNA integrity was assessed by electrophoresis on 1.1% agarose/formaldehyde/formamide gels (39). To ensure that the RNA samples prepared using the Ultraspec® method were free from any potential contaminating DNA, aliquots (25µg) of total RNA were treated with 6.25U RQ DNase I in the presence of 40U RNasin® ribonuclease inhibitor, 50mM Tris-HCl, pH 7.5., 10mM MgCl₂ for 15 minutes at 37°C in a total volume of 50µl. Reactions were terminated by the addition of 2.5µl 0.5M EDTA, pH 8.0.
Phenol:chloroform extraction and precipitation of the RNA were performed by standard methodology (39). The lyophilised RNA pellet was resuspended in 20μl diethyl pyrocarbonate (depc) treated H2O.

**Reverse Transcription and Polymerase Chain Reaction (RT-PCR)**

DNase I treated total RNA from immortalised cell lines and total RNA extracted from human tissue were converted to first strand (1°) cDNA with MMLV RT. Briefly, 1.4μg of total RNA was denatured for 10 minutes at 70°C in the presence of random hexamers (100μM), then chilled on ice. Reaction buffer, deoxynucleotides, RNasin® and MMLV RT were then added to give a final reaction mix of 50mM Tris-HCl, pH 8.3, 75mM KCl, 3mM MgCl2, 10mM DTT, 40U RNasin, 0.8mM deoxyribonucleotides, 400U MMLV RT in a total volume of 25μl. 1° cDNA synthesis was performed at 37°C for 40 min, then at 42°C for 40 min. Reactions were heat inactivated at 80°C for 10 min. In each RT experiment, the following negative control reactions were routinely carried out: a) 1° cDNA reactions carried out in the absence of MMLV-RT; b) all RT reagents excluding template RNA. Aliquots (3.5μl) of each 1° cDNA were then used as templates in subsequent PCR reactions (25μl) using primers pairs selective for TPα or TPβ.

The general organization of Exon 2 - Intron 2 - Exon 3 of the human TP gene corresponding to the region encoding the unique C-terminal cytoplasmic tails of TPα and TPβ are shown in Figure 1. Oligonucleotide primers were designed to specifically amplify TPα and TPβ mRNA sequences in PCR reactions based on the published cDNA sequences of the placental TPα (28) and the endothelial TPβ (30). In all cases, the common Primer A with the sequence 5’GAGATGATGGCTCAGCTCCT3’ corresponding to nucleotides 724-743 of Exon 2 was utilised as the 5’ or Sense primer; whereas Primer C (5’CCAGCCCCCTGAATCCTCA3’; nt 1123-1106 of TPα) was used as specific Antisense primer for TPα and Primer B (5’AGACTCCGTCTGGGCCG3’; nt 1651 - 1643 plus 983 - 976, which corresponds to nt 992-976 of TPβ mRNA ) was used as specific antisense primer for TPβ. An additional Primer D (5’TGGGCCACAGAGTGAGACTC3’; nt 1665-1646) was designed to co-amplify both TPα and TPβ sequences. These primers (Primers A-D) were designed to span across Intron 2 (4.3 kB) such that only PCR products derived from 1° cDNA would be amplified, thereby eliminating genomic artefacts. As an internal control for each experiment, oligonucleotides were also designed to direct PCR amplification of DNA from the constitutively active gene, glyceraldehyde-3-phosphate dehydrogenase (GA3PDH), namely Gf 5’TGAAGGTCGGAGTCAACG 3’ (nt 71-89) and Gr 5’CATGTGGGCCATGAGGTC3’ (nt 1053-1035).

The random primed first strand (1°) cDNA was used as a template for the PCR amplification of TPα, TPβ, TPα plus TPβ and GA3PDH specific sequences. In brief, aliquots (3.5 μl) of 1° cDNA were used as templates in each PCR reaction (25 μl) in the presence of 10 mM Tris-Cl, pH 8.3., 50 mM KCl, 2 mM MgCl2, 0.2 mM dNTPs, 6.7 % glycerol, 1 μM Sense primer, 1 μM Antisense primer, 1 U Taq DNA polymerase. PCR amplifications were carried out using the following repeat cycle conditions for 40 cycles: (denaturation at 95 °C, 1 min; primer annealing at 50 °C, 30 sec; elongation at 72 °C for 3 min) followed by a single final extension reaction ( 95 °C, 1 min; 50 °C, 30 sec; 72 °C for 10 min). In the case of primer pairs A/D, PCR reaction components were initially assembled without any Taq DNA polymerase and were pre-heated to 95 °C for 5 min, then cooled on ice for 1 min. Thereafter, Taq DNA polymerase was added and PCR amplifications were carried out using the following repeat cycle conditions for 40 cycles: (95 °C, 1 min; 54 °C, 30 sec; 72 °C, 3 min) followed by a single final extension reaction (95 °C, 1 min; 54 °C, 30 sec; 72 °C, 10 min). In each PCR experiment the following negative control
reactions were routinely carried out for each primer pair: a) PCR reactions carried out in the absence of 1\(^\circ\) cDNA template; b) template DNA resulting from 1\(^\circ\) cDNA reactions carried out in the absence of MMLV-RT; c) template DNA resulting from 1\(^\circ\) cDNA reactions carried out in the absence of template RNA.

