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Chapter 1 - General Introduction and Outline of the thesis

The coagulation cascade

The coagulation system is a vital mechanism that helps to prevent blood loss. Coagulation is the result of a complex cascade of enzymes that was first proposed in 1905 by Morawitz [1]. The coagulation cascade is divided in two distinct parts; the extrinsic pathway which plays a major role in the initiation phase, and the intrinsic pathway which is responsible for amplification and propagation of clotting. The initiator of the extrinsic pathway is Tissue Factor (TF), a membrane tethered protein mainly expressed by the cells that reside in the medial and adventitial layer of the vessel wall (i.e. vascular smooth muscle cells and fibroblasts). TF is normally not expressed on endothelial cells as direct contact with circulating coagulation factors may cause excessive clotting. However, stimulation with inflammatory mediators results in the expression of TF on endothelial cells and may be responsible for thrombotic complications [2-5].

Coagulation is initiated when vascular integrity is compromised, such as after wounding. As a consequence the endothelium is damaged and TF is exposed to the blood. The blood-borne zymogen FVII, which is produced in the liver, forms a high-affinity complex with blood-exposed TF upon which FVII is converted to the enzymatically active protease FVIIa. The TF:FVIIa complex then activates coagulation factor X (FX) which leads to the formation of trace amounts of thrombin. Thrombin amplifies its own production through activation of a feedback-loop consisting of subsequent activation of factor XI (FXIa), the tenase complex (protease FIXa in complex with its co-factor VIIIa (FVIIIa)) and the prothrombinase complex (protease FXa in complex with its co-factor factor Va (FVa)). As a result, fibrinogen will be converted to fibrin and a clot will form. This feedback loop takes place on the surface of activated platelets that provide the negatively charged phospholipid layer essential for coagulation factor activation

Blood coagulation is subject to regulation by coagulation inhibitors. Coagulation initiation is regulated by TFPI which FXa-dependently inhibits TF:FVIIa function. In addition, coagulation propagation is effectively regulated by antithrombin that targets FIXa, FXa and thrombin [6]. The Protein C/Protein S pathway is another negative regulator of the coagulation cascade. As the levels of thrombin increase, thrombin binds to thrombomodulin on endothelial cells. This results in thrombin-dependent cleavage of Endothelial Protein C Receptor (EPCR)-bound Protein C. Generated Activated Protein C (APC) in complex with protein S can proteolytically inactivate FVIIIa and FVa to terminate blood clotting [7] (**Fig 1**).

The complex nature of the coagulation cascade assures tight regulation of this process in order to prevent excessive or inadequate clotting. Nevertheless, aberrant expression or

activation of coagulation zymogens and cofactors may cause clotting and bleeding problems. For instance, deficiency in FVIII or FIX cause bleeding problems in hemophilia A and hemophilia B patients respectively. In contrast, excessive activation of coagulation factors, or defects causing prolonged activity (e.g. Factor V^{Leiden} mutation, yielding a FV variant that is resistant to APC) may result in a hypercoagulable state, and thrombus formation in veins [7, 8].

