

New insights into the clearance of tissue factor pathway inhibitor (TFPI) and unfractionated heparin (UFH)



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**New insights into the clearance of tissue factor pathway
inhibitor (TFPI) and unfractionated heparin (UFH)**

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LIST OF PAPERS

This thesis is based on the following papers:

- I. Cristina Ionica Øie, Ellen Brodin, Rupa Shree Appa, Bård Smedsrød, John-Bjarne Hansen. Asialoglycoprotein Receptor (ASGP-R) in Liver Parenchymal Cells is Involved in Elimination of Recombinant Human TFPI – manuscript
- II. Oie, C.I., Olsen, R., Smedsrød, S., Hansen, J.B. Liver sinusoidal endothelial cells are the principal site for elimination of unfractionated heparin from the circulation. *Am J Physiol Gastrointest Liver Physiol*, 2008. 294(2): p. G520-8
- III. Cristina Ionica Øie, Ellen Brodin, Rupa Shree Appa, Ida Hilden, Bård Smedsrød, John-Bjarne Hansen. Effect of Unfractionated Heparin on TFPI Elimination – manuscript
- IV. Cristina Ionica Øie, Rupa Shree Appa, Ida Hilden, Helle Heibroch Petersen, Albrecht Gruhler, Bård Smedsrød, John-Bjarne Hansen. Rat Liver Sinusoidal Endothelial Cells (LSECs) express functional Low Density Lipoprotein Receptor-Related Protein-1 (LRP-1) – submitted

ABBREVIATIONS

AGE = advanced glycation end products
APP = amyloid precursor protein
ASGP-R = asialoglycoprotein receptor
ASOR = asialo-orosomucoid
CHO = Chinese hamster ovary
EC = endothelial cell
EEA1 = Early Endosome Antigen 1
EGF = epidermal growth factor
EPI = extrinsic pathway inhibitor
GAGs = glycosaminoglycans
GPI = glycosylphosphatidylinositol
HDL = high-density lipoprotein
HSPGs = heparan sulphate proteoglycans
IL = interleukin 1
KCs = Kupffer cells
LACI = lipoprotein-associated coagulation inhibitor
LDL = low density lipoprotein
LDL-R = low-density lipoprotein receptor
LMWH = low molecular weight heparin
LRP/LRP-1 = low-density lipoprotein receptor-related protein
LSECs = liver sinusoidal endothelial cells
MANN/COLL-R = mannose/alpha-collagen receptor
MPS = mononuclear phagocyte system
NPCs = non-parenchymal cells
oxLDL = oxidized low density lipoprotein
PARs = protease-activated receptors
PCs = parenchymal cells
RES = reticuloendothelial system
SR = scavenger receptor
TNF = tumor necrosis factor
TF = tissue factor
TFPI = tissue factor pathway inhibitor
UFH = unfractionated heparin
uPA = urokinase-type plasminogen activators
VLDL = very low density lipoprotein
vWF = von Willebrand Factor

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1. INTRODUCTION

1.1. Structural organization of the liver: anatomical localization and characteristics of the major liver cell types – parenchymal cells (PCs) and sinusoidal endothelial cells (LSECs)

The structural organization of the cellular and vascular elements of the liver is adapted to its special function as a key organ interposed between the digestive tract and the rest of the body. Representing a central metabolic processor of the body the liver functions both to

- i) produce an array of bio-molecules including for instance several coagulation enzymes and albumin as well as a great number of low molecular weight metabolites, and
 - ii) take up blood borne nutrient components absorbed in the intestine and bring about their subsequent metabolism, storage and distribution to blood and bile.
- The uptake function also includes the removal of physiological and foreign waste from the blood.

The liver tissue is arranged in lobules; each has a central vein which carries blood to the hepatic veins. The lobules consist of thin cords of liver cells, separated by spaces called sinusoids. The sinusoids are arranged in a radial pattern around the central vein (Figure 1).

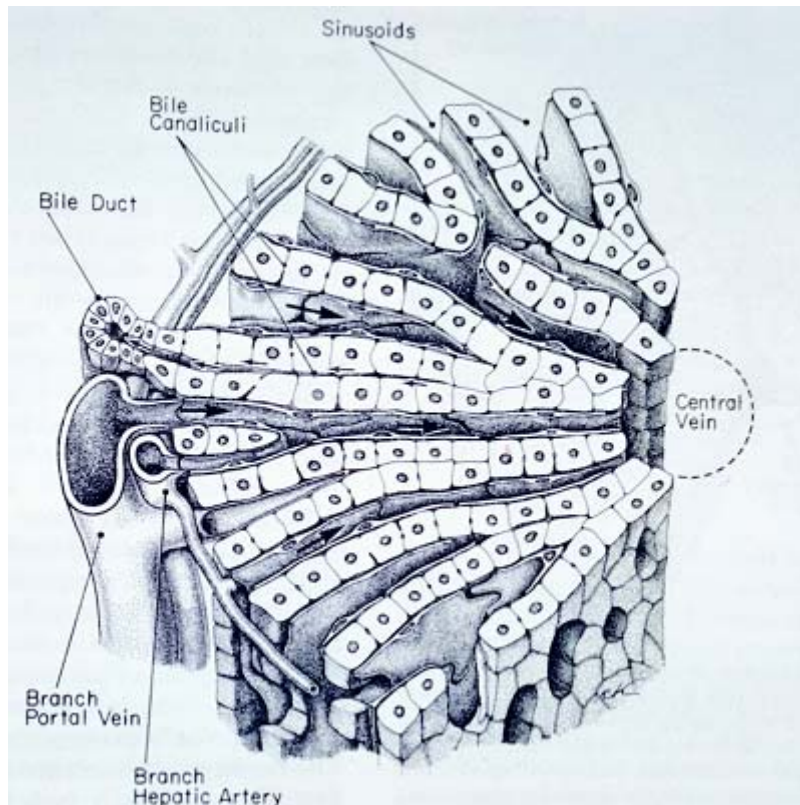


Figure 1. Schematic drawing of the liver sinusoids (reproduced with permission of Prof. Robert S McCuskey from A.W. Ham, “A Textbook of Histology”, J.B. Lippincott Co., Philadelphia, 1965)

Sinusoidal cells consist of various cell types, usually classified in two major groups: the parenchymal cells (PCs) or hepatocytes and the non-parenchymal cells (NPCs). The NPCs consist of four cell types: liver sinusoidal endothelial cells (LSECs), Kupffer cells (KCs), stellate cells and pit cells (also called liver associated lymphocytes or natural killer cells) (Figure 2).

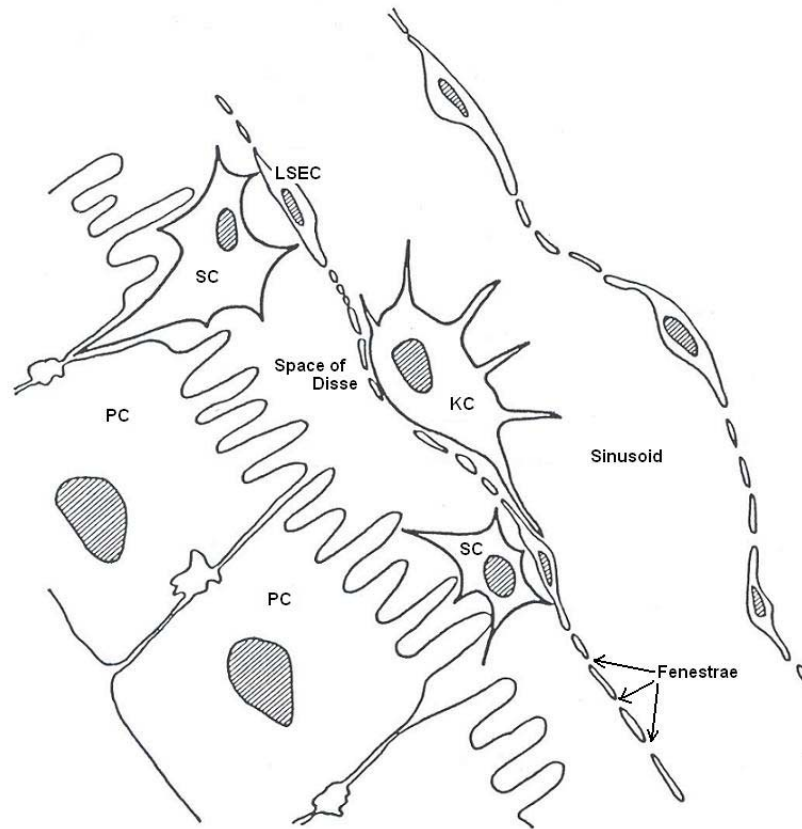


Figure 2. Schematic drawing of the liver sinusoidal cells (reproduced with permission of Dr. Grete Mørk Kindberg [1])

PCs are the largest cells in the liver, with a diameter of $>20 \mu\text{m}$ and are polyhedral with eight or more surfaces; many of them are polyploid (up to octaploid) (Table 1). LSECs form a continuous lining of the liver sinusoids and represent a barrier between the PCs and the sinusoidal blood. In the early 1970s a number of electron microscopic studies by Eddie Wisse indicated that the LSECs were a unique cell type of the liver sinusoids [2, 3], that differ from other vascular endothelial cells in several aspects: (a) LSECs lack a basement membrane, (b) von Willebrand factor, or factor VIII related antigen (an often used immunohistochemical marker of vascular endothelial cells), is not expressed by LSECs. Rather, LSECs have been reported to synthesize procoagulant factor VIII [4], (c) the long cytoplasmic processes of LSECs contain abundant pores or fenestrae with a mean diameter of approximately 100 nm, which are arranged in so-called sieve plates and function as a barrier between particles in the

sinusoidal lumen and the PCs [5], (d) intracellularly, LSECs are rich in coated pits and vesicles and other organelles associated with endocytosis.

| Cell Type | Number (%) | Volume (%) | Cells/g liver (x 10⁶) | Cell diameter (µm) |
|------------------------------|-------------------|-------------------|---|---------------------------|
| Parenchymal cells | 65 | 92.5 | 115 | 10-34 |
| Non-parenchymal cells | 35 | 7.5 | 63 | 6-15 |
| Sinusoidal endothelial cells | 21 | 3.3 | 38 | 6-11 |
| Kupffer cells | 8.5 | 2.5 | 15 | 7-15 |
| Stellate cells | 5.5 | 1.7 | 10 | 10-13 |
| Pit cells | <1 | | <0.3 | 6-8 |

Table 1. Cellular composition of rat liver (reproduced with permission of Prof. Bård Smedsrød [6])

1.1.1. Receptor-mediated endocytosis

Endocytosis is the process of vesicle formation from the plasma membrane, and in this process, plasma membrane-associated proteins are internalised into membrane-bound transport vesicles. The endocytic pathway begins at the plasma membrane and ends up in the lysosomes, and along this pathway cargo is either destined for recycling back to the plasma membrane or for degradation. As cargo passes through early and late endosomes, communication with the *trans*-Golgi network and the secretory pathway takes place. The secretory pathway functions to deliver secretory and transmembrane proteins and lipids from the ER, via the Golgi apparatus, either to intracellular compartments, to the plasma membrane or to the exterior of the cell. At all stages in this vesicle-mediated transport between the plasma membrane and various intracellular compartments, recognition, tethering and fusion of vesicles are essential for proper destination of the cargo.

Endocytosis supports various cellular functions including nutrient uptake, waste removal, growth-factor signaling, and membrane homeostasis [7]. Categorically, endocytosis can occur by multiple mechanisms, and can be divided into phagocytosis or “cell eating” of large particles (> 200 nm) typically restricted to specialized cells such as macrophages and neutrophils [8] and pinocytosis or “cell drinking”, the uptake of fluid and solutes that occurs in all cells.

Pinocytosis occurs by at least four basic mechanisms: 1) clathrin-dependent endocytosis, 2) caveolin-dependent endocytosis, 3) macropinocytosis, and 4) caveolae-, dynamin-, and clathrin-independent endocytosis [7]. These pathways are thought to vary mechanistically with respect to how the vesicles are formed, which cargo molecules are internalized, how entry is regulated, and to which intracellular destination the cargo is delivered.

Clathrin-mediated endocytosis is the best characterized endocytosis pathway (Figure 3). It ensures uptake of nutrients and waste and provides a way of transferring and regulating signalling from the exterior to the interior of the cell through surface receptor internalization. Receptor-mediated uptake of macromolecules via clathrin-coated pits constitutes a selective concentration mechanism that largely increases the efficiency of ligand internalization, such that even minor components of the extracellular environment can be taken up in large amounts without internalization of correspondingly large amounts of extracellular fluid.