Following amplifications, products of the PCR reactions (7\(\mu\)l) were analysed by agarose gel electrophoresis (39); the gels were then subjected to densitometry by scanning on a UVP GDS800 gel documentation system. The levels of TP\(_a\) and TP\(_b\) mRNA expression were determined by measurement of PCR product band intensities on the densitometric scans; in each case, expression levels, in arbitrary units, are represented as a ratio relative to GA3PDH expression (i.e TP\(_a\)/GA3PDH ± standard error of the mean (S.E.M.); TP\(_b\)/GA3PDH ± S.E.M., in arbitrary units) and the relative levels of TP\(_a\) to TP\(_b\) are represented as a ratio of these values in each case, i.e TP\(_a\)/TP\(_b\) ± S.E.M., arbitrary units. For each cell or tissue type screened, at least three independent experiments were carried out. Results are expressed as mean ± S.E.M. where n ≥ 3. For each independent cell / tissue type screened, the ratio of TP\(_a\)/GA3PDH and TP\(_b\)/GA3PDH were analysed using the unpaired Student t-test. P values of less than or equal to (≤) 0.05 were considered to indicate a statistically significant difference and, where values were found to be significant, are indicated in the Figures.

**Southern Blotting and Phosphor Image Analysis.**

Southern Blot analysis of PCR generated fragments was carried out using standard methodology essentially as described by Sambrook et al., 1989.

Briefly, following agarose gel electrophoresis, PCR products were transferred to Duralon -UV nylon membrane (Stratagene) by upward capillary transfer (39). Aliquots (10 pmoles) of the radiolabelled oligonucleotides Probe X (5’ CTGTCCCGCACCACGGAG 3’, corresponding to nucleotides 844-861 of the TP\(_a\) and TP\(_b\) mRNA) or the Probe Gp (5’ CAGAAGACTGTGGATGGC 3’, corresponding to nucleotides 552-569 of the GA3PDH mRNA) were each 5’end labelled with 16 units of T4 polynucleotide kinase for 45 min at 37\(^\circ\)C in a final reaction volume of 25\(\mu\)l in the presence of 70mM Tris-Cl, pH 7.6, 10mM MgCl\(_2\), 5mM DTT and 20 pmoles [\(\gamma\) -\(^{32}\)P] ATP (6000Ci/mmol; 10mCi/ml). Carrier nucleic acid (55\(\mu\)g yeast tRNA) was added and phosphorylated oligonucleotide primers were co-precipitated with 0.1 volumes of 3M sodium acetate, pH 5.2 and 2.5 volumes of absolute ethanol at -20\(^\circ\)C for 30 min. The resultant pellet was washed in 70% ethanol and dried in vacuo. The lyophilised pellet was then re-suspended in 20 \(\mu\)l dH\(_2\)O and used as a probe for hybridization in the presence of 6x SSC, 0.5% SDS and 100\(\mu\)g/ml denatured, sonicated salmon sperm DNA overnight at 44\(^\circ\)C. Membranes were washed as previously described (39). Radioactive images were captured by autoradiography on Fuji New RX Film and quantified by Phosphor Image analysis using a GS 250 Molecular Imager (BioRad).

**Cloning and sequencing of TP\(_a\) and TP\(_b\) PCR generated fragments**

In order to confirm the absolute identity of the TP\(_a\) and TP\(_b\) specific PCR products, generated using primer pairs A/C and A/B, respectively, each product was subcloned into the vector pBluescript II SK(-) and then subjected to DNA sequence analysis. To facilitate subsequent subcloning, PCR amplifications were carried out in the presence of oligonucleotide primers that had been 5’ phosphorylated using T4 polynucleotide kinase prior to the PCR reactions.
Briefly, 500 pmoles of the required oligonucleotide primers (A, C or B) were 5’ phosphorylated with 16 units of T4 polynucleotide kinase in the presence of 50μM ATP, 10mM MgCl₂, 70mM Tris-Cl., pH 7.6 in a final volume of 100μl. Reactions were incubated at 37°C for 90 min and were heat inactivated at 65°C for 10 min. Carrier nucleic acid (5.5μg yeast tRNA) was added and phosphorylated oligonucleotide primers were co-precipitated with 0.1 volumes of 3M sodium acetate., pH 5.2 and 2.5 volumes of absolute ethanol at -20°C for 30 min. The resultant pellet was washed in 70% ethanol and dried in vacuo. The lyophilised pellets were resuspended in 20μl distilled H₂O. Aliquots (1.25μl) of each phosphorylated primer was used to direct PCR amplification of either TPα or the TPβ from 1° cDNA template as previously described. Following amplification, any recessed DNA ends were filled in by the addition of 10 units of DNA polymerase I Klenow fragment to each of the resulting 25μl PCR reactions and were further incubated at 30°C for 15 min. Thereafter, the Klenow treated PCR fragments were subjected to 1.2% agarose gel electrophoresis and the TPα (400bp) and the TPβ (269bp) fragments were gel purified using the GeneClean II® kit. Phenol-chloroform extraction and precipitation of the gel purified PCR products was performed in the presence of 0.1 volumes of 3M sodium acetate, pH 5.2 and 2.5 volumes of absolute ethanol at -20°C. The washed pellet was resuspended in distilled H₂O. PCR fragments were then subcloned by blunt end ligation into the Sma I site of pBluescript II SK (-) using standard methodology (39). Recombinant plasmids containing either the TPα or the TPβ specific PCR products were sequenced using the Sequenase Version 2.0 DNA sequencing kit.