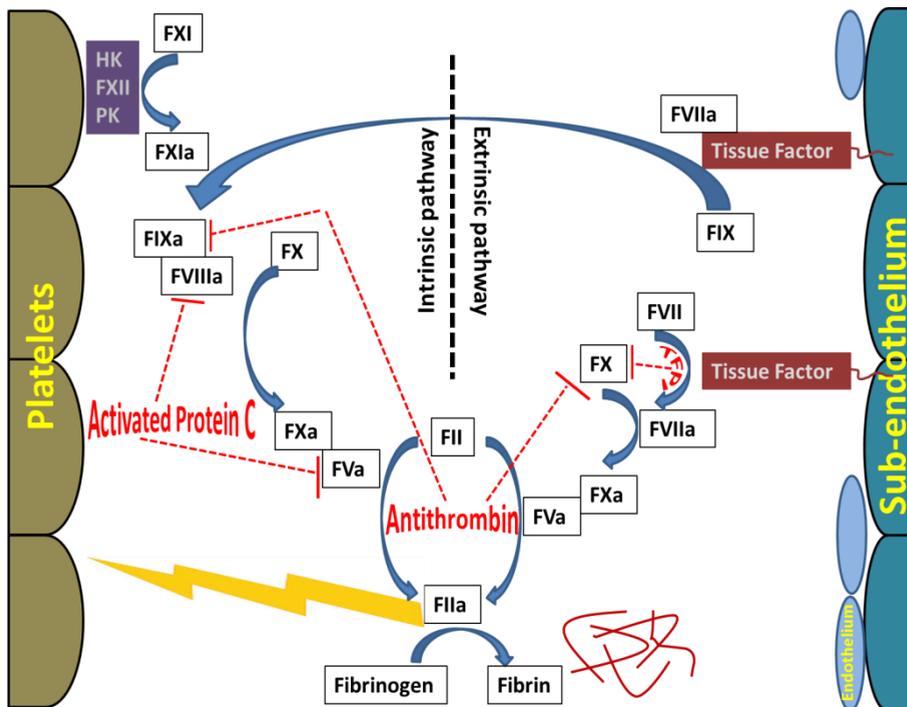


Fig.1 The coagulation cascade Sub-endothelial cells exposing TF, and platelets facilitate activation of a complex pathway regulating coagulation. Blue arrows represent activation and red lines indicate inactivation of the coagulation factors.

Coagulation factor signaling

Other than regulating blood clotting, coagulation factors may also signal via G-protein coupled Protease Activated Receptors (PARs) on cells. PARs are seven-span transmembrane proteins belonging to a family consisting of four members: PAR1-4. Upon activation, their N-terminus is cleaved and the newly formed N-terminus binds to the second extracellular loop of the receptor thus initiating downstream signaling. PARs are targeted by specific proteases. PAR1, PAR3 and PAR4 are typically cleaved by thrombin [9]. However, PAR1 can also be activated by plasmin [10], APC [11], FXa [12] and matrix

metalloproteases [13]; PAR2 is the only PAR that cannot be activated by thrombin but it is responsive to trypsin [14], mast cell tryptase [15], membrane-type serine protease 1 [16], bacterial proteases [17], TF/FVIIa [18], TF/FVIIa/FXa [19] and FXa-dependent cleavage [18].

Platelet activation and aggregation is a crucial step in coagulation. Platelet activation by thrombin is mainly orchestrated by PAR1/PAR4 on human platelets [20, 21]. PAR1 regulates platelet activation at relatively low levels of thrombin while PAR4 cleavage results in platelet activation when thrombin concentration is high. Most likely, PAR1 and PAR4 act in concert on human platelets [21]. On mouse platelets, thrombin-dependent activation occurs through PAR3/PAR4 targeting [22]. PAR3 does not appear to be directly activated by thrombin but to act as a coreceptor for PAR4 by optimally positioning thrombin on the platelet surface towards PAR4 [23].

All four PAR members are expressed on endothelial cells which allows for a broad spectrum of actions regulated by thrombin [24, 25]. PAR1 activation by thrombin leads to vWF secretion from Weibel Palade bodies in order to amplify coagulation by recruiting platelets to the wound area and acting as a carrier for FVIII [26]. Additionally, to avoid uncontrolled trafficking of biological substances, endothelial cells form a structural barrier that is sealed with tight junctions [27]. PAR1/thrombin activity increases the permeability of endothelial cells which results in an influx of coagulation factors to the tunica media. Overall, the relocalization of these factors across the endothelium may lead to more efficient coagulation, but potentially also to pro-thrombotic complications [28]. Apart from coagulation, thrombin/PAR signaling is also involved in inflammatory responses. Thrombin stimulation of endothelial cells increases cell surface P-selectin levels to promote leukocyte binding [29, 30] and triggers the release of cytokines [31].

Apart from PARs, endothelial cells express/expose a unique set of proteins modulating the anti-coagulant Protein C pathway. APC activates PAR1 in an EPCR-dependent manner [11, 32]. Interestingly, APC-induced PAR1 activation and thrombin-induced PAR1 activation result in opposing cellular effects: APC-driven PAR1 cleavage triggers anti-apoptotic and anti-inflammatory signaling [32, 33], and decreases endothelial permeability [34] while thrombin-directed PAR1 activation increases endothelial permeability [28] and is involved in inflammatory responses [31]. These differences are most likely dictated by the strength of the downstream signal. Thrombin/PAR1 results in a relatively strong activation of the G_{12/13} and Rho pathways, to disrupt the barrier function [35] whereas a weak signal resulting from APC-induced PAR1 signaling triggers Sphk1 and S1P release resulting in the opposite [36].