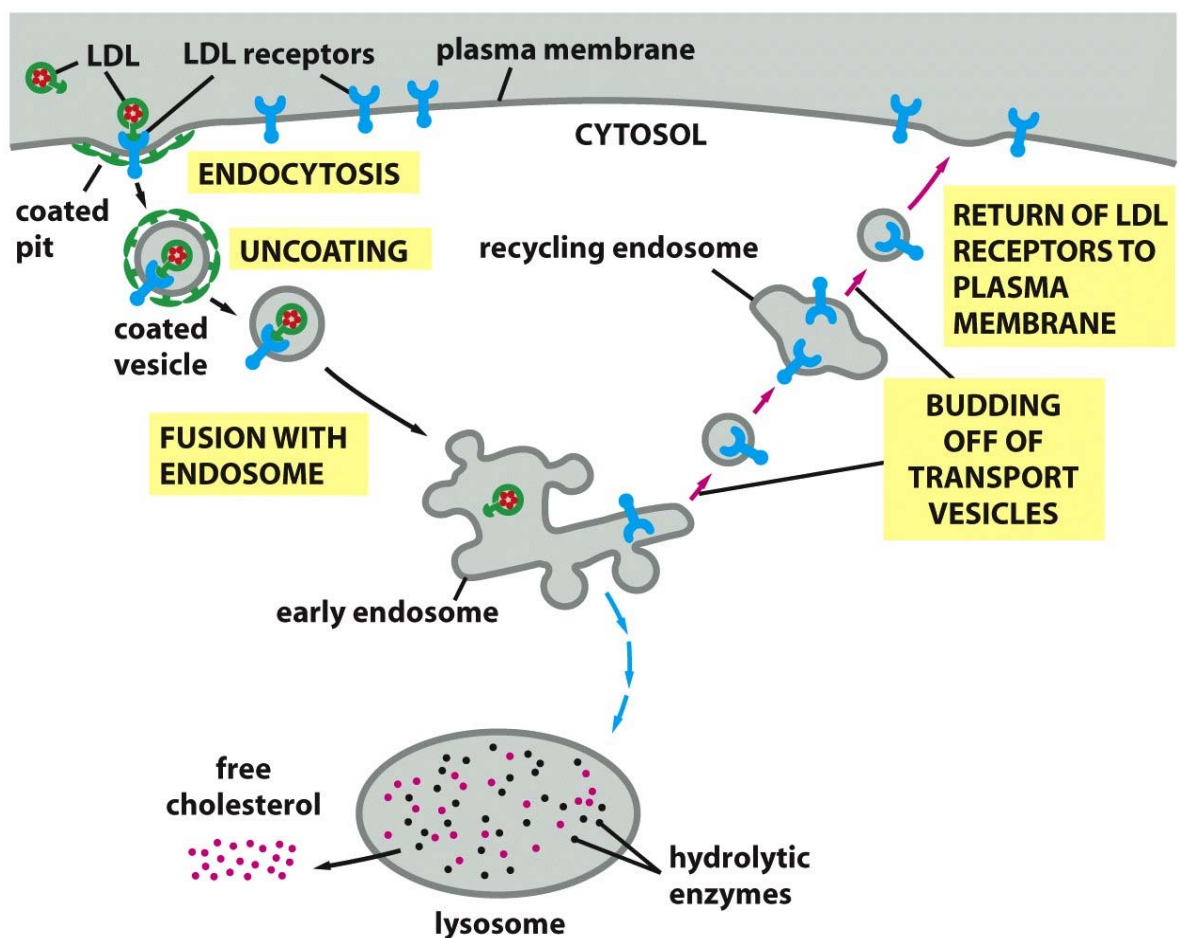


Figure 3. The receptor-mediated endocytosis of Low Density Lipoprotein (LDL)
 LDL receptor binds LDL at the plasma membrane and the complex assembly in a coated pit. The internalized pit is converted into a clathrin-coated vesicle that fuses with early endosomes (EEs) after the removal of the clathrin coat. The LDL dissociates from its receptor in the acidic environment of the EEs and ends up in lysosomes, where it is degraded. Reproduced with permission of Garland Science/Taylor and Francis LLC from Molecular Biology of the Cell 5th Ed. by Alberts et al.

Clathrin-mediated endocytosis is used for clearance of receptor-bound hormones and growth factors from the cell surface, control of the number of channels and transporters, internalization and degradation of extracellular material by some cells [9], recycling of synaptic vesicles in nerve terminals and is implicated in cell invasion by a variety of pathogens [10].

Clathrin is a vesicle coat protein involved in the assembly of membrane and cargo into transport vesicle at the plasma membrane [11]. Several proteins are involved in and essential for the formation of clathrin coated pits and vesicles and for the concentration of transmembrane receptors into these pits. The clathrin-mediated endocytosis starts with the binding of ligand to the luminal or extracellular domain of a transmembrane receptor, followed by concentration of receptor through interaction with the protein coat. Formation of an endocytic clathrin-coated vesicle is initiated by binding and oligomerisation of clathrin adaptor protein at the cytoplasmic surface of the plasma membrane. This leads to polymerization of clathrin into a lattice that pulls the plasma membrane inside [12].

Once the inward budding of the membrane is complete, interactions between the adaptor protein and the GTPase dynamin allow separation of the forming vesicle from the membrane [13]. After the pit is internalized and converted into a clathrin-coated vesicle, the clathrin coat is removed and the vesicle is able to fuse with target early endosomes, a process involving Rab5 and Early Endosome Antigen 1 (EEA1) [14]. Rab5 belongs to a superfamily of approximately 70 proteins that regulate many steps of membrane traffic [15] and EEA1 is a protein that binds phospholipid vesicles containing phosphatidylinositol 3-phosphate, which is necessary for endosomal trafficking [14]. Acidification of early endosomes leads to dissociation of most receptor-ligand complexes, and ligands destined for degradation travel with late endosomes to lysosomes, while receptor-enriched vesicles are recycled back to the

cell surface [16, 17]. The intracellular membrane trafficking system uses vesicles and tubulovesicular structures to deliver cargo proteins and lipids from one compartment to the next. Several proteins including the Rab guanosine triphosphate enzymes (GTPases) and the Soluble N-ethylmaleimide-sensitive factor Attachment Protein Receptors (SNAREs) are involved in recognition, docking and fusion of donor and acceptor compartments to ensure proper transport and delivery of cargo molecules [18].

1.1.2. Endocytic receptors on liver sinusoidal endothelial cells (LSECs) and parenchymal cells (PCs)

1.1.2.1. Liver sinusoidal endothelial cells (LSECs)

Eddie Wisse [3] was the first to present convincing evidence that the liver sinusoidal endothelial cell (LSEC) is a distinct cell type clearly different than the Kupffer cell and other sinusoidal liver cells. Moreover, Wisse's findings gave the first hint that these cells are active in endocytosis of blood plasma proteins [3]. At that time it was believed by most scholars that the cellular blood clearance system or the reticuloendothelial system (RES) was identical to the macrophages, or mononuclear phagocyte system (MPS). Wisse's suggestion that the LSECs endocytose plasma proteins was therefore not acted much upon. It was not until the beginning of the 1980's that scientists found the first evidence that the LSECs play an important role in the clearance of blood borne physiological macromolecular waste products [19, 20]. During the subsequent years several studies showed that the LSEC exhibits an unsurpassed blood clearance capacity [9]. In fact, an array of soluble waste colloids and macromolecules were shown to be removed by the LSECs and not by the KCs. Based on this solid body of evidence it was proposed by the end of the 1990's that the existing paradigm of "RES \equiv MPS" be shifted to "RES \equiv MPS + LSECs [9]. In spite of this, current text books in pathology and immunology still stick to the old incorrect paradigm of "RES \equiv MPS".

Moreover, most of the scientific literature published today still reveals that the old paradigm prevails. This is unfortunate, because it obscures interpretations of clearance studies. The novel paradigm holds that the LSECs are responsible for the clearance of blood borne colloids and soluble macromolecules (<200 nm), while KCs eliminate circulating particulate material (>200 nm).

Notably, animal species of all vertebrate classes contain a special population of scavenger endothelial cells [21]. In mammals and the 3 other land based vertebrate classes the LSECs carry the function of scavenger endothelial cells. However, in phylogenetically older vertebrates these cells are located in heart or kidney (bony fishes) or gills (cartilaginous and jawless fishes). In all vertebrates these cells play a pivotal homeostatic role by removing an array of physiological and foreign molecules from the blood [22]. To cope with the daily burden of grams of endocytosed material, LSECs are geared for rapid intracellular transport to degradation organelles [23], high capacity degradation of ligands by a large pool of active lysosomal enzymes, and release of degraded low molecular weight material to the surroundings [24].

So far, three specific receptors for endocytosis have been identified and characterized in LSECs, i.e., the scavenger receptor (SR), the mannose/collagen receptor (MANN/COLL-R), and the Fc γ receptor.

The scavenger receptor (SR)

LSECs express a number of SRs, including SR-A (a.k.a. macrophage scavenger receptor) [25, 26], SR-B (SR-B1 and CD36) [27] and SR-H (Stabilin 1/FEEL-1 and Stabilin 2/FELL-2/HARE) [26, 28-31]. The other SRs, namely SR-C (not found in mammals), SR-D (CD68: macrophage specific), SR-E (LOX-1), SR-F (SREC) and SR-G (SR-PSOX) are not

normally expressed on LSECs, but LOX-1 expression can be induced on LSEC with *in vivo* exposure to malondialdehyde-acetaldehyde-bovine serum albumin [32].

Despite the expression of three SR sub classes in LSEC, the main work-horse SR in LSEC appears to be Stabilin 2 (possibly together with Stabilin 1), based on the following: i) SR-A knockout mice clear SR ligands equally well as wild type mice [33-35], and cultured LSECs from the same knockout mice endocytose and degrade SR ligands equally well as wild types [36, 37]; ii) an antibody to CD36 that inhibits CD36 mediated uptake of SR ligands in other cells has no effect on the uptake of SR ligands by LSEC [38].

Several categories of waste substances are eliminated by LSECs via the SRs: i) N-terminal propeptides of types I and III procollagen (PINP and PIIINP) [39], and ii) atherogenic molecules: oxidized LDL (oxLDL) [40] and advanced glycation end products (AGEs) [41]. Clearance of these substances represents an important physiological mechanism contributing to maintaining homeostasis, and preventing atherosclerosis.

The mannose/collagen receptor (MANN/COLLA-R)

The mannose receptor (MANN-R) is an endocytic protein expressed in macrophages [42], dendritic cells [43], LSEC [9], kidney mesangial [44], tracheal smooth muscle [45], and retinal pigment epithelial cells [46]. The receptor is a 180 kDa monomeric transmembrane glycoprotein [47] and shows affinity for D-mannose, L-fucose and N-acetyl-D-glucosamine residues, and mediates endocytosis and phagocytosis of glycoproteins, glycolipids and particles that expose these monosaccharides in terminal positions of their carbohydrate side chains [42].

The MANN-R mediates receptor-mediated endocytosis of various soluble macromolecules, such as tissue plasminogen activator (tPA) [48], C-terminal propeptide of

type I procollagen [49], salivary amylase [50] and lysosomal enzymes [51-55]. Soluble mannose-terminated waste glycoproteins in blood circulation end up in liver, in the LSECs, rather than in KCs or other macrophages [9], probably due to the higher level of receptors on LSECs than on KCs [56].

Until recently it was believed that LSECs express a separate receptor, the collagen α -chain receptor (COLLA-R), that recognizes only denatured collagen [57]. However, research conducted to identify the COLLA-R expressed on rat and pig LSECs resulted in purification of a 180 kDa cell surface protein [58], which was identified as the MANN-R. Thus, the MANN-R and COLLA-R in LSECs represent differently located binding domains of the same receptor protein.

The Fc γ receptor

In humans, Fc γ receptors (Fc γ Rs) have been classified into 3 major classes comprising multiple isoforms: Fc γ RI/CD64 (Fc γ RIa, Fc γ RIb, and Fc γ RIc), Fc γ RII/CD32 (Fc γ RIIa, Fc γ RIIb, and Fc γ RIIc), and Fc γ RIII/CD16 (Fc γ RIIIa and Fc γ RIIIb). All these receptors except Fc γ RIIIb, which is a glycosyl phosphatidyl inositol anchored variety, are type 1 transmembrane proteins that, despite similarities in their extracellular domains, differ by ligand-binding specificity, cellular distribution, and regulatory functions [59]. These receptors recognize the Fc domain of immunoglobulin G (IgG), and are expressed on virtually all cells of the immune system [60-62].

The liver is the main organ for uptake of IgG-immune complexes (IgG-ICs) from the circulation [62, 63]. Fc γ R-mediated elimination of circulating IgG-ICs has generally been assumed to be mediated by KCs [64, 65]. However, while internalization of IgG-opsonised particles occurs via phagocytosis in the KCs [8], small immune complexes and soluble

aggregated IgG are internalized through receptor-mediated endocytosis in clathrin-coated pits by LSECs [62, 63, 66]. Studies using monoclonal antibodies to Fc-receptors and immunohistochemistry suggested that the Fc γ RII, and not Fc γ RIII is expressed in human LSECs [67]. By RT-PCR and Western blotting, it was demonstrated that purified rat LSECs express only one Fc γ R, the Fc γ RIIb2 [59]. Moreover, binding of ICs to the LSECs was completely blocked by the presence of the monoclonal antibody against the ligand binding site of Fc γ RIIb2 [59]. A recent study showed that an antibody (SE-1) which is specific to LSECs in rat does in fact recognize the antigen CD23b (Fc γ RIIb2) [68]. Fc γ RIIb2 may therefore be considered a biomarker for LSECs.