**Saturation Radioligand binding assay**

Cells were harvested by scraping, centrifuged at 500 x g at 4°C for 5 min and then washed three times in phosphate buffered saline (PBS). Protein concentrations were determined using the Bradford assay (40). Cells were then harvested and were resuspended in HBSS/1B (modified Ca²⁺/Mg²⁺-free Hanks’ buffered salt solution, containing 10mM HEPES pH 7.67, 0.1% bovine serum albumin) at a final concentration of 1mg/ml. Saturation radioligand binding experiments with the TP antagonist [³H]SQ29,548 (20 nM, 50.4 Ci/mmol) were carried out at 30°C for 30 min in 100μl reactions using approximately 100μg cell protein per assay. Non-specific binding was determined in the presence of excess nonlabeled SQ29,548 (10μM). Reactions were terminated by the addition of ice-cold 10mM Tris, pH 7.4 (4 ml) followed by filtration through Whatmann GF/C glass filters, and subsequent washing of the filters 3 times with 4 ml 10mM Tris, pH 7.4, followed by liquid scintillation counting of the filters in 5ml of scintillation cocktail. Results were expressed as the fmol [³H]SQ29,548 incorporated per mg cell protein ± S.E.M, where n ≥ 4.
Results.

In this study, we have developed a semi quantitative reverse transcriptase (RT)-PCR based approach to screen for and determine the relative expression of TPα and TPβ mRNA sequences in a variety of human cell and tissue types of relevance to TXA2 biology. Where possible, in order to confirm actual TP protein expression, measurements of mRNA expression levels were complimented by radioligand binding studies using the selective radiolabelled TP antagonist [3H]SQ29,548.

Figure 1 outlines the general organisation of the human TP gene in the region where the differential splicing event giving rise to the two receptor isoforms occurs and the oligonucleotide primer pairs which were used in the RT-PCR reactions to amplify either TPα (Primers A/C; nucleotides 724 - 1123; 400bp) or TPβ (Primers A/B; nucleotides 724 - 992 of TPβ mRNA; 269bp) specific sequences. As a confirmatory PCR reaction, an additional primer pair was used to co-amplify both TPα and TPβ (Primers A/D; nucleotides 724 - 1665 of TPα; 942bp and nucleotides 724 - 1006 of TPβ; 283 bp) specific sequences. In all cases, the 5’ and 3’ primers of the TPs were designed to flank the large 4.3kB Intron 2 thereby ensuring that the PCR products derived from 1° cDNA could readily be distinguished from those which might be generated from trace genomic DNA contamination of the RNA preparations. As an internal control for a constitutively transcribed gene, oligonucleotide primers (Primers Gf / Gr; nucleotides 71 - 1053; 983 bp) were also used to amplify GA3PDH mRNA sequences in each experiment.

A typical electrophoretogram of RT-PCR generated products from the platelet like human erythroleukemic (HEL) megakaryocyte cell line is presented in Figure 2A. Clearly, TPα (Primer A/C, lane 2), TPβ (Primer A/B, lane 1), TPα plus TPβ (Primer A/D, lane 9) as well as GA3PDH (Primer Gf/Gr; lane 3) DNA fragments of the predicted sizes were specifically amplified in each case. The amplified fragments were subsequently cloned into pBluescript II SK(-) vector and were confirmed to be correct by DNA sequence analysis (data not shown). Whereas HEL cells express both TPα and TPβ mRNA sequences at ratio’s of 0.87 ± 0.06 and 0.40 ± 0.008 relative to GA3PDH, respectively, these cells express 2.32 ± 0.34 (p ≤ 0.05) fold more TPα than TPβ mRNA (Figure 2B). Consistent with previous data (32), TP expression in HEL cells was confirmed by radioligand binding studies and were found to express 36.7 ± 6.52 fmol [3H]SQ29,548 / mg cell protein (Figure 2C).

Routinely, in order to validate data obtained from densitometric scans of ethidium bromide stained gels, PCR fragments were also screened by Southern Blot analysis using an internal 32P radiolabelled oligonucleotide Probe X (Nucleotides 844 - 861 of TPα and TPβ mRNA sequences) as specific TP cDNA probe and radiolabelled oligonucleotide Probe Gp (Nucleotides 552 - 569 of GA3PDH mRNA) as specific GA3PDH cDNA probe. Southern blots containing the PCR generated cDNA fragments (primer pairs A vs C to ampify TPα; primers A vs B to amplify TPβ cDNA; Gf vs Gr to amplify GA3PDH cDNA) were screened by hybridization, using standard methodology. Thereafter, the Southern Blots were subjected to autoradiography and densitometric scanning by Phosphor Image Analysis using a BioRad GS 250 Molecular Imager. Results of a typical autoradiogram are presented in Figure 2D. In each case, data generated by Phosphor Image analyses of the Southern Blots were consistent with the data generated from the ethidium bromide stained gels.

TP expression in uterine and vascular smooth muscle.

The immortalised smooth muscle cells lines derived from adult aortic (ALTR), foetal aortic (VLTR) and uterine (ULTR) smooth muscle cells (SMC’s) have been previously described (38). These cells were used as model cell
lines and using the RT-PCR approach, were each found to co-express both TP\textsubscript{a} and TP\textsubscript{b} isoforms. Specifically, foetal and adult SMC’s express comparable levels of TP\textsubscript{a} mRNA with ratio’s of TP\textsubscript{a} / GA3PDH were 0.90 ± 0.06 and 0.81 ± 0.08, respectively (Figure 3A). In contrast, there is greater expression of TP\textsubscript{b} in foetal VSM compared to adult VSM, with ratio’s of TP\textsubscript{b} / GA3PDH mRNA’s found to be 0.81 ± 0.14 and 0.36 ± 0.06, respectively. Hence, the adult aortic SMCs express 2.37 ± 0.43 fold more TP\textsubscript{a} than TP\textsubscript{b} (Figure 3B, p ≤ 0.05) whereas foetal SMC express 1.16 ± 0.16 fold greater levels of TP\textsubscript{a} than TP\textsubscript{b}.