Tissue Factor signaling

Apart from being the initiator of coagulation cascade, TF supports cellular signaling. FVIIa in complex with TF activates PAR2 [18]. FVIIa-dependent PAR2 signaling is further supported by integrins. Antibodies either inhibiting $\beta 1$ integrins or disrupting $\beta 1$ /TF complexes have a negative effect on PAR2 signaling [37]. Upon PAR2 activation, PKC α localizes to the cell membrane via the phosphatidylcholine-dependent phospholipase C pathway, and phosphorylates the TF cytoplasmic tail (TF-ct) on Ser 253 followed by p38 α -dependent Ser 258 phosphorylation [38, 39]. TF's extracellular domain is involved in the regulation of coagulant activity and cell survival by the phosphorylation of STAT5 [40]. In addition, the FVIIa:TF complex regulates the transcription of wound repair response genes (i.e IL-1 β , egr-1, hbEGF) in keratinocytes [41]. TF's cytoplasmic domain does not play a role in PAR-dependent p42/44 activation [42]. In contrast, activation of p38 requires the presence of TF-ct [43] and the same holds true for adhesion, migration and spreading of fibroblasts [44]. In an angiogenic context, the TF-ct inhibits PAR2-dependent angiogenesis while its phosphorylation reverses this inhibition [45]. Similarly, the TF-ct blocks $\alpha 3\beta 1$ integrin function and consequently cell migration, but upon PAR2-dependent TF-ct phosphorylation this inhibition is released [46]. Overall, these data suggest that TF drives cellular events in TF-ct-dependent manners (e.g. migration and angiogenesis), and in TF-ct-independent manners (e.g. gene expression and coagulation).

In addition to physiological settings, TF-dependent signaling also plays a role in pathophysiological (i.e. cancer) setting. In breast cancer, disease progression is influenced by the TF/FVIIa/PAR2 axis. Deletion of PAR2, but not PAR1 in a spontaneous model of breast cancer resulted in reduced tumor size, metastasis and angiogenesis [47]. Additionally, injection of MDA-MB-231 mfp cells into the mice in the presence of PAR2-blocking antibodies resulted in smaller tumors whereas PAR1 antibodies were without effect [37]. The same proliferative and angiogenic effect of TF/FVIIa/PAR2 was observed in melanoma models [48]. TF/FVIIa/PAR2 signaling increases the expression of pro-angiogenic factors (i.e. VEGF, Cxcl-1, Cyr61, IL-8) [49-51] and there is a correlation between TF expression and microvessel density in lung [52], gastrointestinal [53], prostate cancer [54] and gliomas [55]. FVIIa also increases uPAR levels in pancreatic cancer cells [56, 57] and ovarian cancer cells [58] which is believed to regulate tissue reorganization and metastasis [56, 57]. In support, FVIIa signaling was shown to directly regulate melanoma metastasis [59]. TF/FVIIa also upregulates Bcl2 in cancer cells to inhibit apoptosis [60].

TF may also signal and regulate cellular processes independent of PARs. In endothelial cells, TF in complex with Akt increases CCL2 levels that attract smooth muscle cells to form

mature vessels [61, 62]. Moreover, downregulation of TF results in diminished angiogenic potential and stimulation with PAR2 agonist rescued the angiogenic phenotype only partially which suggests the involvement of PAR2-independent pathways in TF-driven angiogenesis [62]. Incubation of endothelial cells only with exogenous TF activates the JNK-SAPK pathway and increases proliferative Elk-1 levels [63]. The increasing numbers of endothelial cells may allow the incorporation of those cells into the newly formed vessels in order to support angiogenesis. Moreover, TF in complex with a proteolytically inactive form of FVIIa (FVIIai) activates CREB and NFκB which are both involved in cell survival [63]

Tissue Factor decryption

Cellular levels of TF antigen do usually not correlate with cellular pro-coagulant activity, as most of the TF pool resides in a non-coagulant/cryptic form on the cell membrane [64]. So far, the exact mechanism regulating the activation of TF remains controversial. Several theories were suggested to explain the decryption process: phosphatidylserine exposure, localization of TF in lipid rafts, TF dimerization and disulfide switch model.