1.1.2.2. Liver parenchymal cells (PCs)

The PCs are equipped with the following major endocytosis receptors: the asialoglycoprotein receptor (ASPG-R), the low-density lipoprotein receptor (LDL-R), the low-density lipoprotein receptor-related protein (LRP) and the scavenger receptor class B type I (SR-BI).

The asialoglycoprotein receptor (ASPG-R)

The hepatic ASGP-R represents the “pioneer endocytosis receptor” as it was discovered and characterized already in 1974 [69]. This receptor is one of the best characterized model system for receptor-mediated endocytosis via the clathrin-coated pit pathway [69-73]. ASGP-R mediates the endocytosis and degradation of a wide variety of desialylated glycoproteins and neoglycoproteins that contain terminal galactose (Gal) or N-acetylgalactosamine (Gal-NAc) residues on their N-linked carbohydrate chains [69]. The most commonly used test ligand is asialoorosomuroid (ASOR), which contains tri- and tetra-antennary N-linked glycans. The ASGP-R is expressed along the entire surface of PC,

enriched in clathrin-coated pits, most abundantly over the sinusoidal plasma membrane domain, and one PC contains $1-5 \times 10^5$ binding sites [52, 74]. The affinity of the ASGP-R increases for mono-, di-, tri-, and tetra-antennary oligosaccharides [75]. The ligand receptor interaction is reversible on addition of competing Gal-exposing derivatives, in the absence of Ca^{2+} and on acidification [76, 77]. Recycling of internalized ASGP-Rs back to the plasma membrane occurs with high efficiency [78, 79]. In isolated rat PCs, it takes about 5-7 min for internalized ASGP-Rs to reappear on the cell surface [80, 81].

Involvement of the ASGP-R in the clearance of coagulation proteins was also recently shown. Coagulation Factor VIII (FVIII) is recognized by ASGP-R as a ligand *in vitro*, and its binding is driven by the oligosaccharide structures of the FVIII B domain, which has 15 complex-type N-linked oligosaccharide branches [82]. Studies on mice deficient in ST3Gal-IV, an enzyme that mediates attachment of sialyl groups to terminal galactose residues, showed that the half-life of endogenous von Willebrand Factor (vWF) is reduced 2-fold in mice [83]. Enzymatic removal of sialyl groups reduces the half-life of vWF in rabbits from 240 min to 5 min [84]. The importance of the nature of terminal carbohydrate residues is most strikingly illustrated by RIIS/J-mice, a strain characterized by vWF levels that are several fold lower compared with other strains. This level is caused by a rapid clearance of vWF through ASGP-R due to a surplus of terminal N-acetylgalactosamine residues [85].

The low-density lipoprotein receptor (LDL-R)

The low-density lipoprotein receptor (LDL-R) plays a critical role in the homeostatic control of blood cholesterol by mediating the removal of cholesterol-containing lipoprotein particles from circulation [86]. The most important physiological ligand for the receptor is

low density lipoprotein (LDL) [87, 88], which carries approximately 65% to 70% of plasma cholesterol in humans.

The LDL-R consists of five distinct domains with individual function: 1) ligand binding domain at the N-terminus containing complement-type repeats involved in LDL binding; 2) epidermal growth factor (EGF) precursor-homology repeats that contain YWTD motifs responsible for ligand dissociation; 3) an O-linked sugar domain acting as a spacer; 4) a membrane-spanning domain for anchorage; and 5) a cytoplasmic tail (NPxY motif) involved in internalization of LDL particles into coated pits [89, 90] (Figure 4).

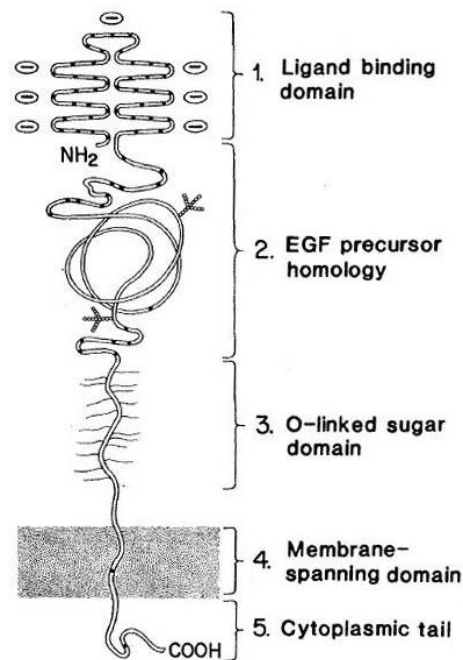


Figure 4. Structure of the LDL receptor From Brown, M.S. and J.L. Goldstein, *A receptor-mediated pathway for cholesterol homeostasis*. Science, 1986. 232(4746): p. 34-47., Reproduced with permission of AAAS and Dr. Brown.

There are eight members of the family besides LDL-R. These are: the low-density lipoprotein receptor-related protein (LRP), Megalin, very-low-density lipoprotein (VLDL) receptor, apoER2 and SorLa/LRP11, LRP1b, MEGF7, LRP5/6 (Figure 5). Each member of this receptor family undergoes receptor-mediated endocytosis; yet each member is expressed

in a number of different tissues and has a wide range of different ligands, not specific to the recognition of the LDL particle [91-93].

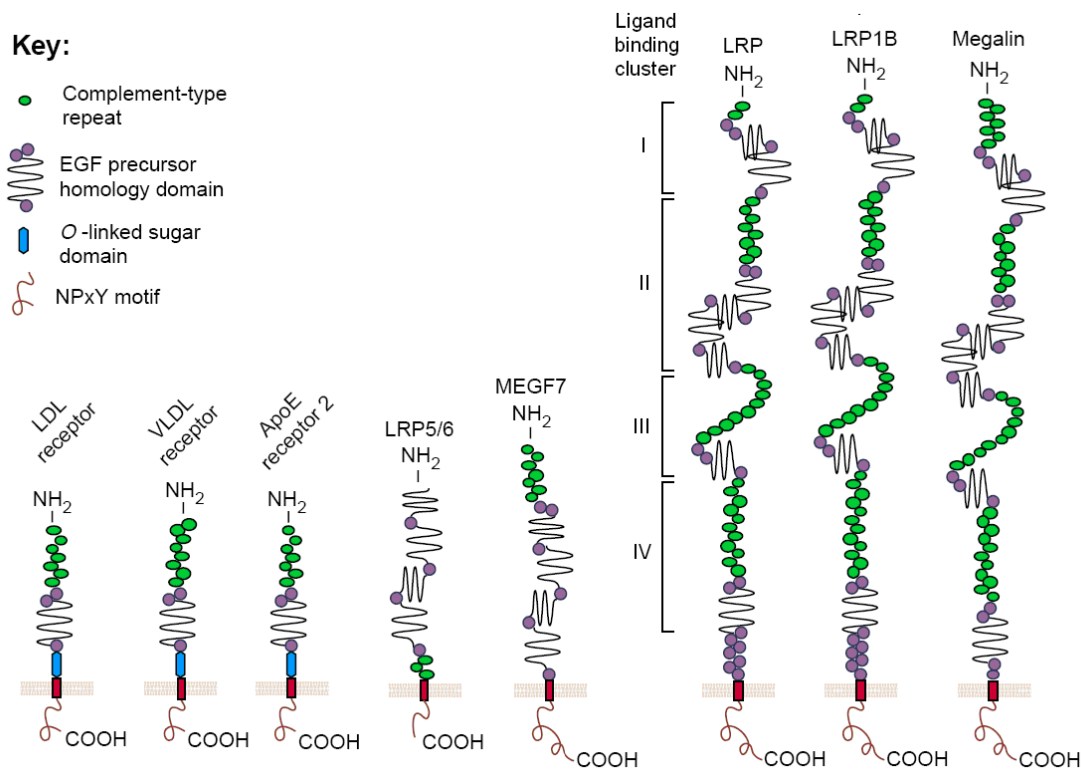


Figure 5. Structural organization of mammalian receptors of the low-density lipoprotein (LDL) receptor family (modified with permission of Nykjaer and Moestrup [91, 94])

Low-density lipoprotein receptor – related protein (LRP)

The low density lipoprotein receptor-related protein (LRP) is one of the largest member of the family (600 kDa). LRP is a multifunctional endocytic scavenger receptor expressed in a number of different cell types, mostly in hepatocytes, macrophages, trophoblasts, neurons, activated astrocytes and fibroblasts, pneumocytes and smooth muscle cells [95-97]. Mature LRP contains two subunits, a 515 kDa extracellular domain (α -chain), noncovalently attached to a 85 kDa intracellular and transmembrane domain (β -chain), which are produced by proteolytic cleavage from a single polypeptide precursor of 600 kDa in the trans-Golgi network [95, 98, 99].

Due to its high expression in the liver, LRP mediates the cellular uptake of lipoprotein particles containing apoE and lipoprotein lipase [100-102]. It cooperates with LDL receptor in the removal of cholesterol containing remnant lipoproteins from the circulation; thus acting as a chylomicron remnant receptor [100, 101, 103]. Despite lipoprotein recognition, it has a wide range of other ligands from urokinase-type plasminogen activators (uPA), amyloid precursor protein (APP), tissue factor pathway inhibitor (TFPI), protease/inhibitor complexes, toxins, viruses and activated α_2 -macroglobulin [93, 99, 104-107]. All these ligands deviate both in structure and function and, characteristically, do not cross-compete for binding to LRP [108]. The major ligand-binding sites within LRP are contained in clusters II and IV (Figure 5) and most ligands bind equally well to both clusters, suggesting a functional duplication within LRP [109].

LRP gene depletion in mice has demonstrated a failure of LRP^{-/-} embryos to develop after implantation. Thus, LRP seems to be important during foetal development, and mutations within the LRP gene can induce embryonic death within 10 days. [99]. In addition, LRP has been associated with the progression of Alzheimer's disease [110-112].

The Scavenger Receptor Class B type I (SR-BI)

SR-BI is a cell surface glycoprotein of 82 kDa [113] consisting of a horseshoe-like large extracellular loop, short N- and C-terminal cytoplasmic domains, adjacent N- and C-terminal transmembrane domains, and the bulk of the protein in a heavily N-glycosylated, disulfide-containing extracellular domain [114].

SR-BI is highly expressed in organs with critical roles in cholesterol metabolism (liver) and steroidogenesis (adrenal, ovary, testis) [114-116]. SR-BI has binding specificity for high-density lipoprotein (HDL) and mediates selective uptake of lipids from HDL without

endocytic uptake of the lipoprotein itself [115, 117]. Besides HDL, SR-BI binds a wide array of ligands, including anionic phospholipids [118], advanced glycation end products (AGE) [119], apoptotic cells [120], oxidized LDL (oxLDL), maleylated BSA, apoB-containing lipoproteins, including LDL and VLDL [121], apoE, an important ligand for VLDL removal from the circulation [122] and native and modified lipoproteins [115, 123-125].

1.2. Tissue factor pathway inhibitor (TFPI)

1.2.1. History

TFPI is an endogenous anticoagulant protein, a serine protease inhibitor, and the only known regulator of the TF-dependent pathway of blood coagulation. It is known to play an important role in the control of thrombogenesis at both cellular and plasmatic sites.

Experiments performed early in the second half of the last century demonstrated the presence of an endogenous inhibitor of TF-induced coagulation activation [126-128]. Subsequently, Hjort (1957) reported that convertin, now known as TF-FVIIa catalytic activity, was inhibited by a component present in serum [129]. He described the calcium dependence and reversibility of the inhibition by calcium chelators, and suggested from indirect methods, that the inhibitor to convertin was calcium dependent, and named the inhibitor anticonvertin. The nature of this inhibition remained obscure until 25 years later, when Dahl et al. published a chromogenic substrate assay system, for the determination of the inhibitor [130]. They demonstrated that anti-convertin activity was present in two high molecular weight peaks, identified by gel filtration of plasma. Then Sanders et al. reported the remarkable finding that inhibition of TF-FVIIa requires the presence of FX [131], and it was quickly shown that FXa rather than FX was responsible for the inhibition of TF-FVIIa. The inhibitor was isolated in 1987 by two independent groups [132, 133], and was cloned and characterized in 1988 by Wun et al. [134].

The name of the inhibitor varied during the years [anithromboplastin, anticonvertin, the factor VIIa/tissue factor inhibitor, tissue factor inhibitor, extrinsic pathway inhibitor (EPI) and lipoprotein-associated coagulation inhibitor (LACI)], until a consensus meeting of the Scientific and Standardization Committee of the International Society of Thrombosis and Haemostasis in 1991 agreed on the name “Tissue Factor Pathway Inhibitor” (TFPI).

