

Functional genomics of endothelial cells treated with anti-angiogenic or angiopreventive drugs

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Abstract Angiogenesis is a highly regulated physiological process that has been studied in considerable detail given its importance in several chronic pathologies. Many endogenous factors and hormones intervene in the regulation of angiogenesis and classical as well as targeted drugs have been developed for its control. Angiogenesis inhibition has come off the bench and entered into clinical application for cancer therapy, particularly for metastatic disease. While the clinical benefit is currently in terms of months, preclinical data suggest that novel drugs and drug combinations could lead to substantial improvement. The many targets of endogenous angiogenesis inhibitors reflect the complexity of the process; in contrast, current clinical therapies mainly target the vascular endothelial growth factor system. Cancer chemopreventive compounds can retard tumor insurgence and delay or prevent metastasis and many of these molecules hinder angiogenesis, a mechanism that we termed angioprevention. Angiopreventive drugs appear to prevalently act through the

inhibition of the pro-inflammatory and anti-apoptotic player NF κ B, thus contrasting inflammation dependent angiogenesis. Relatively little is known concerning the effects of these angiogenesis inhibitors on gene expression of endothelial cells, the main target of many of these molecules. Here we provide an exhaustive list of anti-angiogenic molecules, and summarize their effects, where known, on the transcriptome and functional genomics of endothelial cells. The regulation of specific genes can be crucial to preventive or therapeutic intervention. Further, novel targets might help to circumvent resistance to anti-angiogenic therapy. The studies we review are relevant not only to cancer but also to other chronic degenerative diseases involving endothelial cells, such as cardiovascular disorders, diabetes, rheumatoid arthritis and retinopathies, as well as vessel aging.

Keywords Anti-angiogenesis · Endothelium · Functional genomics · Mechanisms of action

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Introduction

Tumors are the second cause of death after cardiovascular/cerebrovascular diseases in industrialized nations, and cancer incidence is rapidly increasing among developing nations. Notwithstanding massive efforts and investments in improving cancer therapy, most of the progress made towards reducing overall mortality has been achieved through early diagnosis. For most cancer patients with metastatic disease, the improvements made in therapeutic efficacy in recent years can be measured on an average of months. Most current therapeutic strategies are based largely on directly killing tumor cells with cytotoxic agents, a traditional approach that inherently harbors extensive systemic side effects, now increasingly used in combination

with more targeted therapies. In contrast to oncology, the mortality rates for cardiovascular disease have been declining over the last decades, a success attributable in large part to an active prevention approach. If we are to gain further improvement on treatment of cancer patients, we need to: (1) target the tumor microenvironment, by interrupting the tumor-host interactions that fuel tumor growth and metastatic spread, and (2) apply more effective prevention approaches. One approach that fits both of these categories is targeting tumor angiogenesis [1].

During development, vessels are formed by proliferation of endothelial progenitor cells (EPCs) that are derived from hematopoietic stem cells of the bone marrow (vasculogenesis). Tumor vascularization depends, however, mainly on sprouting from pre-existing vessels in the vicinity of the tumor through the release of the strongly angiogenic growth factors such as VEGF and bFGF (angiogenesis). Hence, tumor induced angiogenesis does not rely on EPC activation but rather on reactivation of quiescent endothelial cells. The incidence of tumors correlates with age. Endothelial cells of elder subjects may have accumulated many genotoxic insults since almost all carcinogens pass in the blood before they are destroyed in the liver or the kidney. Endothelial cells therefore need a particularly tight control of genome integrity since upon activation, the effects of mutations could lead to aberrant proliferation. In fact, malignant transformation of endothelial cells is extremely rare. A tight genome surveillance in endothelial cells most probably corresponds to a pre-commitment to apoptosis which in turn becomes an important target of anti-angiogenic therapy.

Anti-angiogenesis: clinical efficacy and resistance

Targeting angiogenesis clinically is currently largely limited to interruption of a single pathway, the VEGF pathway, yet has shown significant improvement on survival for several cancers, and provided novel therapeutic efficacy that was lacking for some difficult to manage cancers such as renal cancer. However, since to date the clinical benefit is largely in terms of months, there is vast room for improvement. Targeting pathways other than VEGF must be evaluated [2–5], as is also needed for the role of components of the tumor microenvironment, in particular inflammation [6–8]. Leukocyte recruitment and inflammatory cytokine induction have been suggested to precede even VEGF induced angiogenesis [9].