Uterine SMCs express over 3-fold greater levels of TP\textsubscript{a} relative to TP\textsubscript{b} (Figure 3B, p ≤ 0.025). In contrast, uterine tissue, which comprises uterine SMC, fibroblasts and a number of other cell types, expresses similar, high levels of both TP isoforms (ratio TP\textsubscript{a} and TP\textsubscript{b} mRNA’s relative to GA3PDH were 1.35 ± 0.36 and 1.22 ± 0.36, respectively).

Expression of TP in the immortalised foetal, adult and uterine smooth muscle cells were confirmed by radioligand binding studies (Figure 3C), however, as the radioligand [\textsuperscript{3}H]SQ29,548 is not receptor isoform selective, no direct correlation between the level of isoform-specific TP protein and mRNA expression could be made.

### Analysis of TP expression in HUVEC’s.

Primary human umbilical vein endothelial cells (1\textsuperscript{o} HUVECs) were confirmed to express TP\textsubscript{b} mRNA, albeit at low levels (ratio of TP\textsubscript{b} / GA3PDH was 0.07 ± 0.005; Figure 4A & 4B). In contrast however to previous reports (Raychowdhury et al., 1994), 1\textsuperscript{o} HUVEC’s were also found to express TP\textsubscript{a} mRNA (Figure 4A); in fact, these cells were found to express 5.8 fold greater levels of TP\textsubscript{a} relative to TP\textsubscript{b} (p ≤ 0.01; Figure 4B & C). These data were also confirmed by Southern Blot followed by Phosphor Image analysis where the ratio of TP\textsubscript{a} / TP\textsubscript{b} mRNA expression was found to be 6.09 (Figure 4D). Consistent with these findings, the spontaneously transformed HUVEC-derived cell line, ECV-304, was also found to express both TP isoforms, with greater levels of both TP\textsubscript{a} and TP\textsubscript{b} mRNA expression relative to 1\textsuperscript{o} HUVECs (Figure 4B & 4C). TP protein expression in the immortalised ECV-304 cells was also confirmed by radioligand binding studies (13.9 ± 3.51 fmol / mg protein).

### Expression of TP in trophoblasts.

Primary trophoblast cell lines were generated from four independent placental donors and were termed ED-27, ED-31, ED-77 and Tm-1. Both TP isoforms are expressed at the mRNA level in the ED-27, ED-31, ED-77, and Tm-1 trophoblast cell lines (Figure 5A-5C). However, variations occur in the relative expression of the TP isoforms; TP\textsubscript{a} is expressed at approximately equivalent levels in all four cell lines (Figure 5B). Considerable differences in the expression of TP\textsubscript{b} mRNA were found with lowest levels of TP\textsubscript{b} being expressed in ED-27 (ratio of TP\textsubscript{b} / GA3PDH was 0.23 ± 0.08), TP\textsubscript{b} mRNA is most abundantly expressed in ED-77 and Tm-1 (ratio of TP\textsubscript{b} / GA3PDH were 0.87 ± 0.08 and 0.87 ± 0.03, respectively). Thus, TP\textsubscript{a} predominates in ED-27 and ED-31, with significantly greater levels of TP\textsubscript{a} relative to TP\textsubscript{b} expressed in ED-27 cells (p ≤ 0.005). No significant differences in the expression of TP\textsubscript{a} relative to TP\textsubscript{b} were observed in ED-77 or Tm-1 cells. Radioligand binding studies confirmed protein expression and indicated similar clonal variation in TP expression levels (Figure 5D).
Expression of TP isoforms in brain tissue, small intestine and thymus.

Foetal and adult brain tissue expressed both TP<sub>a</sub> and TP<sub>b</sub> mRNA with 2-fold greater expression of TP<sub>a</sub> relative to TP<sub>b</sub> in both cases (ratio TP<sub>a</sub>/TP<sub>b</sub> were 2.12 ± 0.25; p ≤ 0.05 and 1.97 ± 0.33, p ≤ 0.05 for foetal and adult brain tissue, respectively). Hence, there were no significant differences in the level or relative expression of the TP isoforms in foetal brain tissue compared to adult brain tissue.

Human thymus and small intestine tissue were also found to express both TP<sub>a</sub> and TP<sub>b</sub> mRNAs. The TP<sub>a</sub> predominated in both tissues with greater levels of TP<sub>a</sub> relative to TP<sub>b</sub> mRNA expressed in thymus (ratio TP<sub>a</sub>/TP<sub>b</sub> was 3.31 ± 0.15, p ≤ 0.01) and small intestinal (ratio TP<sub>a</sub>/TP<sub>b</sub> was 1.51 ± 0.12) tissue.

Exclusive expression of TP<sub>a</sub> in a hepatoblastoma cell line.