1.2.2. Molecular structure

The translated product of the human TFPI mRNA is a 304 amino acid protein. The removal of a classical 28 residue signal peptide yields the mature 276 amino acid TFPI [134]. TFPI contains 3 Kunitz-type domains arranged in tandem, each containing 3 disulphide bonds. There is a nonuniform charge distribution within the TFPI molecule. The amino-terminal contains several negatively charged acidic residues. The carboxy-terminal sequence includes 15 positively charged basic amino acids (Figure 6). The predicted molecular weight of the polypeptide backbone of TFPI is 32 kDa, and due to posttranslational modifications, the mature secreted protein size can increase to about 43 kDa [134]. TFPI is *N*-linked glycosylated at Asn117 and Asn167. *O*-linked carbohydrate attachment occurs at Ser174 and Thr175 [135].

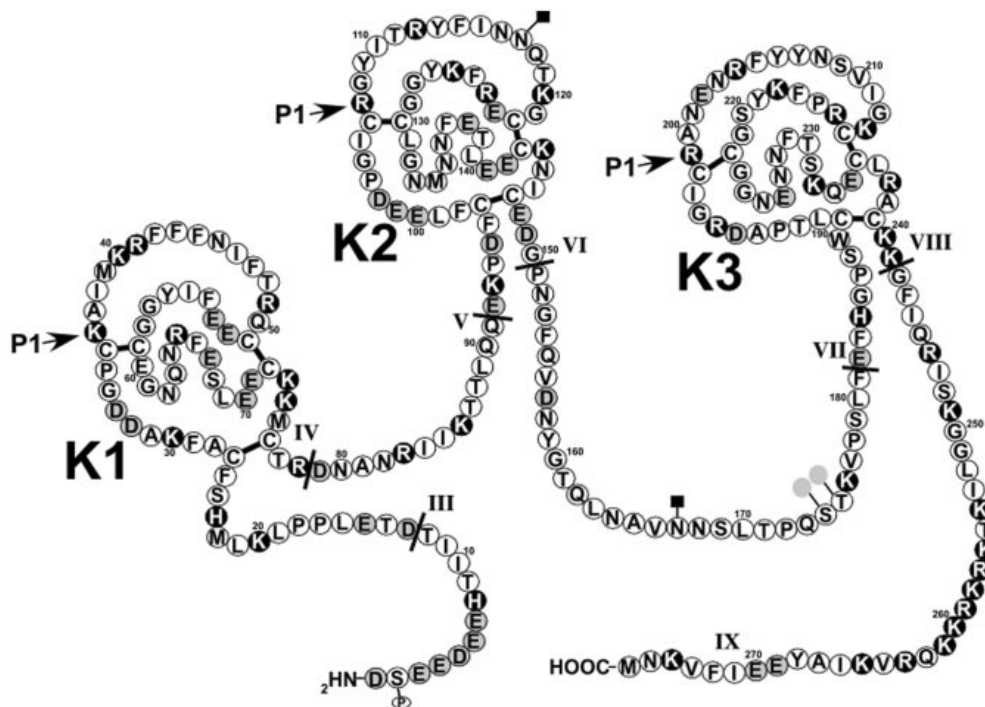


Figure 6. Primary amino acid sequence of mature TFPI Exon boundaries are numbered in roman numerals. *N*-linked glycosylation sites at Asn117 and Asn167 (black squares). *O*-linked glycosylation sites at Ser174 and Thr175 (gray circles). The Kunitz domains (K1, K2, K3) contain 3 disulphide bonds each. Black arrows indicate the P1 residues. P1 in K1 interacts with FVIIa in the TF-FVIIa complex. P1 in K2 interacts with FXa. The predicted P1 in K3 has no described inhibitory role. (Reproduced with permission of Dr. James Crawley [136])

The TFPI mRNA found in the endothelium and various cell types exists as a 4 kb and 1.4 kb species [137, 138]. The difference between the two mRNA sizes has been attributed to the presence of 2.6 kb additional, not translated sequences in the 4 kb band. The TFPI gene resides on the long arm of chromosome 2, at region 2q31-2q32.1, and contains nine exons, which are separated by eight introns [134]. Although the nucleotide sequence of the promoter region, containing several binding sites for transcription factors, has been determined, it remains to be established how endothelial cells specifically synthesize TFPI, and how the expression is regulated. Recently both the TGF- β -like response elements and GATA sequences have been reported [139-141]. The GATA-sequences act as cis-regulatory elements in the expression of several genes, and appear to be active in the expression of genes in the endothelium and haematopoietic cells [142, 143]. GATA-motifs in TFPI-gene may bind GATA-2 transcription factor, also expressed in the endothelium and thereby regulate TFPI gene expression [141, 144].

To date, no patients with TFPI-deficiency have been reported, perhaps because homozygous TFPI deficiency is likely to be lethal. This is supported by observations of embryonic death, from unregulated consumptive coagulopathy in mice embryos, with TFPI gene disruption [145]. Additionally, a few polymorphism sites in the TFPI-gene have been reported in the normal population, and in patients with acute coronary syndrome, as well as with arterial and venous thrombosis [146-148], but do not seem to play a significant pathophysiological role in either arterial or venous thrombosis [149].

Plasma TFPI-levels vary across species [150]. The homology of rabbit and rat TFPI to human TFPI is about 60% [151, 152], whereas the homology of monkey TFPI to human TFPI is about 94% [153]. The differences between rabbit and rat TFPI, and those of humans or

monkeys, may be due to differences in the amino acid sequences, or post-translational modification of TFPI.

TFPI α is a soluble form of TFPI. It is a 43 kDa glycoprotein, and consists of a highly negative acidic N-terminal region, followed by three tandem Kunitz-type inhibitory domains, and a highly positive C-terminal region. Studies of cultured endothelial cells and human placenta have demonstrated that TFPI associates with the cell surface through a glycosylphosphatidylinositol (GPI)-anchor in a manner that is not dependent on glycosaminoglycans (GAGs) or altered by heparin. TFPI α is not directly bound to the GPI-anchor; instead it appears to bind to a GPI-anchored protein, a protein that appears to be necessary for the proper trafficking of TFPI to the cell surface [154-156]. Site-directed mutagenesis experiments indicate that domain 1 (K1) of TFPI binds to FVII and domain 2 (K2) binds to FXa, respectively [157]. The precise function of the third Kunitz-type domain is not fully understood. It appears that it has no inhibitory activity, but is probably involved in the association with lipoproteins [158], and is mandatory for the anticoagulant function of TFPI in TF-induced coagulation *in vitro* [159, 160]. The region between residues 181 and 242, including the third Kunitz domain, contains a heparin binding site, but whether this site is important for TFPI-function or -physiology is not known [161]. The heparin-induced enhancement of TFPIs FXa-inhibition has been shown to become gradually greater, as more of the C-terminal portion is intact [162]. Truncated forms of TFPI, lacking most of their C-terminal domains, exhibit reduced affinity for vascular wall proteoglycans [163]. Whether or not the N-terminal acidic region of TFPI plays a role in physiological inhibition of TF-induced coagulation remains to be determined. Posttranslational modifications in the TFPI-molecule include *O*-linked glycosylation at Ser174 and Thr175, as well as three potential sites for *N*-linked glycosylation: Asn117, Asn167 and Asn228 [157, 164, 165]. The extent of *N*-linked glycosylation in human plasma TFPI appears to be less than that of TFPI^{HepG2} or

TFPI^{CHO}; N-linked glycosylation is linked only at Asn117 and Asn167 [135, 166]. Although these posttranslational modifications do not seem to function directly in the inhibitory function of TFPI, they may influence its cell binding properties and plasma clearance, possible through their interactions with the basic carboxy-terminal. Recombinant bacterial TFPI (TFPI^{E.Coli}), lacking post-translational modifications, may show functional differences to TFPI, that is endogenously synthesized or released from endothelium [167]. TFPI^{E.Coli} does not interact with cell surface in the same manner as endogenously expressed TFPI α [168]. The cellular binding of TFPI^{E.Coli} is of relatively low affinity, and appears to involve an interaction with surface glycosaminoglycans [163, 167].

TFPI β is an alternatively spliced form of TFPI, in which the Kunitz-3 domain and the C-terminal region of TFPI α are replaced with an alternatively spliced C-terminal region, that signals direct attachment of a GPI-anchor [169, 170]. Based on protein mass, TFPI β is considerably smaller than TFPI α , suggesting a difference in post-translational modifications, i.e. TFPI β containing O-linked carbohydrate with considerably greater sialic acid content than TFPI α [169]. Although TFPI β accounts for only 20% of total surface TFPI, it is responsible for most of the FXa-dependent anti TF-FVIIa-activity, suggesting a potential alternative role for cell-surface TFPI α [169]. The binding of TFPI α to its cellular receptor appears to interfere with its interaction with TF-FVIIa, perhaps because of steric effects or by limiting the movement of TFPI α at the membrane surface. Piro and Broze suggested another role of cell-surface TFPI α than just the inhibition of TF-FVIIa. They speculated that the binding of endogenously expressed TFPI α , but not TFPI^{E.Coli}, may affect protease-activated receptors (PARs) signalling [169]. When TFPI^{E.Coli} was used to attempt inhibition of excessive TF expression on vascular endothelial cells, coagulation was more efficiently blocked than cell-

signaling. Therefore, although TF procoagulant function may be blocked by TFPI^{E.Coli}, TF signaling function may continue [171].

Truncated forms of TFPI also exist in the circulation. They lack most of the carboxy-terminal and often also most of the K3 [172], and so also exhibit reduced inhibitory effects, and a lower affinity for GAGs. Although it is not known how the truncated forms are generated physiologically, *in vitro* data have demonstrated that TFPI is cleaved into degraded forms by various proteases that TFPI might encounter physiologically. These include thrombin, plasmin, neutrophil elastase, and certain matrix metalloproteinases [173, 174].

1.2.3. Mode of action

TFPI exerts its function by neutralizing the catalytic activity of FXa, and by feedback inhibition of the FVIIa-TF-complex, in the presence of FXa [175, 176]. In the first step, TFPI inhibits FXa in a 1:1 stoichiometric complex by binding at or close to the active site serine of FXa. This binding is reversible and does not require calcium ions. Heparin moderately enhances the inhibition of FXa by TFPI through a template mechanism in which the simultaneous binding of FXa and TFPI to the same heparin molecule increases their interaction [161, 177]. In the second step, TFPI associated with FXa inhibits the TF-FVIIa-complex in a stoichiometric complex which is calcium ion dependent. This leads to the formation of the stable quaternary complex TFPI-FXa-TF-FVIIa (Figure 7) which does not possess catalytic activity on FX and FIX. Experiments in a model system surprisingly showed that protein S enhances the inhibition of TF/FVIIa-catalyzed FX-activation by TFPI [178]. This observation provides an important role for protein S in the down regulation of coagulation, and suggests that the increased risk of venous thrombosis associated with protein

S deficiency may, in part, be explained by an impaired down-regulation of the extrinsic coagulation pathway by TFPI at low protein S concentrations.

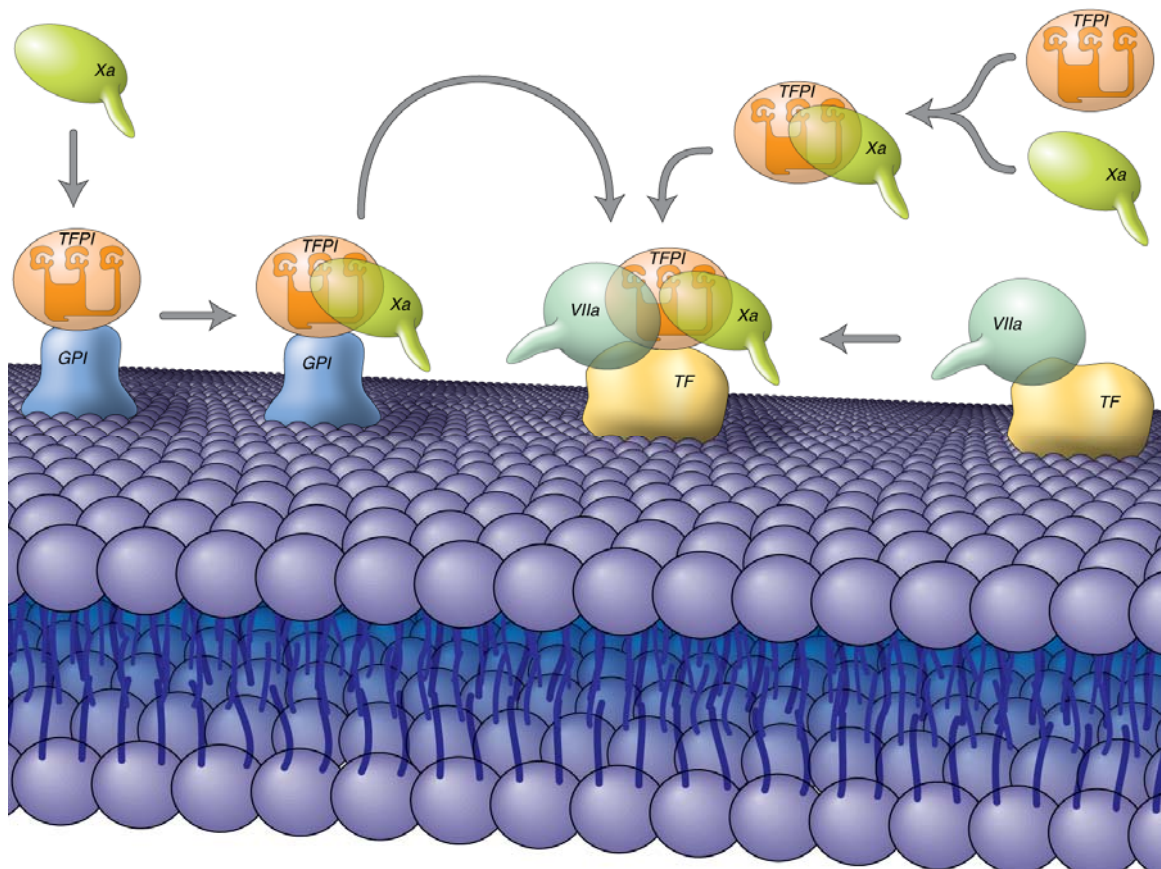


Figure 7. Mechanism for regulation of coagulation by TFPI

However, the requirement of FXa for the inhibition of TF-FVIIa by TFPI is not absolute, and very high concentrations of TFPI may inhibit the activation of FIXa by TF-FVIIa in the absence of FXa. This FXa-independent inhibition by TFPI is of questionable physiological relevance, but could be important when TFPI is used as a therapeutic agent, and when plasma levels of TFPI reach 10 to 50-fold that of normal plasma concentrations [179].