The successful prevention approaches in cardiovascular disease give further support to the concept of cancer chemoprevention, an active intervention to prevent cancer insurgence and progression [1, 10]. Cancer chemoprevention is defined as use of molecular approaches to inhibit or delay tumor onset and growth [10]. Many chemoprevention

agents and substances (including dietary habits) associated with cancer prevention appear to target angiogenesis, a concept known as angioprevention [1, 11]. Angioprevention may represent a feasible and efficacious approach to preventing cancer, however, more effective drugs will be necessary for putting this into clinical practice. Angiopreventive drugs may have the potential to repress angiogenesis during early steps of carcinogenesis where they might retard the angiogenic switch, preventing unrestrained tumor growth. The identification of common molecular hubs targeted by the structurally diverse angioprevention compounds identified to date will provide insight into drug design and drug combinations to provide effective prevention with minimal or no deleterious side effects, as discussed below, leading to reduction of angiogenesis, thus delaying tumor growth, progression and metastasis.

The scope of this review is to summarize what we have learned on the response of the endothelial cell to anti-angiogenic and angiopreventive treatments with special regard to changes in the endothelial gene expression profile. The transcriptome of treated endothelial cells can help to (1) identify new molecular targets, (2) design combination therapies, (3) prevent or stimulate senescence of vascular cells, (4) circumvent resistance to anti angiogenic therapy and (5) design array specific diagnostic tools.

Endogenous inhibitors of angiogenesis

Not surprisingly, a range of endogenous negative regulators of angiogenesis have been found, as expected from the angiogenesis “balance” concept in homeostasis where normally inhibitors of angiogenesis dominate over angiogenic stimuli. However, many of these are in surprising forms, in particular a number of proteolytic fragments have been found to harbor anti-angiogenic activity even though the parental intact protein is not involved in regulation of angiogenesis. These are often fragments of extracellular matrix proteins, such as collagen type IV chains, including Arresten (*COL4A1*) [12], Canstatin (*COL4A2*) [13, 14] and Tumstatin (*COL4A3*) [15]; the Collagen XVIII fragment Endostatin [16]; the perlecan fragment Endorepellin [17] and the fibronectin fragment Anastellin [18]. One of the most potent and physiologically relevant angiogenesis inhibitors is the intact extracellular matrix protein Thrombospondin [19, 20]. Long pentraxin 3, a molecule associated with inflammation and matrix assembly in the ovary [21], is a potent inhibitor of FGF2 induced angiogenesis that appears to be responsible for the paucity of angiogenesis in systemic sclerosis patients [22, 23]. In contrast, the activity of the Tissue inhibitors of metalloproteinases [24] (TIMPs 1–4) also show repression of angiogenesis by inhibiting degradation and processing of

extracellular matrices, in particular the basement membrane, necessary for endothelial cell migration and invasion during angiogenesis. Another class of parental molecules giving rise to angiogenesis inhibitory fragments are involved in regulation of thrombosis, including the first member identified, Angiostatin [25], a fragment of plasminogen, and a peptide derived from Antithrombin III [26], while Vasostatin [27] is instead derived from the endocrine modulator Chromogranin-A. The predominance of extracellular matrix and proteolysis products among known endogenous inhibitors of angiogenesis is striking, suggesting that endothelial cells may have inherent mechanisms for sensing areas of extensive tissue damage where revascularization may well be too premature. One particularly important defense mechanism whereby tissue degradation should inhibit angiogenesis would be in areas of infection with an intense immune reaction in progress; revascularization of the hypoxic infected tissue is blocked so as to prevent systemic dissemination of the infection. As we will see below, some of these inhibitors appear to target immune cells, suggesting this may be a key regulatory mechanism. The immune system is capable of sensing at least some forms of proteolytically generated peptides [28], a role for the immune system in the function of this class of angiogenesis inhibitors could be speculated, in keeping with the immunomodulatory properties of the calreticulin fragment vasostatin [29]. This also suggests that there may be a pattern recognition system involved in mediating the response to these proteolytic fragments.

Several molecules involved in cell signaling appear to interfere with angiogenic cell signaling, including chemokines (Platelet factor 4 [30–32]), Soluble Fms-like tyrosine kinase-1 (S-Flt-1) [33], Pigment epithelium derived factor (PEDF) [34] and Angiopoietin 2 [35]. Interestingly, an alternate splice variant of VEGF that is produced by normal tissues, designated VEGFxxxB [36], appears to inhibit VEGF signaling.

Angiostatin is a large peptide fragment of plasminogen endowed with anti-angiogenic properties originally isolated from the urine of tumor-bearing mice [37, 38]. Angiostatin and related forms consisting of the first 1–5 kingles in plasminogen are generated by the action of diverse proteases, including metalloproteases (MMP2, MMP12, MMP9) and serine proteases (PSA, neutrophil elastase) [39, 40].