Liver tissue express both TP<sub>a</sub> and TP<sub>b</sub> mRNAs with significantly (p ≤ 0.05) greater levels of TP<sub>a</sub> expressed relative to TP<sub>b</sub> (ratio of TP<sub>a</sub> / GA3PDH was 0.78 ± 0.11; ratio of TP<sub>b</sub> / GA3PDH was 0.29 ± 0.05; Figure 7B). However, in contrast to the tissue sample, the hepatoblastoma (Hep) G2 clonal cell line express TP<sub>a</sub> mRNA exclusively with no detectable expression of TP<sub>b</sub> mRNA in these cells (Figure 7A -7C). Furthermore, TP<sub>a</sub> is expressed at equivalent levels in both HepG2 cell and total liver (ratio of TP<sub>a</sub> / GA3PDH were 0.78 ± 0.11; ratio of TP<sub>a</sub> / GA3PDH were 0.80 ± 0.09, in total liver and HepG2 cells, respectively; Figure 7C). TP protein expression in HepG2 cells was confirmed by saturation radioligand binding, with 44.4 ± 16.1 fmoles [³H]SQ,29548 bound/mg protein (Figure 7D).
Discussion

Prostanoids, autocoids synthesised mainly from membrane derived arachidonic acid, mediate diverse physiological and pathophysiological actions throughout the body. Distinct G-protein coupled receptors (GPCRs) have been cloned for each of the primary prostanoids including receptors for TXA$_2$ (TP, 23), prostaglandin (PG) D$_2$ (DP,41), PGE$_2$ (EP$_1$ - EP$_4$,42-47), PGF$_{2a}$ (FP, 48) and PGI$_2$ (IP, 49). Among the large superfamily of GPCRs, the prostanoid receptors are somewhat unique in that receptor isoforms, derived from alternative mRNA splice variants, have now been cloned and identified for the EP$_3$ (50, 51), the TP (30) and the FP (52) receptors. In each case, the specific isoforms are identical throughout their seven transmembrane domains but diverge exclusively within their C-terminal cytoplasmic tail regions. The significance of the existence of isoforms for prostanoid receptors is unclear, but in the case of EP$_3$ isoforms, differences in receptor / G-protein coupling (50, 53 - 55) and receptor desensitization (56) have been found. In the case of the TP$_a$ and TP$_b$ isoforms, studies to date indicate that both receptors exhibit identical ligand binding profiles, identical coupling to phospholipase C but may oppositely regulate adenylyl cyclase activity (31, 37). In terms of receptor localization, PCR analyses indicated that HUVECs express TP$_b$ mRNA only (30) and platelets express mRNAs for both TP$_a$ and TP$_b$ isoforms (31). In view of the diverse actions attributed to TXA$_2$ and its receptor, in both physiological and pathophysiological situations, it was considered imperative to investigate the distribution of TP$_a$ and TP$_b$ in tissues of relevance to TXA$_2$ biology, and indeed, pathophysiology. Hence, in this study, we have developed a semi-quantitative RT-PCR approach to examine the relative expression of the individual TP$_a$ and TP$_b$ isoforms. In all, 17 different human cell / tissue types were examined, including 6 whole tissue samples and 5 primary cell lines. In the absence of available tissue or primary cells, a number of representative immortalised cell lines were also examined including platelet-like megakaryocytes, adult and foetal aortic and uterine SMC’s, human umbilical vein endothelial cells and hepatoblastoma cell lines which may usefully reflect the relative expression of the TP isoforms in the progenitor tissues / cells.

Initially, vascular tissue and an erythroleukemia-like cell line were chosen for analysis since TXA$_2$ is known to play a role in platelet aggregation (57), vascular smooth muscle mitogenesis (58) and contraction (59, 7). The mRNAs coding for both TP isoforms were identified in the platelet-like HEL 92.1.7 cell line. In addition, mRNAs for both TP isoforms were identified in vascular and uterine smooth muscle. However, greater levels of TP$_b$ were found in foetal VSM relative to adult VSM, which may imply an age dependant down-regulation of TP$_b$ mRNA expression in adult tissue, with no alteration of TP$_a$ expression.

Uterine tissue, which encompasses a milieu of cell types, including uterine SMC, blood vessels, stromal cells, endometrial glands and fibroblasts (60) was also found to express both TP isoforms. A previous study reported the existence of a 2.8kb TP transcript in proliferative phase human uterus (60). In our study, uterine tissue expresses greater levels of both TP isoforms relative to that expressed by the uterine smooth muscle ULTR cell line which may indicate essential differences between uterine tissue and uterine derived smooth muscle cells. However, there may, of course, be essential differences in TP expression between primary and immortalised smooth muscle cells which will require further investigation.

The endothelial TP$_b$ has been so called since this novel spliced variant of TP was first cloned from HUVECs (30) which were reported to express TP$_b$ exclusively with no detectable expression of TP$_a$ mRNA in these cells. However, in direct contrast to those studies reported by Raychowdhury et al (30), in the present study we found that whereas the endothelial TP$_b$ was expressed, albeit at low levels in 1° HUVECs, TP$_a$ mRNA was also
identified in these cells. Furthermore, TPα mRNA levels far exceeded those of TPβ. The immortalised HUVEC-derived cell line, ECV-304 was also found to express both TP isoforms, with expression of TPβ being greater in the immortalised cell line. TPα was also expressed at greater levels in the immortalised cell line when compared to the 1st HUVECs.