In addition to its direct function as an endothelial-bound anticoagulant, surface bound TFPI may also have an indirect anticoagulant impact, by regulating the clearance of FXa and FVIIa from the circulation via cellular internalisation and degradation [180].

1.2.4. Synthesis and intravascular distribution

TFPI is distributed in three pools *in vivo*; 80-85% is associated with vascular endothelial cells (EC); localized to the cell surface, the Golgi apparatus, and to the endocytic compartment [181]. In plasma, 10% circulates primarily in association with lipoproteins and a small amount in free form, and 3-5% is present within circulating/resting platelets [182, 183] (Figure 8).

TFPI secreted by endothelial cells circulates in plasma as a concentration of about 2.5 nmol/l [184, 185] but fluctuates temporally in humans because of their natural circadian rhythms [186, 187]. Plasma levels of total TFPI are increased 1.5-to 3-fold after administration of heparin [188].

The major site of TFPI production is in endothelial cells, which constitutively express the protein under normal physiological conditions [137], where it is thought to contribute, in part, towards maintaining lumen in an antithrombotic state. In immunohistochemical analysis of normal human tissues TFPI was found to be restricted to the micro vascular endothelium and megakaryocytes [189]. The expression of TFPI-gene by endothelium of different organs appears to vary, perhaps based on the physiologic demands of the tissue [190]. The human lung and heart appear to express the highest quantities of TFPI mRNA [190]. These findings are corroborated by studies in mouse [90]. Small amounts of TFPI are also expressed by monocytes [191], within platelets [192], macrophages [189], lung fibroblasts and vascular smooth muscle cells [137], laryngeal squamous epithelial cells [193], astrocytes [190], cardiomyocytes and mesangial cells fibroblasts [194]. In addition, TFPI has been detected in macrophages and T cells in atherosclerotic lesions [195]. Importantly, cells that do not synthesize TFPI in the adult under physiological conditions are normal hepatocytes, erythrocytes, neutrophils and lymphocytes [137, 196]. In the human foetus, TFPI is expressed

in the endothelium, liver, as well as in epithelium of the lung, kidney and intestine [197]. Further, TFPI is abundantly expressed in placental syncytiotrophoblasts and cytotrophoblasts, where it helps maintain the blood in a fluid state [197].

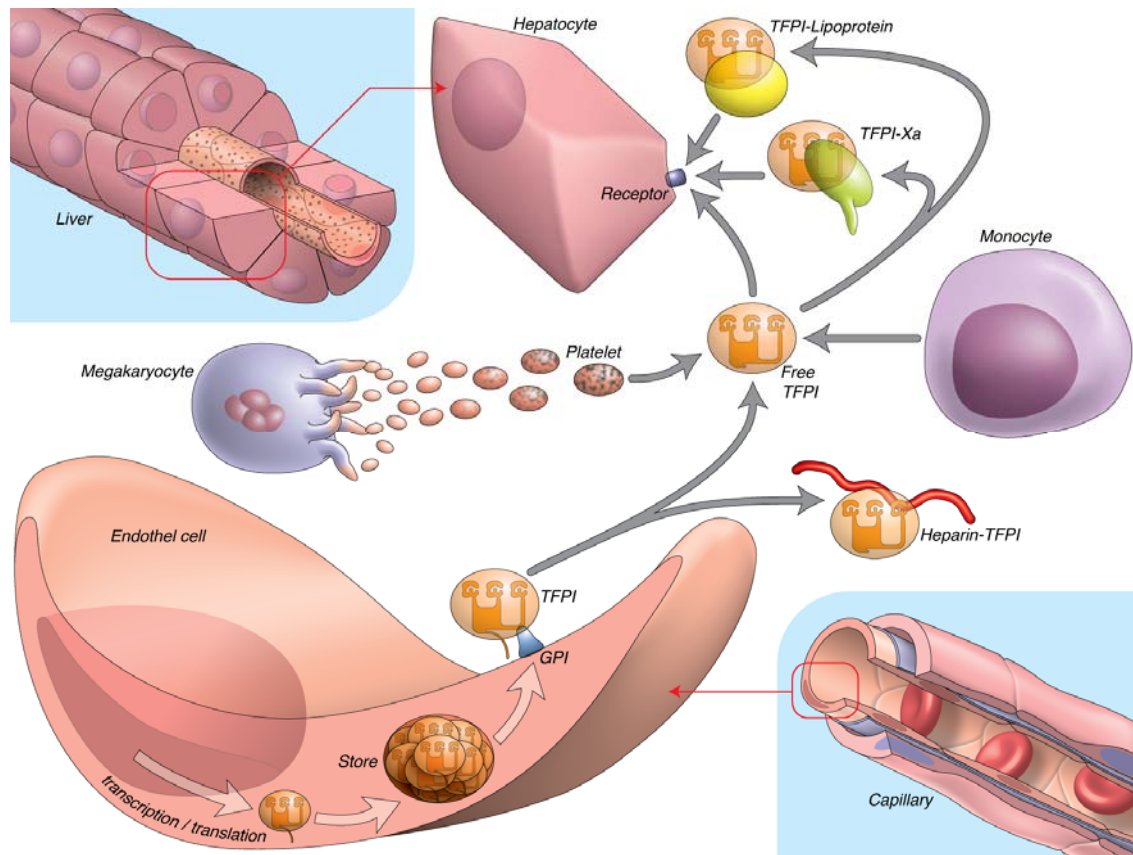


Figure 8. Distribution of TFPI *in vivo*

TFPI expression can be modulated in several cell types in response to various inflammatory stimuli. Shear stress applied to human endothelial cells is reported to increase the expression of TFPI twofold [198]. In addition, thrombin may release cellular TFPI from the vascular endothelium and contribute to an increase in endothelial surface TFPI [199]. Upregulators of TFPI expression *in vitro* that might be of physiological significance include endotoxin, interleukin (IL)-1, tumor necrosis factor (TNF)- α , platelet-derived growth factor, heparin, basic fibroblast growth factor, and elevated shear stress [144, 200-202]. However, endotoxin only slightly upregulates TFPI expression in normal human monocytes and in a

monocytoid cell line U937 [203, 204]. The exposure of different cell types to such agonists or conditions may represent a physiological mechanism by which local anticoagulant activity is upregulated in response to a given challenge.

1.2.5. Elimination and degradation

It was previously assumed that TFPI secreted from ECs became reattached to sulphated proteoglycans at the cell surface glycocalyx through electrostatic bounds between the positively charged C-terminus of TFPI and the negatively charged sulphate group in GAGs. Heparin was simply thought to displace TFPI from binding site on the EC surface and release it into the blood stream in the form of heparin-TFPI complexes. However, heparin treatment of cultured endothelial cells induces a significant release of TFPI in the medium without affecting its surface concentration [163, 201, 205]. This result suggests that TFPI is released from intracellular stores in response to heparin, rather than from the cell surface, or displaced from the membrane surface followed by a very rapid replacement of cell surface TFPI from intracellular stores [201].

Recently, more pieces of evidence have been gathered to point out a possibly more important role for the endogenous cell-associated TFPI than of the circulating form of the inhibitor in maintaining the anticoagulant properties of the endothelium. Studies in cultured endothelial cells have reported that endothelium-associated TFPI was bound to GPI membrane anchors and could be released by phospholipase treatment [170]. Furthermore, GPI-anchored TFPI is located in glycosphingolipid-rich domains, in caveolae [154, 156] and mediates the formation and translocation of TF-FVIIa-FXa complexes in activated endothelial cells [154]. Thus, it is possible that the endothelium plays a key role in regulation of coagulation by TFPI.

A separate clearance system is responsible for the removal of TFPI from the circulation. The primary organs involved in TFPI clearance are the liver and kidneys [206]. Pharmacokinetic studies showed that recombinant TFPI^{E.Coli} has a biphasic and rapid clearance from the circulation with a plasma half-life of approximately 2 minutes in rabbits [206] and less than 1 minute in rats [207]. These characteristics of TFPI^{E.Coli} clearance are reminiscent of other ligands whose cellular uptake and degradation are mediated by the LRP. LRP is particularly abundant in liver, brain and placenta [208], and a closely related receptor, glycoprotein 330 (gp330) that binds many of the same ligands is located in the kidney [209].

Both *in vivo* and *in vitro* studies have demonstrated that LRP in liver mediates the cellular degradation of TFPI^{E.Coli}. Furthermore, *in vitro* studies in HepG2 cells have shown that receptor-associated protein (RAP), an inhibitor of all the ligand interactions with LRP, inhibits degradation of TFPI^{E.Coli} [167, 210]. The initial hepatic cell surface binding in this cell culture requires the carboxy-terminus of TFPI, and is inhibited by clinically achievable levels of heparin [207]. Thus, it was initially proposed that LRP-mediated clearance of TFPI^{E.Coli} involves a two-step process, in which TFPI first binds to heparan sulphate proteoglycans (HSPGs) on the liver endothelial surface, before its transfer to LRP and subsequent internalization. However, later studies demonstrated that receptor-mediated endocytosis of TFPI^{E.Coli} by LRP occurred independently of HSPGs [211]. More recently, it was shown that recombinant human full-length TFPI expressed in mouse C127 cells (TFPI^{C127}, glycosylated) had substantially prolonged survival in the circulation and an apparently different route of elimination independent of LRP [167]. Although it has never been demonstrated whether glycosylation of the molecule could explain the difference between the two TFPI species, it must be considered that data from clearance studies using bacterially expressed TFPI (non-glycosylated) may not reflect precisely the normal physiological clearance of endogenous TFPI.

1.3. Heparin

1.3.1. History

Heparin was first discovered in 1916 by Jay McLean. He was investigating procoagulant preparations when he isolated fat soluble phosphatides from heart and liver tissues that inhibited blood coagulation. This type of fat soluble anticoagulant present in the liver was termed heparin in 1918. In the beginning, heparin was isolated from dog liver but was scarce, causing toxic side reactions and extremely expensive. It was not until the early 1930s that Connaught Medical Research Laboratories (Toronto, Canada) developed a method for making available a purified, plentiful and inexpensive supply safe for human use. Instead of using dog liver as a source they changed to beef liver, and later to beef lungs and intestines [212].

The first human trials began in May 1935, which soon involved hundreds of complex surgical cases where Connaught's heparin played an essential role. By 1937 it was clear that Connaught's heparin was easily available, safe and effective blood anticoagulant, and by the early 1940s it was available both for experimental and clinical use. Its routine application to medical procedures did not occur however until after the Second World War.

1.3.2. Structure

Heparin is a naturally occurring polysaccharide produced in the granules of mast cells that are closely associated with the immune response. Thus, the ability of heparin to regulate the major activities of the complement cascade is an area of active interest [213].

The biosynthesis of heparin includes formation in ER/Golgi of a polypeptide core containing characteristic extended ser-gly sequences. Following substitution of these serine

residues with gal-gal-xyl sequences the polysaccharide chain is built by adding alternating D-glucuronic acid and N-acetyl-D-glucosamine units. The resulting highly sulphated polysaccharide chains are converted to heparin through a series of modification reactions [214-216].

Heparin is normally polydisperse, with a molecular weight within 3-30 kDa, and an average molecular weight of about 15 kDa. Heparin has the highest negative charge density of any known biological macromolecule. This is the result of its high content of negatively charged sulfo- and carboxyl-groups [216]. The main repeating structure of heparin is a disaccharide of alternating N- and 6-O-sulfated alpha-D-glucosamine and 2-O-sulfated alpha-L-iduronic acid (90%) [217], with a minor proportion of N-acetyl glucosamine and beta-D-glucuronic acid (10%). Determination of the structural motif in heparin with high affinity for antithrombin came from Petitou et al. 2003 [218] (Figure 9).