Following identification with *in vivo* studies, numerous *in vitro* studies have sought to identify the effects of angiostatin on endothelial cells. Angiostatin has been demonstrated to produce an array of events ranging from apoptosis/activation of endothelium to inhibition of endothelial cell migration, [41–44] and tube formation [45]. Potential endothelial cell surface angiostatin receptors identified to date include cell surface ATP synthase, angiotensin and various integrins (see [40] for review).

Angiostatin inhibits migration of neutrophils and macrophages *in vitro* and neutrophil mediated angiogenesis *in vivo*, [44] and inhibits neutrophil and monomyeloid cell adhesion [46]. It also inhibits angiogenesis induced by HIV-tat, a molecule with chemokine-like and VEGF-like properties [47], reduces macrophage numbers in atherosclerotic plaques [48], and tumor-associated macrophage infiltration *in vivo* [49]. This activity was associated with repression of macrophage infiltration into matrigel sponges *in vivo* and inhibition of macrophage migration *in vitro*.

The effects of angiostatin on cellular infiltrates could dictate the alterations in the cytokine profile at the local microenvironment or systemic levels following angiostatin treatment. Using microarray analyses, we noted that exposure of endothelial cells to angiostatin *in vitro* strikingly limited effects on gene expression profiles as compared to that generated by cytokines such as interferons (unpublished observations and [50]). The range of modulation observed was modest (maximum 2.8-fold); only few genes found to be up-regulated over twofold being MMP14 (2.8-fold), IL-15 (2.6-fold), a lymphoid-specific helicase (HELLS) and its interacting protein protein MX2 (myxovirus resistance 2) and HSF2BP, a heat shock transcription factor 2 binding protein. PCDH7 (brain–heart–protocadherin, was the only gene substantially (0.5-fold) down-regulated. However, these data are based on two technical replicates and the lack of biological replicates does not permit to firmly conclude that these genes were indeed modulated by angiostatin. Further, modulation of IL-15 to a similar extent (3.4-fold) was also observed on endothelial cells treated with IL-12; however, analyses of numerous microarray analyses show that these human umbilical vein endothelial cells (HUVEC) express low or absent levels of the IL-12Rb1 and IL-12Rb2 subunits, consistent with previous observations [51] and the lack of biological effects of IL-12 on HUVE cells *in vitro* examining growth, migration or invasion [52, 53]. Altogether, the limited transcriptional effects observed suggested that non-endothelial cell types, such as immune cells, are primary targets *in vivo*.

Previous array studies found substantial modulation of the endothelial transcriptome when using diverse angiostatin forms (K1–3, the “canonical” K1–4, and k1–5) that were transduced into A549 lung carcinoma cells using and adenoviral vector. The effects of supernatants from the transfected cells, as compared to the null vector control, was the tested on HUVECs treated for 4 h containing 75% of the transduced A549 cell supernatants and final concentrations of 5% heat inactivated FBS, 5 ng/ml VEGF-A and 0.1% BSA [54]. Unfortunately, these authors did not investigate the effects of angiostatin transduction on the transcriptome of the A549 cells themselves, which may have undergone significant alterations as well, thus

skewing the results. Further, the platform used, cDNA chips of 6,388 human unigenes, was limited in scope and quality control, although 3 biological replicates were used. Treatment of HUVE cells with these supernatants resulted in inhibition of proliferation, migration, tube formation and induction of apoptosis. Induction of apoptosis appeared to be related to FasL induction and was blocked by antibodies targeting fas, the α -ATP synthase and the $\alpha v\beta 3$ integrin. The array analyses indicated 189 genes were differentially induced or repressed by at least twofold, most (161) of these were induced. These induced genes were dominated (70%) by functional groups related to growth/proliferation, inflammation, apoptosis/survival, extracellular matrix/adhesion and migration/cytoskeleton (in order of predominance). Of note, one gene up-regulated by angiostatin in this approach was E-selectin, both expression and function [54]. Expression of E-selectin, a downstream target of NF- κ B, is generally associated with angiogenesis [55], and we have found that E-selectin is repressed by angioprevention agents [56]. These data could reflect the action of cytokines such as IL-1 β that could have been induced by angiostatin in the A549 cells.