Trophoblasts mediate the transport of nutrients and immunoglobulins from the maternal to the foetal circulation and also functions as an endocrine organ (61). Recently, TXA synthase mRNA was identified in trophoblasts (62). In addition, serotonin-induced vasoconstriction in the human fetoplacental circulation appears to be mediated by TXA2 release and action (63). Increased fetoplacental resistance, a feature of pre-eclampsia, may be due, in part, to TXA2 as it is known to be a potent vasoconstrictor (59). Because of the role trophoblasts play in fetoplacental circulation, examination of TP isoform expression in trophoblast was undertaken. Both TP isoforms were identified in all trophoblast cell lines; however, differences were observed in the relative expression of the mRNA’s for the individual isoforms. Whereas TPα mRNA is expressed at approximately equivalent levels in all 4 cell lines, up to 4 fold differences in the level of TPβ mRNA were observed. Corresponding differences in TP expression by the clonal trophoblast lines were observed in radioligand binding studies using the non-discriminatory TP antagonist SQ29,548 as a radioligand. The significance of the differential expression of TPα and TPβ in trophoblasts is currently unknown. However, taking into account the inter-individual variation in endogenous mRNA and protein levels which were observed in trophoblast cell lines derived from normal individuals in this study, it is possible that the individual isoforms may have distinct roles to play in pregnancy-induced hypertensive disorders including pre-eclampsia and pregnancy-induced hypertension.

TXA2 is thought to play a pathophysiological role in neuronal death during cerebral ischaemia (64). Previous studies have shown that the level of brain TXB2, the non-enzymatic degradation metabolite of TXA2, increases 55 fold in cerebral ischaemia, and has thus been implicated in post-ischaemic hypoperfusion and the development of cerebral injury after ischaemia (65). Using ligand based (SQ31,491) affinity chromatography, Borg et al., (66) identified two distinct TP receptors of 52kDa and 55kDa in rat brain. Recently, a TXA2 receptor was cloned from rat astrocytes (67) and was found to be 71.8% homologous to the human TPα cDNA. Interestingly, no alternatively spliced variant of the TP gene was identified in rat brain tissue (67). In this study, we identified both TPα and TPβ mRNAs in normal human foetal and adult brain tissue, with no age-related alterations in TP expression levels. TPα expression predominates in both adult and foetal brain tissue. The significance of this is unclear but may point to TPα playing a greater role in mediating cerebral ischaemia. Our finding of TP expression at the mRNA level correlates with Blackman et al., (68) who reported the existence of functional TP protein in both rat neonatal oligodendrocytes and human oligodendroglioma cells by radioligand binding analysis and immunocytochemistry.

Northern blot analysis indicated that, in the mouse, TP mRNA is most abundantly expressed in thymic tissue (36). Additional studies indicated that the TP is most highly expressed in CD4+8- and CD4+8+ immature thymocytes, followed by CD4+8- and CD4+8+ cells (17). Previous studies have shown that the TXA2 agonist, STA2, induces apoptotic cell death in immature thymocytes and mediates thymocyte maturation and selection (17). Therefore, we examined thymic tissue for the presence of TPα and TPβ encoding mRNA’s. We found that both TP isoforms are expressed at the mRNA level in thymic tissue, with 3-fold greater expression of TPα relative to TPβ. The relative role of each TP isoform in DNA fragmentation and apoptosis remains to be determined.
Northern blot analysis of various mouse organs revealed the presence of TP mRNA in thymus, spleen, lung, kidney, uterus, heart and brain tissue but not liver, stomach and ileum (36). In contrast, another study reported the existence of TP in endothelial cells, hepatocytes and Kupffer cells of rat liver, with an increase in TP mRNA expression observed with experimentally induced alcoholic liver disease in each of these cell types (69). Moreover, Taniguchi et al., (70) reported that TXA$_2$ antagonists may prove useful in the treatment of inflammatory bowel disorder implicating the importance of TP in intestinal tissue. In view of these findings, we investigated the existence of mRNAs encoding the TP isoforms in human liver and small intestine tissue. Both TP isoforms were expressed in small intestine and liver tissue, with TP$_a$ expression predominating in both cases. Furthermore, RT-PCR analyses for TP mRNAs in the immortalised hepatoblastoma cell line, HepG2, revealed the expression of TP$_a$ exclusively with no detectable expression of TP$_b$ mRNA. The differential expression of TP$_a$ and TP$_b$ mRNA’s in these cells clearly indicates that the 2 receptor isoforms are subject to distinct gene regulatory events in HepG2 cells, at least.

In conclusion, the TP is abundantly expressed at both the mRNA and protein level in tissues of relevance to TXA$_2$ biology, such as erythroleukemia cells, vascular and uterine smooth muscle, uterus and placental tissue, endothelium, epithelium, trophoblasts, thymus, liver and small intestine with TP$_a$ expression predominated in most tissues examined. Whereas relative to GAP3DH mRNA, TP$_a$ is expressed at approximately equal levels in all cell / tissue types analysed (0.80 ± 0.04, n = 47), considerable differences in TP$_b$ mRNA (0.49 ± 0.04, n = 47) expression were observed. The apparent greater physiological requirement for TP$_a$ over TP$_b$ remains to be studied in the future. In addition, the hepatoblastoma cell line, HepG2, exclusively expresses TP$_a$, implicating a redundant physiological role for TP$_b$ in this cell type. Contrary to previous reports, HUVECs express both the TP$_a$ and TP$_b$ mRNA’s with significantly greater levels of TP$_a$ than TP$_b$ expressed. Thus, it is evident from this study that mRNA’s for both isoforms are co-expressed in placental/platelet tissue, in endothelial cells and, indeed, in a number of other cell/tissue types. This fact raises doubts as to whether the TP$_a$ should be referred to as the platelet/placental TP and the TP$_b$ referred to as the endothelial receptor (30). Our findings also suggest that the molecular mechanisms responsible for TP$_a$ and TP$_b$ mRNA expression are subject to subtle regulation in different tissues and cell types. Further investigations are required to understand the molecular regulation in TP$_a$ and TP$_b$ mRNA expression.