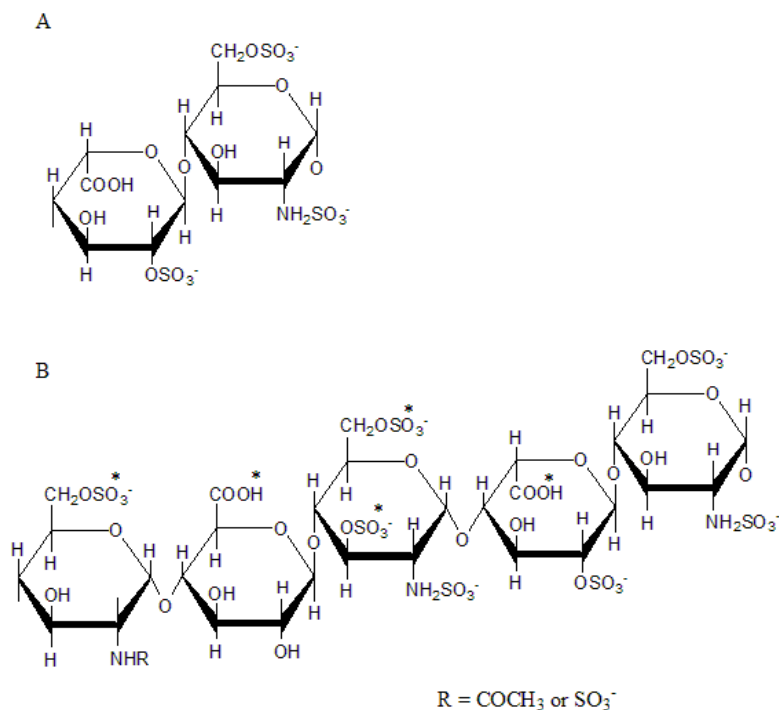


Figure 9. Structure of heparin

A) The main repeating unit of heparin. B) the pentasaccharide in heparin, which is the minimal structure with high affinity for antithrombin. (Reproduced with permission of the American Physiological Society [219])

1.3.3. Mode of action as an anticoagulant

Heparin exerts its anticoagulant effects by accelerating the interaction between the enzyme inhibitor antithrombin (AT) and various serine proteases, such as thrombin, FX and FIXa [220, 221]. Binding of heparin to AT causes a conformational change that results in its active site being exposed. The activated AT then inactivates thrombin and other proteases involved in blood clotting, among them factor Xa. Thus, heparin inhibits blood coagulation by binding to AT, thereby promoting inactivation of the protease factors of the coagulation cascade mechanism. In the absence of heparin, the reactions between AT and coagulation proteases are slow. With optimal amounts of heparin present, these reactions can be accelerated up to 2000-fold, thereby efficiently preventing the formation of fibrin in blood [222]. The reason for heparin's desirability as an anticoagulant is its safety, rapid onset of activity, and reversibility [223]. For controlling heparin therapy and in assay techniques, several other inorganic and organic substances have been reported to have antagonistic properties to heparin, such as protamine, clupein, polylysine, lysozyme, polybrene, toluidine blue, fuchsin, and tryptophan [223].

1.3.4. Pharmacology

Heparin and low molecular weight (LMW) heparins are the most commonly used clinical anticoagulants. The main clinical use of heparin is in acute coronary syndrome, e.g. myocardial infarction, vascular and cardiac surgery, atrial fibrillation, deep-vein thrombosis and pulmonary embolism.

Heparin is involved in a rising number of other physiological and pathological processes, such as tumor cell metastasis and immune cell migration and inflammation [224-228]. For instance, heparin is able of attenuating the neurotoxic and proinflammatory activity

of amyloid-beta protein, which is implicated in the pathogenesis of the Alzheimer disease because of its neurotoxicity and ability to trigger local inflammation [224]. This suggests that heparin could represent a new strategy to reduce the progressive neurodegeneration in the Alzheimer disease. Furthermore, peripheral treatment with the low molecular weight Enoxaparin has been shown to reduce plaques and beta-amyloid accumulation in a mouse model of the Alzheimer disease, which offers promise as a tool for slowing the progression of the disease [225].

1.3.5. Elimination

Because heparin is a widely prescribed drug, it is very important to understand its clearance mechanisms. Heparin clearance involves a combination of rapid saturable and much slower clearance kinetics [229-231]. The elimination of heparin from blood can follow three potential pathways. The first pathway is attachment to the vascular endothelium [232]. This binding was assumed to contribute significantly to the rapid phase of the UFH clearance. This assumption was supported by experimental studies on vascular endothelial cells *in vitro*, showing binding to saturable and specific binding sites at the endothelial surface. However, the capacity for internalization of heparin was reported to be very low in these cells [233-235]. The second pathway is by uptake and metabolism by cells of the RES. Studies in hepatectomized dogs [236] and patients with liver cirrhosis [237] showed increased circulatory half life of intravenously administered UFH in the circulation, indicating that the liver plays a crucial role in UFH removal. Both in humans [238] and in animal models [239, 240], the plasma half-life of heparin increased with dose. Whole body autoradiography of rats injected with tritiumlabeled heparin showed that the ligand was retained by the organs belonging to the RES, with the largest uptake in the liver [241]. However, little is known about the cells involved in the clearance of UFH from the circulation. The first evidence was

published in 1939 by Asplund et al. [242], when they observed heparin in the “sternzellen” of the liver sinusoids of rabbits, rats, and guinea pigs, but not in liver parenchymal cells (PCs) following injection of single and repeated doses of heparin. More than 40 years later, Hiebert observed that repeated administration of heparin into normal and atherosclerotic rabbits was succeeded by heavy accumulation of the polysaccharide in Kupffer cells (KCs) and in endothelial-like cells lining the liver sinusoid [243]. Most studies on distribution of heparin in liver performed *in vitro* using fractionated heparin report that the KCs and the PCs represent the main cellular site of uptake [244-247]. A specific binding and uptake via scavenger-like receptors in KCs and PCs has been suggested [246, 248]. The third pathway of heparin elimination involves the kidney, either via direct excretion into the urine, or by involvement of cellular clearance implicating a metabolic process. LMWH binds to the endothelial cells much less than UFH and is therefore more dependent on the renal, non-saturable elimination process than UFH [249]. It was shown that in nephrectomised rabbits, about 40% of UFH and 70% of the LMWH was eliminated by the kidney and that the elimination in case of the LMWH was due to urinary excretion [250]. In the same study RES was blocked by dextran sulphate, a ligand for the SR, which resulted in a prolonged half-life for UFH but not for LMWH.

1.4. Heparin and TFPI

Numerous proteins of physiological and pathophysiological importance interact with heparin [216]. These interactions lead to an interest in using heparin in roles outside its normal application as an anticoagulant/antithrombotic agent, and offer a large number of potential therapeutic applications for heparin.

In 1963, Nordøy [251] reported that polybrene completely neutralized the anticoagulant effect of heparin added to plasma *ex vivo*, whereas polybrene was unable to

abolish the anticoagulant effect in plasma collected from persons receiving heparin. This phenomenon was referred to as the post-heparin effect, and later attributed to TFPI [252]. TFPI and heparin are known to exert synergistic inhibitory effects on TF-induced coagulation *in vitro* [104, 253], and TFPI may account for as much as 30-50% of the prolongation in a diluted prothrombin time assay, caused by a bolus administration of heparin [252].

Although both UFH and LMWH are known to upregulate the synthesis and release of TFPI in endothelial cells *in vitro* [201, 205], prolonged administration of UFH, but not LMWH, is known to cause partial depletion of both plasma-free TFPI and heparin-releasable-TFPI *in vivo* [254, 255]. The reason for this discrepancy is unknown. Only trace amounts of endogenous TFPI is excreted into the urine in a native, non-degraded form under physiological conditions in humans [256], suggesting passive leakage rather than active excretion in the kidneys. Prolonged UFH treatment has been shown to decrease excretion of TFPI into the urine in humans, most probably by abrogating renal leakage due to formation of large molecular weight UFH-TFPI complexes in the circulation [256]. Furthermore, *in vivo* studies have shown that LMWH prolonged the β half-life clearance of TFPI^{BHK} in rabbits [257], and both LMWH and UFH inhibited binding of TFPI^{E.Coli} to rat hepatoma MH₁C₁ cells *in vitro* [207]. TFPI^{E.Coli} was shown to bind to the endothelial cell surface proteoglycans or glycosaminoglycans [207], but inhibition of this interaction with protamine promoted increased TFPI^{E.Coli} degradation by LRP-positive cells (rat hepatoma MH₁C₁ cells and mouse embryonic fibroblasts heterozygous PEA10 cells), most probably by increasing the availability of TFPI for receptor-mediated endocytosis [211]. Thus, it remains a puzzle to understand the physiology and pharmacology beyond the apparent paradox of depleted intravascular stores, increased endothelial synthesis and inhibited elimination of TFPI by UFH.

2. AIMS OF THE STUDY

- 2.1. To carry out a more detailed pharmacokinetics study during the first phase of clearance, to identify the organ(s) involved in removal of recombinant human TFPI purified from BHK cells (TFPI^{BHK}) from the circulation, and to determine the hepatocellular site of uptake, as well as to identify the main cell (s) and their receptor(s) involved in the clearance.
- 2.2. To study the role of liver sinusoidal endothelial cells (LSECs) in the clearance of unfractionated heparin (UFH)
- 2.3. To study the mechanism of TFPI depletion during UFH treatment by investigating the effect of UFH *in vivo* and *in vitro* on the clearance of a recombinant full length glycosylated TFPI purified from baby hamster kidney cells (TFPI^{BHK}) as compared to recombinant full length non-glycosylated TFPI purified from *E.Coli* (TFPI^{E.Coli})
- 2.4. To investigate if low density lipoprotein receptor-related protein-1 (LRP-1) is expressed on LSECs

3. SUMMARY OF THE RESULTS

Paper I: Asialoglycoprotein Receptor (ASGP-R) in Liver Parenchymal Cells is Involved in Elimination of Recombinant Human TFPI

We here report on a study carried out to determine the early clearance kinetics, and organ, cell(s) and receptor(s) responsible for the clearance of full length TFPI purified from BHK cells (TFPI^{BHK}). Following intravenous administration, ¹²⁵I-TFPI^{BHK} was cleared with a biphasic elimination curve, and with a significantly slower $t_{1/2\alpha}$ compared to recombinant human TFPI from *E. Coli* (TFPI^{E.Coli}) (1.95±0.10 versus 1.42±0.07 min, respectively, p<0.001). Studies on organ and cell distribution revealed that liver parenchymal cells (PCs) were responsible for 96% of the uptake of TFPI^{BHK} and 81% of TFPI^{E.Coli}, whereas the non-parenchymal cells (NPCs) were responsible for uptake of 4% and 19%, respectively. Pre-administration of excessive amounts of unlabeled TFPI^{BHK} prolonged blood clearance of ¹²⁵I-TFPI^{BHK}. Unlabelled TFPI^{BHK} inhibited endocytosis of ¹²⁵I-TFPI^{BHK} in PCs *in vitro*, whereas blocking of LDL-receptor related protein-1 (LRP-1) by receptor-associated protein (RAP) affected neither blood clearance nor endocytosis of ¹²⁵I-TFPI^{BHK} in PCs. In addition, TFPI^{BHK} was also found in the kidneys and this could be reduced in the presence of RAP. Asialoorosomucoid (ASOR), a potent inhibitor of the asialoglycoprotein receptor (ASGP-R), prolonged the circulatory survival of ¹²⁵I-m-TFPI by 1.5-fold (p<0.001). *In vitro*, ASOR and other ASGP-R antagonists significantly inhibited endocytosis of ¹²⁵I-TFPI^{BHK} in PCs. Moreover, unlabelled TFPI^{BHK} markedly decreased endocytosis of ¹²⁵I-asialofetuin. In conclusion, our findings suggest that ASGP-R mediated endocytosis in the liver is involved in the clearance of TFPI^{BHK}.