Endostatin was the next endogenous anti-angiogenic fragment to be discovered [16]. The effects of on HUVE cells of endostatin treatment for 30 min, 1, 2, 4, and 8 h was examined by microarray analyses [57] using a human cDNA 10 k array (Hs-UniGem2, produced by the NCI/NIH ATC) and compared to that of fumagillin, an anti-angiogenic fungal metabolite. The authors focused on a series of genes that showed rapid up-regulation (at 1–2 h of treatment) followed by down-regulation. These were transcription factors, in particular KLF4 and ID1, that have been shown to be involved in regulating angiogenesis, consistent with the evidence that endostatin influences signal transduction [58–60].

The group of O'Reilly and Folkman, following their discoveries of angiostatin and endostatin, found that tumor cells in culture generated a fragment of bovine anti-thrombin III that strongly inhibited angiogenesis [26]. Transcriptome analyses of the effects of the anti-thrombin fragment on endothelial cells based on Stanford 43 K human cDNA microarrays initially showed a dramatic down-regulation of perlecan [61], a heparan sulfate proteoglycan [62] involved in presentation of angiogenic growth factors to their receptors [63] that also gives rise to an anti-angiogenic fragment [17]. More in-depth analyses showed modulation of 128 transcripts over twofold, in particular those of proteins associated with the extracellular matrix [64], including up-regulation of TIMPs 1, 2 and 3 and the proteoglycans agrin and vitronectin, and down-regulation of biglycan and syndecan 3. Syndecan 1, whose involvement in angiogenic signaling is complex [63] instead showed a unique rapid up-regulation followed by

down-regulation. Interestingly, most of the transcripts were down-regulated.

The Tissue Inhibitors of Metalloproteinases, or TIMPs, have a complex relationship with angiogenesis, metastasis, and several other cell regulatory pathways. While TIMPs have anti-angiogenic activities, largely assigned to their capacity to block invasion, the effects of TIMPs have not been tested on endothelial cells. The effects of TIMP1 on differential gene expression in JD38 Burkitt lymphoma cells using NIH ATC 10 K microarrays [65] indicated most transcripts were repressed. The effects were centered on gene categories such as those regulating B-cell growth and differentiation, transcription and cell cycle regulators, again suggesting the complex signaling role of these molecules dominated. We note that CD44, a gene associated with matrix and metastasis, was among the most up-regulated, while the alpha 4 integrin subunit was strongly down-regulated. A quite different picture was obtained with TIMP3 transfected into Gli36 human glioma cells using Affymetrix GeneChip HG-U133A microarrays [66]. Here most genes were up-regulated, 3 major gene classes could be identified: (1) A series of disintegrin metalloprotease ADAM proteins (including ADAM-9, ADAM-10, ADAM-17, ADAM-19, ADAM-21, and ADAM-23), probably related to the regulatory role that TIMP3 is known to exert on membrane-anchored proteinases, (2) Numerous proteins associated with apoptosis, most likely related to the apoptotic activity associated to TIMP3, (3) Matrix/angiogenesis associated genes, including up-regulation of MMP2 and MMP9, chains of collagen IV, V and VI, laminins, PDGFs, FGF2&5 and FGFR1, several interleukins and other cytokines, TNF and its receptors, and finally VEGFA, B, C and neuropilin-1. This would imply induction of angiogenesis and a finite risk of enhancement of tumor growth, however, in vivo assays demonstrated that the TIMP3 transfected tumors grew slower [66], although histological analyses on tumor vascularization, apoptosis, and eventual microenvironment effects were not reported.

Hormones with anti-angiogenic activity

The endogenous metabolite of estrogen, 2-methoxyestradiol, has been described as a potent inhibitor of endothelial cell proliferation, migration and angiogenesis in vitro [67]. The metabolite is a strong inhibitor of superoxide dismutase [68] and this activity might be related to the anti-angiogenic effect inasmuch as superoxides stimulate inflammation as well as endothelial cell activation and proliferation.

Human beta-chorionic hormone (β HCG) has been studied following initial reports of its activity against the

endothelial cell derived Kaposi's sarcoma [69]. β HCG inhibits MMPs [70] but the precise mechanism has not been elucidated. Gene expression profiling of β HCG treated breast cancer cells using dedicated arrays with about thousand genes hints at cell proliferation, apoptosis, cell trafficking, and DNA repair without a clear relation to anti-angiogenic functions [71].

Somatostatin inhibits angiogenesis by binding to its receptors on the surface of endothelial cells that leads to the activation of the nitric oxide synthase and the MAP-kinase pathway [72]. Gene expression profiling of somatostatin treated pancreatic cancer cells led to the identification of several angiogenesis related genes including angiogenin, a potent pro-angiogenic RNase [73].