TF encryption/decryption was originally thought to be dependent on phosphatidylserine exposure. In a resting cell, phosphatidylserine (PS) is kept in the inner leaflet of the lipid bilayer by flippases whereas floppases transport phosphatidylcholine (PC) to the outer leaflet, thus creating an asymmetrical cell membrane. Stimulation of cells with Ca^{2+} ionophore or apoptotic signals block the action of flippase and enable scramblase activity which in turn transports PS and PC across the lipid bilayer in an unselective manner [65]. Due to increased PS levels on the outer leaflet, a negatively charged surface is formed which allows the optimal complex formation between coagulation factors [66].

Alternatively, it has also been suggested that TF's positioning in different membrane compartments might be involved in decryption. Lipid rafts are rigid microdomains that contain elevated levels of cholesterol and glycosphingolipids [67]. Some researchers argue that rafts provide the optimal environment for TF to perform its coagulant function whereas others claim that these domains are unsuitable for efficient coagulation [68-70]. Obviously, further research is required to prove or refute this theory.

A third model argues that TF homodimers are cryptic and TF monomers are the coagulant pool [71]. Stimulation of HL60 cells with TF activity inducing reagent, calcium ionophore [72], leads to a decrease in TF cross-linking [71]. Conversely, the fusion of a leucine zipper motif to soluble TF not only promotes TF dimerization but also does not affect TF's amidolytic or Xa generation activity [73]. On the basis of the aforementioned observations, it is clear that more studies should be performed to clarify the dimerization theory.

The last theory to explain TF encryption/decryption is the disulfide switch model. Both human TF (hTF) and mouse TF (mTF) contain an allosteric cysteine-cysteine bond in their extracellular domain (Cys¹⁸⁶-Cys²⁰⁹, Cys¹⁹⁰-Cys²¹³ respectively) which is subject to regulation by protein disulfide isomerase (PDI). Reduction of these disulfide bonds results in the formation of cryptic or signaling TF whereas oxidation causes an increase in TF-dependent coagulation [74, 75]. TF contains an additional extracellular disulfide bond between cysteines at the positions 49 and 57. Although this disulfide bond but does not appear to have an influence on TF's coagulant function, it was suggested that this disulfide bond may be involved in the regulation of redox activity at the C186-209 positions [76, 77]. Finally, the TF allosteric disulfide bond appears to be regulated by nitric oxide and glutathione, as both agents are capable of disrupting the disulfide bond and TF activity [74, 78].

There are also studies supporting the notion that Cys¹⁸⁶-Cys²⁰⁹ disulfide bond is not essential for the regulation of TF's pro-coagulant activity [79]. It is important to note that in these studies in order to mimic the reduced form of TF, cysteines were exchanged into alanine or serine residues which cause a misfolding problem in TF. As a result, the mutants have lower surface antigen levels than wild type TF. Although these studies attempted to express coagulant activity per TF molecule, excessive membrane surface might have caused an overestimation of the coagulant function for the mutants.

Alternatively Spliced Tissue Factor

A decade ago, another TF isoform, alternatively spliced Tissue Factor (asTF), was discovered [80]. The splicing machinery may choose between the inclusion or exclusion of exon 5 of the TF gene to form TF (nowadays often referred to as full length TF; flTF, to avoid confusion) or asTF respectively. Exclusion of exon 5 also causes a frameshift in the TF mRNA sequence. Consequently, human asTF (hasTF) contains a 40 amino acid unique C-terminus, while the first 166 amino acids in human flTF (hflTF) and hasTF are identical [81]. In addition, asTF lacks the transmembrane domain and is a soluble protein. The expression of asTF is tissue and cell type specific. HasTF is expressed by promyelocytic leukemia cells (HL-60), CD14+ monocytes, TNF- α and IL-6 treated endothelial cells, smooth muscle cells, gastric carcinoma (KATO III, SNU-5 and MKN-74), colon carcinoma (HCT 116), neuronal glioblastoma (U343), squamous cell carcinoma (A431), melanoma (WM1341B, WM983A), pancreatic carcinoma (Capan-2) cell lines, and is also expressed in pancreas, placenta, lung and human thrombi [80, 82-84]. hasTF also has a mouse homologue (masTF) with a slightly longer C-tail [85] that is localized in kidney, lung, stomach and murine thrombi [85, 86].

Exon 5 of the TF pre-mRNA contains exonic splicing enhancer (ESE) sequences that interact with a set of splicing factors (i.e. SR proteins) to regulate inclusion or exclusion of exon 5 (Fig.2).