Paper II: Liver Sinusoidal Endothelial Cells are the Principal Site for Elimination of Unfractionated Heparin from the Circulation

The mechanism of elimination of blood borne heparin was studied. To this end unfractionated heparin (UFH) was tagged with FITC, which served as both a visual marker and a site of labeling with ¹²⁵I-iodine. UFH labeled in this manner did not alter the anticoagulant activity or binding specificity of the glycosaminoglycan. Labeled heparin administered intravenously to rats (0.1 IU/kg) had a circulatory $t_{1/2}$ of 1.7 min, which was increased to 16 min upon coinjection with unlabeled UFH (100 IU/kg). At 15 min after injection, 71% of recovered radioactivity was found in liver. Liver cell separation revealed the following relative uptake capacity, expressed per cell: liver sinusoidal endothelial cell (LSEC)-parenchymal cell-Kupffer cell = 15:3.6:1. Fluorescence microscopy on liver sections showed accumulation of FITC-UFH only in cells lining the liver sinusoids. No fluorescence was detected in parenchymal cells or endothelial cells lining the central vein. Fluorescence microscopy of cultured LSECs following binding of FITC-UFH at 4°C and chasing at 37°C, showed accumulation of the probe in vesicles located at the periphery of the cells after 10 min, with transfer to large, evenly stained vesicles in the perinuclear region after 2 h. Immunogold electron microscopy of LSECs to probe the presence of FITC following injection of FITC-UFH along with BSA-gold to mark lysosomes demonstrated colocalization of the probe with the gold particles in the lysosomal compartment. Receptor-ligand competition experiments in primary cultures of LSECs indicated the presence of a specific heparin receptor, functionally distinct from the hyaluronan/scavenger receptor (Stabilin 2). The results suggest a major role for LSECs in heparin elimination.

Paper III: Unfractionated Heparin Promotes Elimination of Recombinant TFPI in a Rat Model

Background: Tissue factor pathway inhibitor (TFPI) plays an important role for the anticoagulant effect of heparin. Depletion of intravascular TFPI by treatment with unfractionated heparin (UFH), and not by low molecular weight heparin (LMWH), has been suggested to explain the superiority of LMWH in treatment of both arterial and venous thrombosis. The present study was undertaken to investigate the impact of UFH on clearance kinetics, and organs and cells responsible for the clearance of recombinant human full length TFPI purified from baby hamster kidney cells (TFPI^{BHK}) and from *E. Coli* (TFPI^{E.Coli}).

Methods: Male Sprague-Dawley rats were used as research animals. TFPI^{BHK} and TFPI^{E.Coli} were labelled with ¹²⁵I, and used to study clearance *in vivo*.

Results: Surface Plasmon Resonance (SPR) analysis revealed that both types of TFPI bound to UFH *in vitro*, but TFPI^{E.Coli} exhibited a faster association rate and a much slow dissociation rate. Intravenous administration of 100 IU/kg UFH immediately prior to TFPI decreased the circulatory survival ($t_{1/2\alpha}$) of TFPI^{BHK} from 1.99 ± 0.10 min to 1.17 ± 0.13 min ($p < 0.001$) without affecting the fast clearance of TFPI^{E.Coli}. Presence of UFH significantly increased the circulatory survival during the slow $t_{1/2\beta}$ phase of TFPI^{E.Coli} from 27.44 ± 1.91 min to 36.88 ± 1.87 min ($p < 0.05$) without affecting the $t_{1/2\beta}$ of TFPI^{BHK}. Hepatocellular distribution of radiolabeled ligands showed that both forms of TFPI were mainly taken up by PCs in the absence of UFH ($\geq 90\%$). UFH administration switched the hepatocellular distribution of TFPI^{E.Coli} from PCs towards LSECs, without affecting the distribution of TFPI^{BHK}.

Conclusions: Our findings revealed a specific increase in the elimination of TFPI^{BHK} during UFH treatment. This observation may represent the underlying mechanism for depletion of endogenous TFPI in humans during UFH treatment.

Paper IV: Rat Liver Sinusoidal Endothelial Cells (LSECs) express functional Low Density Lipoprotein Receptor-Related Protein-1 (LRP-1)

The low density lipoprotein receptor-related protein-1 (LRP-1), a member of the LDL receptor family, is a large, multifunctional endocytic receptor highly expressed in liver parenchymal cells (PCs), neurons, activated astrocytes and fibroblasts. Receptor associated protein (RAP), the antagonist for all known ligands to members of the LDL receptor family, was used in this study as a tool to investigate whether liver sinusoidal endothelial cells (LSECs) express LRP-1, and, if so, to what extent they contribute to the clearance of exogenously administered RAP. We found that ^{125}I -RAP was rapidly cleared from the circulation with the liver as the principal site of elimination. Liver cell separation following administration of radiolabeled-RAP showed accumulation mainly in parenchymal cells (PCs) (91%) and the rest in liver sinusoidal endothelial cells (LSECs) (8%). Studies *in vitro* showed that RAP endocytosis is specific and is followed by degradation. Excess amounts of unlabeled ligands to known endocytosis receptors in LSECs had no inhibitory effect on uptake of RAP, suggesting the involvement of a yet unknown receptor in these cells. Immunofluorescence assay using a monoclonal antibody to LRP-1 showed positive staining in LSECs. Ligand blot analyses using total cell proteins and ^{125}I -RAP followed by mass spectrometry further confirmed and identified LRP-1 in LSECs. **Conclusion:** An important implication of the expression of LRP-1 in LSECs is that these cells may contribute together with the parenchymal cells to the rapid removal of blood borne ligands for LRP-1, including proatherogenic ligands, thus preventing the development of atherosclerosis.

4. GENERAL DISCUSSION

4. 1. Methodological Considerations

4.1.1. Animal Models and Drug Clearance

Cell and tissue cultures, often suggested as an “alternative” to using animals, have been used in biomedical research for many years. But results obtained using such isolated systems may not reflect physiological processes in the intact body. To better understand the elimination mechanisms of different substances and drugs (Heparin and TFPI in the present study), the experiments must be conducted *in vivo*, under normal physiological conditions.

Several approaches are available to monitor the fate and distribution of exogenous ligands in the intact organism. The vast majority of the *in vivo* clearance studies are conducted using radiolabeled ligands, in which tissue distribution is usually reported as radioactivity accumulated in a particular organ at various times after administration [48, 57, 258-260]. In addition, the radioactivity in blood samples collected for a certain length period is used for calculating the decay in blood clearance. Iodogen was used in our studies for labelling of proteins with ^{125}I . Iodogen is an oxidizing agent that gives higher iodine incorporation than the other commonly used oxidizing reagents, chloramine-T and lactoperoxidase [261]. It can be used for a wide range of proteins and peptides, can permit iodine incorporation with minimal oxidation damage, and can produce tracers stable for up to 3 months [262].

The liver has been shown to be the primary organ involved in clearance and metabolism of a large number of physiological and non-physiological circulating macromolecules [22, 248, 263, 264]. However, in order to obtain information about which cell type(s) are involved in the clearance, quantification of radioactivity can be measured in different liver cells separated after injection of the protein labeled with ^{125}I -tyramine

cellobiose (TC) [39, 49] (paper IV) or ^{125}I -FITC (paper II). The technique of labeling macromolecules with TC was introduced in 1983 by Pittman and co-workers [265] and used in several studies since then [49, 266-269]. The advantages of using this technique are i) that the proteins derivatized with this adduct are recognized as unmodified proteins by biological systems, ii) that the TC ligand is labeled to a high specific radioactivity, and iii) that the ^{125}I -TC adduct is stably trapped intralysosomally after uptake and catabolism of the protein, allowing quantitation of the protein at the site of uptake hours or even days after the uptake [265]. Protein labeling with FITC or other fluorochromes have similar advantages when care is taken to modify the protein minimally by keeping the molecular ratio FITC:protein at a minimum. Usually, the isothiocyanate portion of FITC binds to primary amino groups of lysine residues of the ligand to be labeled. This interaction neutralizes the positive charge of the amino group of the ligand. In addition, an extra negative charge is incorporated by the carboxy group of FITC. Thus, with a high FITC:protein ratio it is likely that the net negative charge of the FITC-labeled ligand increases to the extent that it is recognized by the scavenger receptor (SR), a receptor known for its ability to bind negatively charged molecules [270, 271]. Since FITC is also trapped intralysosomally after internalization of FITC-conjugated ligands, it can be traced by fluorescence microscopy, and it may also be detected by gold-labeled FITC-antibodies at the electron microscopic level [23] (paper I and II).

4.1.2. Primary cells vs cell lines

To obtain more detailed information about binding and uptake mechanism and characterize the endocytic pathway involved in the uptake of the protein of interest, *in vivo* studies must as a rule be followed up with studies *in vitro* with isolated cells in culture. Cell lines are often used in such studies, since they are often readily available and easily maintained. Also, a cell line may exhibit many of the characteristics of the original tissue from which the cell line has been derived. As an example, the HepG2 cell line has been found

to exhibit many characteristics of normal hepatocytes, e.g. expressing the LRP-1 [272], ASGP-R [273], and synthesis of serum proteins [274]. However, hepatoma-derived cell lines may differ from primary cell cultures with regard to receptor expression, endocytic capacity and protein synthesis [137, 275-277]. Regarding LSECs, some laboratories culture these cells under conditions that allow cell proliferation and subsequent splitting and passaging before the cells are used in experiments several days or even weeks after isolation [278, 279]. However, many phenotypic features of LSECs change gradually when they are placed in a culture dish, and most importantly, many of the signature functions of LSECs, e.g. scavenger function and fenestration, are also rapidly lost during *in vitro* culture [280, 281]. For these reasons, true primary liver cell cultures (PCs and LSECs) were used in this study each time an *in vitro* experiment was required.

4.2. TFPI and heparin: Elimination and mechanisms of clearance

“How much?”, “How often?” and “How long?” are important therapeutic questions when investigating a drug. To administer a drug optimally, knowledge is needed for the mechanism of absorption, distribution, and elimination. The present thesis aims to increase our understanding of how the liver contributes to the elimination of two important anticoagulants, namely unfractionated heparin (UFH) and tissue factor pathway inhibitor (TFPI).

Because of the central role it plays in thrombus generation, propagation, and stabilization, effective inhibition of thrombin is crucial in the prevention and treatment of thrombotic disorders.

Recombinant tissue factor pathway inhibitor (rTFPI) has been proposed to be a beneficial therapeutic agent as a natural anticoagulant to attenuate pathological clotting

activation. rTFPI purified from *E. Coli* (TFPI^{E.Coli}) or from different mammalian cell lines has been shown in animal studies to be effective against TF-induced coagulopathy [282], to reduce mortality from bacterial septic shock [283, 284], and to prevent arterial thrombosis [179]. In humans, initial results from phase I and II studies indicated that rTFPI is well tolerated, with no clinical significant bleeding side effect [285]. Unfortunately, these earlier encouraging results could not be repeated in a phase III trial (the OPTIMIST). There was no survival benefit with the administration of TFPI^{E.Coli} in humans with severe sepsis [286]. However, patients who did not receive concomitant heparin appeared to benefit from the treatment with TFPI^{E.Coli}. As we have shown in paper III, TFPI^{E.Coli} has a strong affinity binding to UFH, while TFPI^{BHK} does not. Thus, it would be interesting to investigate the effect of a TFPI of mammalian origin in patients with severe sepsis.

Previous studies suggest that depending on the source, rTFPI may have different routes of elimination. The low density lipoprotein receptor-related protein (LRP-1), a multifunctional endocytic receptor, has been shown to be the main receptor responsible for the plasma clearance [210] and degradation of TFPI^{E.Coli} in hepatoma-derived cell lines [106]. In addition, it has been shown that while the majority of TFPI^{E.Coli} binds to cell surface HSPGs, LRP-1 can function independently from HSPGs in the binding and degradation of TFPI^{E.Coli} [211]. On the other hand, LRP-1 is not involved in the clearance of rTFPI purified from mouse C127 fibroblasts (TFPI^{C127}) [167]. Notably, TFPI^{C127} has a prolonged survival in the circulation compared to TFPI^{E.Coli} and it does not compete with TFPI^{E.Coli} for binding or degradation in HepG2 cells [167]. While TFPI^{E.Coli} was mainly found in the liver after intravenous injection [207] (paper I), rTFPI purified from C127 fibroblasts and human SK hepatoma cells was found in liver and kidneys [206].

In our study we used recombinant human full-length TFPI purified from baby hamster kidney (BHK) cell line (TFPI^{BHK}), with the aims to i) carry out a more detailed pharmacokinetics study during the first phase of clearance, ii) to identify the organ(s) involved in removal of TFPI^{BHK} from the circulation, iii) to determine the hepatocellular site of uptake, and iv) to identify the main cell (s) and their receptor(s) involved in the clearance (paper I). We found that TFPI^{BHK} was cleared slower from the circulation than TFPI^{E.Coli}, and while TFPI^{E.Coli} was cleared mainly by the liver, TFPI^{BHK} was taken up in both liver and kidneys. As mentioned above, rTFPI from C127 fibroblasts and human SK hepatoma cells also accumulated in the kidneys [206]. However, the method used in that study, namely whole-body autoradiography, does not give a quantitative measurement of the ligand distribution in different organs. Besides, an error of the assessment of the rTFPI in the kidneys may be induced by evaluating the distribution in the organ without removing the blood. From our study, we could see that even 1h after injection, there is still a lot of TFPI^{BHK} in the circulation (paper I). Based on our results and previous studies, we hypothesized that the possible mechanism for the detection of TFPI^{BHK} in the kidneys is by renal reabsorption in the proximal tubule. Using the Opossum kidney (OK) cell line, we found that RAP significantly inhibited both binding and internalization of ¹²⁵I-TFPI^{BHK}, effect which was not seen on liver PCs. The results suggest that TFPI^{BHK} may bind to megalin or/and cubilin in kidneys, two members of the LDL receptor family [287, 288], but it does not bind to LRP-1 in liver. With the goal of finding the receptor involved in its clearance, we found that TFPI^{BHK} was inhibited both *in vivo* and *in vitro* by ligands to the ASGP-R, suggesting that this receptor is, at least partially involved in the removal of TFPI^{BHK} from the circulation. Recombinant human TFPI^{BHK} differs from bacterial TFPI^{E.Coli} in molecular weight (42 kDa and 35 kDa, respectively) due to post-translational modifications in mammalian cells involving *N*-linked glycosylation at three potential sites; Asn 117, Asn 167, Asn 228 [157, 164, 165]. The

mammalian cells used for synthesis of TFPI^{BHK} in our study, the BHK cells, are known to have a heterogenous glycosylation pattern. However, under certain culture conditions, changes in the oligosaccharide chains occur, and the product secreted by these cells is partially desialylated [289]. The carbohydrate moiety of plasma glycoproteins is known to play a key role in their plasma clearance [290]. Desialylation and subsequent exposure of the penultimate galactose is known to increase the rate of removal of many plasma glycoproteins from the circulation due to recognition by the ASGP-R. The finding that the liver ASGP-R is involved in the clearance of TFPI^{BHK} adds to the important scavenger function of ASPG-R in designing clinical treatments to provide therapeutic levels of glycoproteins in circulation.