Acknowledgements:
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References


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66. C. Borg, CT. Lim, DC. Yeomans, JP. Dieter, D. Komiotis, EG. Anderson and GC. Le Breton. Purification of rat brain, rabbit aorta, and human platelet thromboxane A2/prostaglandin H2
receptors by immunoaffinity chromatography employing anti-peptide and anti-receptor antibodies.


FIGURES:

A. TP PRIMER POSITIONING

![Diagram of TP primer positioning]

B. PREDICTED SIZE FRAGMENTS

<table>
<thead>
<tr>
<th>TP</th>
<th>Primers</th>
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<tr>
<td>TPα</td>
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</tr>
<tr>
<td>TPβ</td>
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<tr>
<td>TPαβ</td>
<td>A vs D</td>
<td>942/283bp</td>
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</table>

C. GA3PDH PRIMER POSITIONING

![Diagram of GA3PDH primer positioning]

Figure 1. Organization of the h. TP gene.

A. The general organization of Exon 2 - Intron 2 - Exon 3 of the human TP gene corresponding to the region encoding the unique C-terminal cytoplasmic tail of TPα and TPβ are shown. Exon 3 spans nucleotides 811 - 1029, encoding amino acid residues 271 - 343 of TPα, plus an additional 942 nucleotides (corresponding to nucleotides 1029 - 1971) of 3' untranslated sequence (3' UTR). Nucleotides 984 - 1642 of the TPα coding sequences behave as a potential intron (Intron 2B) in the TPβ mRNA; splicing of nucleotides 983 / 1643 results in a mRNA which has a new open reading frame and encodes a protein of 407 amino acids, of which amino acids 328 - 427 are unique to the TPβ.

B. The following primer pair combinations were used in the PCR reactions: Primer pairs A/C specifically amplify TPα; Primer pairs A/B specifically amplify TPβ; Primer pair A/D was used to co-amplify TPα and TPβ isoforms. Primer pairs Gf and Gr were used to amplify a 982 bp fragment of GA3PDH cDNA sequences.
Figure 2. Analysis of TP expression in HEL cells.

A. Agarose gel electrophoresis of RT-PCR products (7 μl/lane) derived from megakaryocyte HEL 92.1.7 cell 10 cDNA template: lane 1, TPα, 269bp product versus primers A/B; lane 2, TPα, 400bp product versus primers A/C; lane 3, GA3PDH, 983 bp product versus primers Gf/Gr; lanes 4-6, negative control PCR reactions carried out in the absence of template 10 cDNA in the presence of primers A/B, A/C and Gf/Gr, respectively; lanes 7-8, negative control reactions resulting from 10 cDNA template generated in the absence of MMLV-RT or template RNA, respectively, versus primers A/B; lane 9, TPα and TPβ, 942 bp and 283 bp products, respectively, derived versus primer A/B. Lane M, pGEM® DNA markers; only the 179 - 1,198 bp fragments are shown.

B. In each case, levels of TPα, TPβ mRNA were each represented as a ratio relative to GA3PDH expression (i.e. TPα/GA3PDH ± S.E.M. and TPβ/GA3PDH ± S.E.M., arbitrary units). Expression of TPα relative to TPβ are represented as a ratio of these values (i.e. TPα/TPβ ± S.E.M, arbitrary units). Both TPα and TPβ are expressed in HEL 92.1.7 with significantly greater levels of TPα expressed relative to TPβ (* p<0.05).

C. Saturation radioligand binding data are expressed as fmol [3H]SQ29,548 / mg cell protein ± S.E.M. where n ≥4.

D. Southern blot analysis of TPβ, TPα and GA3PDH specific RT-PCR products, generated using primers A/B, A/C and Gf/Gr, respectively, screened using the [γ-32P] radiolabelled TP specific Probe X and GA3PDH specific Probe Gp.
Figure 3. Analysis of TP expression in vascular SMC and uterus.

A. Levels of TP\(_\alpha\), TP\(_\beta\) and GA3PDH mRNA expression in foetal aortic (VLTR), adult aortic (AALTR) and uterine (ULTR) smooth muscle (SM) cells, and uterine tissue, in arbitrary units, were each represented as a ratio relative to GA3PDH expression (i.e. TP\(_\alpha\)/GA3PDH ± S.E.M. and TP\(_\beta\)/GA3PDH ± S.E.M.).

B. Expression of TP\(_\alpha\) relative to TP\(_\beta\) are represented as a ratio of these values (i.e. TP\(_\alpha\)/TP\(_\beta\) ± S.E.M, arbitrary units). Significantly greater levels of TP\(_\alpha\) relative to TP\(_\beta\) mRNA is expressed in adult aortic (* p<0.05) and uterine (*p<0.025) SM cells.