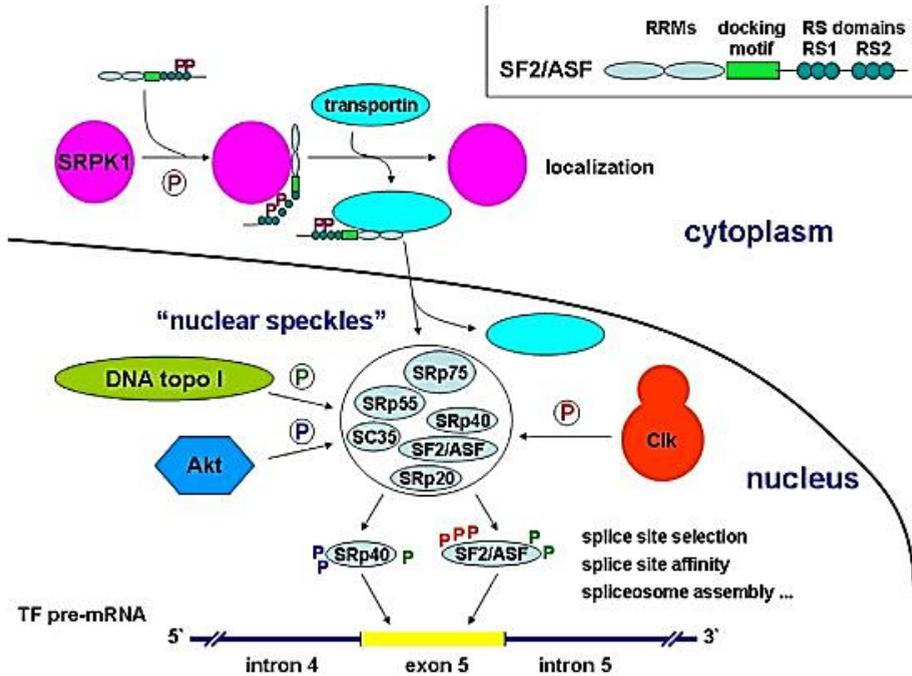


Fig.2 Regulation of TF pre-mRNA splicing by splicing regulator proteins. SR protein resides in the cytoplasm and are transported into the nucleus following phosphorylation by SRPK1. SR proteins are then additionally phosphorylated by a variety of SR protein kinases to regulate their interaction with RNA sequences [87] .

DNA topoisomerase I, Clk ,PI3K and the interaction of different SR proteins with exon 5 play a major role in exon 5 inclusion/exclusion as described in Table I and Table II.

Upstream regulator	Regulated SR proteins	exon 5 inclusion/exclusion	Ref
DNA topoisomerase I	SRp55 and SF2/ASF	inclusion	[88]
PI3K	SRp55 and SF2/ASF ,SRp75	exclusion	[89]
Clk	SRp55 , SF2/ASF, SRp75, SRp40 and SRP20	inclusion, exclusion	[88]
NFkB		inclusion, exclusion	[89]

Table I. Upstream regulator pathways , their effects on SR protein phosphorylation and their effects on alternative splicing of the TF gene.

SR proteins	exon 5 inclusion/exclusion	Ref
SRp75 and SF2/ASF	exclusion	[88-90]
SF2/ASF and SRp55	inclusion	[91]
SRp40 and SRp35	exclusion	[92]

Table II: Unique sets of SR proteins and their effects on exon 5 inclusion/exclusion.

Alternatively Spliced Tissue Factor in Coagulation

The coagulant function of asTF is still under debate. The FVIIa binding site of flTF is conserved in asTF, and asTF localizes to thrombi [80]. Therefore, it is tempting to hypothesize that asTF plays a role in the coagulation. Indeed, addition of recombinant hasTF to platelet poor plasma decreases the clotting time and this pro-coagulant effect of asTF is dependent on the presence of phospholipids. [80]. Similarly, recombinant masTF showed coagulant activity in FXa generation assays [86]. In an other study, incubation of endothelial cells with cytokines resulted in hfITF and hasTF production while hasTF depletion reduced coagulant activity [83]. It should be noted that asTF is not tethered to the cell surface and the lack of such a phospholipid surface may compromise coagulant activity. Thus it remains unclear how asTF/FVIIa complex interacts with the cell surface in order to activate FX.