Traditional anticoagulants, such as heparin, are indirect inhibitors of thrombin. The main clinical use of heparin is in acute coronary syndrome, e.g. myocardial infarction, vascular and cardiac surgery, atrial fibrillation, deep-vein thrombosis and pulmonary embolism. Several studies indicated that the liver plays a key role in heparin elimination [248]. However, little is known about the liver cells and the mechanism involved in the clearance of unfractionated heparin (UFH). Most studies on distribution of heparin, performed *in vitro* using fractionated heparin, reveal that the PCs and KCs are the main cells for uptake [244-247]. However, our *in vivo* experiments showed that LSECs are the principal site for binding and uptake of UFH from the circulation (paper II). An unknown scavenger-like receptor was suggested to be involved in the binding and uptake of heparin [248]. As UFH has the highest negative charge density of any known biological macromolecule [216], it is a likely candidate ligand for the SRs. This group of receptors has only one feature in common, namely the ability to bind negatively charged macromolecules [22]. Our finding that neither hyaluronan, nor AGE-BSA, that are both high affinity ligands for Stabilin 2, or anti-Stabilin 2 antibody could inhibit the uptake of UFH, suggested that Stabilin 2 in LSECs is not involved in the uptake of UFH. Contrary to our finding, Harris and Weigel suggested shortly after the

publication of our paper II that Stabilin 2 is the systemic clearance receptor for heparin [291]. This conclusion from these authors was surprising in light of their previous publication that heparin does not bind Stabilin 2 [292]. Moreover, mapping the binding sites of 8 different ligands within Stabilin 2, the same authors showed that the receptor specifically and simultaneously bind to both heparin and HA, in a non-competitive manner [293]. This property of one and the same receptor to bind different ligands non-competitively is also observed in LRP-1 and MANN/COLLA-R [58, 108]. Of note, we recently purified a major heparin binding protein using heparin-sepharose affinity chromatography of rat LSECs (unpublished data). Although we have not yet characterized this protein, its apparent MW was around 70 kDa, which is clearly different than the MW of the Stabilin 2 of 270 kDa [26]. This evidence support our conclusion that heparin uptake in LSECs is via a receptor that is clearly different than Stabilin 2.

4.2.1. Clearance of TFPI during heparin treatment

Heparin is known to bind a large number of plasma proteins [294]. Formation of heparin-protein complexes during heparin treatment may have important clinical implications by affecting the elimination of the proteins. Administration of heparin is known to cause partial depletion of both plasma free TFPI and heparin-releasable TFPI *in vivo*, an effect not seen by low molecular weight heparin (LMWH) [254, 255]. As mentioned above, the primary organs involved in TFPI clearance are the liver and kidneys. Urinary loss of TFPI has been suggested to explain the selective depletion of intravascular TFPI during continuous UFH treatment. However, a recent study showed that only trace amounts of native TFPI were detected in the urine under basal conditions and during heparin treatment, with a more pronounced reduction during UFH treatment [256]. It was speculated that filtration of TFPI-heparin complexes probably depends on the molecular weight of the complexes; thereby explaining attenuated renal clearance of TFPI during UFH treatment. In paper III we aimed to

elucidate the mechanism of TFPI depletion during UFH clearance by investigating the effect of UFH *in vivo* and *in vitro* on the clearance of recombinant human full length glycosylated TFPI (TFPI^{BHK}) as compared to recombinant full length non-glycosylated TFPI (TFPI^{E.Coli}). We found that TFPI^{BHK} binds weaker to heparin compared to TFPI^{E.Coli}, and that intravenous administration of UFH immediately prior to TFPI significantly decreased the circulatory survival of TFPI^{BHK} during the alpha-phase of elimination, while the circulatory survival of TFPI^{E.Coli} during the beta-phase of elimination was significantly increased. Administration of UFH did not affect the organ distribution of TFPI^{BHK}. Hepatocellular distribution of TFPI^{BHK} was not affected by the presence of UFH, while the uptake of TFPI^{E.Coli} was switched from PCs towards NPCs. Bregengaard et al. reported that the recovery of TFPI^{BHK} after 2 min was increased to 46% in rabbits receiving low molecular weight heparin and TFPI^{BHK} [257]. The discrepancy between the two studies could explain the selective depletion of TFPI^{BHK} with UFH and not with LMWH. Interestingly, UFH administration only affected the distribution of TFPI^{E.Coli} within the liver cells, and not of TFPI^{BHK}, by switching the distribution from the PCs towards the non-parenchymal cells (NPCs). As shown in paper II, LSECs, the largest population among the non-parenchymal cells, is the principal site of UFH elimination. This result suggests that in the presence of heparin, the scavenger receptor on LSECs may have higher affinity for binding of TFPI^{E.Coli}-UFH complexes than the HSPGs and/or LRP-1 receptor on PCs and/or LSECs for binding of TFPI^{E.Coli} alone.

The mechanism by which heparin shorten the circulatory survival of TFPI^{BHK} is not fully understood. Interestingly, the anatomical distribution and the hepatocellular distribution of TFPI^{BHK} were not significantly affected by the presence of UFH. In accordance with previous findings in humans [256], only traces of TFPI^{BHK} were detected in the urine of rats with or without pre-administration of UFH. Moreover, only slightly elevated levels of TFPI^{BHK} were detected in the blood following UFH administration. These findings in addition

to the rapid clearance of TFPI in the presence of UFH clearly demonstrate that the mechanism for depletion of TFPI is not the urinary loss. Previously, we and others have shown that TFPI of mammalian origin, i.e. TFPI^{BHK} and TFPI^{C127} bind very weakly, or even fail to bind to HSPGs, and that their uptake is not mediated by the LRP-1 (paper I, [167, 295]). These findings along with the SPR analysis showing weaker TFPI^{BHK}-UFH interactions compared to TFPI^{E.Coli}-UFH interactions suggest that the faster clearance of TFPI^{BHK} in the presence of UFH is caused by an enhanced binding affinity of the TFPI^{BHK}-UFH complexes to the yet unknown receptor(s) for TFPI^{BHK} on PCs. Our findings may explain why prolonged treatment with UFH causes depletion of intravascular TFPI in humans.

4.3. LRP-1 expression in LSECs

Hepatocellular distribution of TFPI in paper I showed that while the majority of TFPI^{E.Coli} was found in PCs, 19% was also found in NPCs. NPCs consist mainly of KCs and LSECs, with KCs eliminating particles (> 200 nm) from the circulation via phagocytosis, and LSECs removing colloids and soluble macromolecules (< 200 nm) via non-phagocytic receptor-mediated endocytosis [22]. Knowing that liver PCs LRP-1 is involved in the clearance and degradation of TFPI^{E.Coli} [106, 210] we investigated whether LSECs also express LRP-1 (paper IV). Studies on hepatocellular distribution after intravenously injection of ¹²⁵I-RAP showed that, while the PCs were responsible for 90% of the RAP clearance, 8% was also found in LSECs. However, it may be argued that the apparent 8% uptake in LSECs reflects uptake in contaminating PCs. To eliminate the possibility of PC contamination in the LSEC fraction, *in vitro* cultures of LSECs were prepared, where the cells were extensively washed free of any contaminating PCs. This can be very easily visualized by light microscopy, as the two types of cells have very distinct morphology and size. A significant uptake of ¹²⁵I-RAP was observed in the super pure LSECs *in vitro*. As RAP is known to interact also with other members of the LDL receptor family, and not only with LRP-1, we performed an

immunofluorescence assay using LRP-1 antibody. Positive staining was observed in LSECs, which were identified by the presence of the LSEC specific marker, Stabilin 2. Furthermore, ligand blot analyses using LSECs total cell protein and ¹²⁵I-RAP followed by mass spectrometry showed the appearance of a single band, which was identified as LRP-1. The finding that LRP-1 is expressed in liver not only in PCs but also in LSECs, is novel, and gives insight into the role of these cells in the catabolism of a variety of molecules.

5. MAIN CONCLUSIONS

- The clearance of intravenously administered recombinant human TFPI purified from BHK cells (TFPI^{BHK}) has a significantly slower α -phase compared to TFPI^{E.Coli}. While TFPI^{E.Coli} was cleared mainly by the liver, TFPI^{BHK} was found both in liver and kidneys. In the liver, TFPI^{BHK} was found mainly in PCs, while TFPI^{E.Coli} was found in PCs, as well as in NPCs. The uptake of TFPI^{BHK} in liver is not mediated by the LRP-1, as with TFPI^{E.Coli}, but by the ASGP-R. This finding has the important implication that any rTFPI in mammalian cell lines intended for use as a therapeutic agent in antithrombotic treatment must be specifically checked for its clearance by the ASGP-R.
- LSECs are the principal site for binding and uptake of unfractionated heparin (UFH). The receptor for endocytosis of UFH is distinct from the hyaluronan/scavenger receptor (Stabilin 2). Formation of heparin-protein complexes during heparin treatment may have important clinical implications by affecting the elimination of the proteins.
- In contrast to TFPI^{E.Coli}, TFPI^{BHK} was found to bind weaker to UFH. During UFH treatment, TFPI^{BHK} elimination was significantly increased without affecting the target organ and specific cells responsible for binding and endocytosis
- We demonstrate for the first time that the expression of functional LRP-1 in liver is not restricted only to PCs, it is also found in LSECs. This suggests that the atheroprotective activity ascribed to LRP-1 in liver is operative in both PCs and LSECs. In addition, LSECs may work together with the PCs in cleaning the blood from numerous ligands with affinity to LRP-1.

6. FUTURE PERSPECTIVES

To improve anticoagulant treatment strategies in the future it is necessary to increase our knowledge about the mechanism of clearance of key molecular players. The present thesis focused on two major anticoagulants TFPI and heparin.

TFPI^{BHK} was shown to be mainly cleared *in vivo* by the liver PCs. *In vitro* experiments carried out to study the details of the uptake mechanism were obtained using cells cultured in the absence of plasma components. Thus, the *in vitro* system used here is highly simplified compared to the physiological *in vivo* situation. To make more physiologically relevant experimental conditions *in vitro* it would be necessary to include factors such as FXa and TF, lipoproteins and platelets to study if they would influence the uptake process of TFPI^{BHK}.

Our findings that TFPI^{BHK}, which is glycosylated and thereby resembling endogenous TFPI, was eliminated faster in the presence of UFH may explain why prolonged treatment with UFH causes depletion of intravascular TFPI in humans. However, further studies are needed to understand the impact of UFH on cell binding and degradation of TFPI^{BHK}.

Further studies are warranted to elucidate the specific mechanism for binding and uptake of heparin in LSECs, as well as identification and characterization of the binding protein that seems to be specific for the heparin recognition and internalization in LSECs.

Although only one band was visible in the ligand blot in paper IV, RAP is known to associate with most of the LDL receptor family members [296]. Thus, it would be interesting to look more into the physiological importance of the LRP-1 expression in LSECs by investigating the clearance of a more specific ligand for this receptor, such as trypsin activated alpha 2-macroglobulin [297] or uPA-PAI-1 complexes [298]. Another interesting study could be to investigate whether LRP-1 compensates for the clearance of tissue plasminogen

activator (tPA) in the absence of the mannose receptor (MANN-R). tPA was shown to be taken up both in PCs and LSECs, by the LRP-1 and the MANN-R, respectively [299]. Clearance of SR-ligands was shown not to be affected by the lack of MANN-R in MANN-R KO mice [58]. However, with tPA being a ligand for both MANN-R and LRP-1, it would be interesting to investigate whether the LRP-1 clearance function in LSECs would be upregulated to compensate for the lack of MANN-R-mediated uptake in the MANN-R KO mice.

7. REFERENCES

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Paper I

Paper II

Paper III



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