C. Radioligand binding data are expressed as fmol \([^3]H\)SQ29,548 / mg cell protein ± S.E.M. where n ≥4.
Figure 4. Analysis of TP expression in 1° HUVEC and ECV-304 cells

A. Agarose gel electrophoresis of RT-PCR products (7 μl/lane) derived from primary HUVEC cell 1° cDNA template: lane 1, TP\(_{\beta}\), 269bp product versus primers A/B; lane 2, TP\(_{\alpha}\), 400bp product versus primers A/C; lane 3, GA3PDH, 982 bp product versus primers Gf/Gr; lanes 4-6, negative control PCR reactions carried out in the absence of template 1° cDNA in the presence of primers A/B, A/C and Gf/Gr, respectively; lanes 7-8, negative control reactions resulting from 1° cDNA template generated in the absence of MMLV-RT or template RNA, respectively, versus primers A/B. Lane M, pGEM® DNA markers; only the 179 - 1,198 bp fragments are shown.

B. Relative TP isoform expression

C. Relative TP isoform expression data

D. Southern blotting analysis

The 1° HUVECs express significantly greater levels of TP\(_{\alpha}\) relative to TP\(_{\beta}\) (\(* p<0.05\)).
**Figure 5. Analysis of TP expression in 1° Trophoblasts**

**A.** Agarose gel electrophoresis of RT-PCR products (7 μl/lane) derived from primary ED-31 cell 1° cDNA template: lane 1, TP β, 269bp product versus primers A/B; lane 2, TP α, 400bp product versus primers A/C; lane 3, GA3PDH, 982 bp product versus primers Gf/Gr; lanes 4-6, negative control PCR reactions carried out in the absence of template 1° cDNA in the presence of primers A/B, A/C and Gf/Gr, respectively; lanes 7-8, negative control reactions resulting from 1° cDNA template generated in the absence of MMLV-RT or template RNA, respectively, versus primers A/B. Lane M, pGEM® DNA markers; only the 126 - 1,198 bp fragments are shown.

**B.** Relative TP isoform expression

**C.** TP isoform expression data

<table>
<thead>
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<th>Cell line</th>
<th>TP α/GA3PDH</th>
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<tr>
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<tr>
<td>ED-31</td>
<td>0.85 ± 0.12</td>
<td>0.55 ± 0.12</td>
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<tr>
<td>ED-77</td>
<td>0.86 ± 0.11</td>
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<tr>
<td>Tm-1</td>
<td>0.78 ± 0.10</td>
<td>0.87 ± 0.03</td>
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**D.** Saturation radioligand binding data

<table>
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<tr>
<th>Cell type</th>
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<td>ED-27</td>
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<td>ED-31</td>
<td>11.3 ± 3.21</td>
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<tr>
<td>ED-77</td>
<td>48.0 ± 6.41</td>
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<tr>
<td>Tm-1</td>
<td>36.6 ± 5.65</td>
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</table>

**D.** Radioligand binding data are expressed as fmol [3H]SQ29,548 / mg cell protein ± S.E.M. where n ≥ 4.
A. Relative TP isoform expression

B. Relative TP isoform expression data

<table>
<thead>
<tr>
<th>Tissue type</th>
<th>Tissue</th>
<th>TP_a/TP_b ± S.E.M</th>
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<tr>
<td>Brain</td>
<td>Foetal*</td>
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<td></td>
<td>Adult*</td>
<td>1.97 ± 0.33</td>
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<tr>
<td>Thymus</td>
<td>Total thymus*</td>
<td>3.31 ± 0.15</td>
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<tr>
<td>Intestine</td>
<td>Small Intestine</td>
<td>1.51 ± 0.12</td>
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Figure 6. Analysis of TP expression in foetal and adult brain, thymus and small intestine.

A. Levels of TP\_a, TP\_b and GA3PDH mRNA expression in foetal brain, adult brain, thymus and intestine, in arbitrary units, were each represented as a ratio relative to GA3PDH expression (i.e. TP\_a/GA3PDH ± S.E.M. and TP\_b/GA3PDH ± S.E.M.).

B. Expression of TP\_a relative to TP\_b are represented as a ratio of these values (i.e. TP\_a / TP\_b ± S.E.M, arbitrary units). Significantly greater levels of TP\_a relative to TP\_b are expressed in foetal brain tissue (* p<0.05), thymus (*p<0.05) and small intestine.
Figure 7. Analysis of TP expression in liver tissue and HepG2 cells

A. Agarose gel electrophoresis of RT-PCR products (7 µl/lane) derived from HepG2 cell 10⁶ cDNA template: lane 1, TPβ, primers A/B; lane 2, TPα, 400bp product versus primers A/C; lane 3, GA3PDH, 982 bp product versus primers Gf/Gr; lanes 4-5, negative control PCR reactions carried out in the absence of template 10⁶ cDNA in the presence of primers A/B and A/C. Lane M, pGEM® DNA markers; only the 126 - 1,198 bp fragments are shown. Both the TPα and the GA3PDH products were amplified (lanes 2 & 3, respectively). However, TPβ specific product (268bp, lane 1) was not detected. B. Levels of TPα, TPβ and GA3PDH mRNA expression in liver and the HepG2 cell line, in arbitrary units, were each represented as a ratio relative to GA3PDH expression (i.e. TPα / GA3PDH ± S.E.M. and TPβ / GA3PDH ± S.E.M.). C. Expression of TPα relative to TPβ are represented as a ratio of these values (i.e. TPα / TPβ ± S.E.M., arbitrary units). Both TPα and TPβ are expressed in liver tissue with significantly greater levels of TPα expressed relative to TPβ (* p<0.05). D. Radioligand binding data are expressed as fmol [³H]SQ29,548 / mg cell protein ± S.E.M. where n ≥4.