In contrast with the above, other studies using cell lysates or supernatant from HEK293 and Mia-PaCa-2 cells transfected to express hfITF and hasTF, show prominent coagulant activity only when cells were transfected to express flTF and only flTF could be detected in the culture media of these cells, which is in contradiction with asTF's secretable nature [93, 94]. While in all these previously mentioned experimental designs, asTF or flTF were expressed separately, more recent work in which flTF and asTF were co-expressed suggests that asTF enhances flTF's coagulant activity [95]. In these studies, asTF was co-localized with flTF antigen on both cell surfaces and microparticles. Although simultaneous TF isoform expression did not lead to any change in flTF levels on cells, TF activity was significantly higher on cells expressing both isoforms than that on cells harboring solely flTF [95]. Thus, it appears that asTF enhances flTF function and further studies to investigate the thrombogenicity of asTF are warranted.

Alternatively Spliced Tissue Factor Signaling

fITF-dependent PAR signaling is both supported and limited by their membrane tethered nature, as the majority of both fITF and PAR2 localize in lipid rafts. This domain allows the positioning of these proteins in close proximity to trigger downstream signaling events [68]. In contrast, non membrane-tethered asTF may not be optimally positioned on a membrane surface and does not facilitate FVIIa-dependent PAR2 activation. Rather, asTF ligates integrin subsets on the cell surface to activate signaling pathways [96]. Integrins are membrane receptors composed of an α and β subunit. 18 α and 8 β subunits associate to form 24 different integrin receptors. They are involved in cell-cell or cell-extracellular matrix interaction and inform the cells on surrounding conditions. Utilization of different integrin subsets by asTF results in the activation of various signaling pathways that regulate diverse cellular functions. On endothelial cells, hasTF/integrin interaction increases the phosphorylation of FAK, p42/44 MAPK, p38 MAPK and Akt. Particularly, $\alpha v \beta 3$ ligation triggers endothelial cell migration whereas $\alpha 6 \beta 1$ is involved in capillary formation [96]. Although, masTF-induced sprout formation is dependent on $\beta 1$ and $\beta 3$ as well, endothelial cell adhesion is only mediated by $\beta 3$ integrin [97]. The difference in integrin specificity between hasTF and masTF may be the result of the distinct C-termini. asTF also appears to play a substantial role in cancer progression. asTF levels correlate with lower survival and grade among non-small cell lung carcinoma patients [98, 99]. In addition, grafting of asTF- but not fITF- expressing pancreatic MiaPaCa cancer cells into mice yielded larger and more vascularized tumors [100].

Apart from cancer, asTF also appears to influence atherosclerotic progression. $\beta 1$ integrin ligation upregulates the expression of adhesion molecules (i.e. E-selectin, ICAM-1, VCAM-1) on endothelial cells giving rise to enhanced binding and transmigration of monocytes [101]. Despite a role for asTF in pathology, asTF may also dampen progression of certain diseases. In mouse cardiomyocytes asTF activates a signaling cascade composed of $\alpha v \beta 3$, Akt and NF κ B. Activation of this cassette leads to increased expression of anti-apoptotic Bcl-XL and protects cardiomyocytes against TNF- α induced cell death [102]. Survival signals for the cardiomyocytes are vital due to their inability to proliferate. Therefore asTF might play a protective role against cardiac dysfunction by decreasing apoptosis rates.

Outline

In this thesis we aimed to elucidate the specific roles of TF isoforms in coagulation, cell proliferation and angiogenesis. To achieve these objectives, we utilized patient cohorts, *in vivo* and *in vitro* tools.

Chapter 2 outlines the current findings on the contribution of each TF isoform to coagulation, atherosclerosis, cancer progression and cancer associated thrombosis. **Chapter 3** investigates the possible mechanisms regulating fITF coagulant function, in particular the disulfide switch model and fITF dimerization. **Chapter 4** not only zooms into the TF regulated processes which were discussed in Chapter 2 but also summarizes the impact of integrin complexation on these processes. This chapter also gives further directions to improve our knowledge on TF/integrin signaling and disease progression. **Chapter 5** investigates the unique role of TF isoforms, specifically asTF, in breast cancer progression. The chapter is expanded by unveiling the mechanism lying behind asTF dependent tumor growth. The individual impact of each isoform was evaluated in **Chapter 6** is a side-by-side comparison study. The hormonal regulation of breast cancer prompted us to investigate the interaction of asTF and the estrogen pathway in **chapter 7**. Moreover, a widely used breast cancer model that was exploited in this thesis is thoroughly described in **Chapter 8**. Finally, **chapter 9** presents the general summary and discussion.

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