Prolactin, the lactation stimulating hormone that almost exclusively acts on the mammary gland, can give rise to a 16kD fragment with a strong anti-angiogenic activity that is mediated by the inhibition of MAP-kinases [74, 75]. Similar fragments are also released from the other members of the prolactin/human growth hormone family of proteins [75]. Interestingly, a study of the response of endothelial cells to the treatment with the fragment revealed induction of an NF κ B dependent response including chemokines and the endothelial activation marker, E-selectin [76] which is one of the major down-regulated genes by the anti-angiogenic anti-oxidants *N*-acetyl cysteine and epigallocatechin gallate that repress NF κ B signaling [77] (see also below). The authors suggest that enhanced leukocyte infiltration might be responsible for the anti-tumoral effects observed in the melanoma model [76] but it is not clear how enhanced NF κ B activity may determine anti-angiogenic effects. Full length prolactin also induces NF κ B leading to the induction of the anti-angiogenic cytokines CXCL-9, -10, and -11 [78]. The prolactin fragment might therefore share the anti-angiogenic mechanism with interferons (see below).

Anti-angiogenic cytokines

Despite the fact that several cytokines may interfere with angiogenesis in some experimental settings (see Table 1), only a few of them can be considered endogenous angiogenesis inhibitors. Interferon- α (IFN- α), a cytokine with marked therapeutic activity in transplantable tumor models, is possibly the prototype of anti-angiogenic cytokines. Initial evidence for anti-angiogenic effects of type I IFNs stems from observations in immuno-competent DBA/2 mice bearing IFN-resistant erythroleukemia, or ESb lymphoma cells; results indicated that IFN- α/β exerted an anti-tumor effect by damaging tumor blood vessels, thus causing disruption of tumor blood flow, which led to ischemic tumor necrosis [79]. Moreover, it was suggested that IFNs

modulated the signal for angiogenesis produced by the tumor cells [80]. Later on, experiments of IFN- α gene transfer by various delivery systems confirmed and extended these findings (reviewed in [81]). In most of these studies, immuno-deficient mice lacking mature CD8+ lymphocytes and generally also NK cells were transplanted with IFN- α -resistant tumor cells, thus ruling out involvement of immune-based mechanisms or direct anti-proliferative effects in the anti-tumor effects observed.

The anti-angiogenic activity of class I IFN has classically been attributed to inhibition of basic fibroblast growth factor (bFGF) overproduction by tumor cells [82] or down-regulation of IL-8 and vascular endothelial growth factor (VEGF) gene expression [83, 84]. However, reduced production of pro-angiogenic factors is not likely to explain IFN- α -induced anti-vascular effects in experiments involving injection of murine IFN- α into mice bearing human tumor cells [85, 86], due to the relatively strict species-specificity of class I IFN. Moreover, even in the absence of these interspecies barriers, reduced production of VEGF or bFGF was barely observed in TRAMP mice—a transgenic model of prostatic cancer—treated with murine IFN- α , in spite of clear-cut anti-angiogenic effects in the tumors [87]. Thus, suppression of pro-angiogenic factors synthesis by IFNs is one plausible yet not exclusive explanation for the anti-angiogenic effects of this cytokine, and direct effects on endothelial cells (EC) can be envisioned. In this regard, microarray data have shown dramatic transcriptional effects of IFNs in EC, which are accompanied by modulation of some endothelial cell functions, such as in vitro proliferation and migration [88–91]. A key intracellular mediator of these effects could be guanylate binding protein 1 (GBP-1), whose expression in vivo has been almost exclusively associated with EC, where it may exert specific functions (including inhibition of endothelial cell proliferation and migration) in response to class I IFNs and other inflammatory cytokines through MMPs and other as yet unknown mechanisms [92, 93]. Moreover, anti-vascular effects of IFN- α may partially depend upon up-regulation of angiostatic chemokines [94, 95]. In vitro, treatment of human endothelial cells with IFN- α leads to marked transcriptional up-regulation of CXCL10–11, uncoupled from CXCL9 or IFN- γ [88]: these chemokines, which are released at low level by IFN- α -stimulated endothelial cells, could in theory act as biological amplifiers of the primary anti-angiogenic effects of IFN- α .

What are the consequences of these effects of IFN- α on tumor vessels? In vivo, anti-vascular activity in subcutaneous tumor xenografts has been associated to induction of areas of ischemic necrosis [85, 86, 96–99], confirming initial observations [79, 80, 100]. It appears that disruption of tumor microvessels by IFN- α leads to increased hypoxia in these models, a feature shared by other anti-angiogenic drugs [101]. It is important to note that hypoxia and

Table 1 Inhibitors of angiogenesis

Inhibitors of angiogenesis	Gene symbol	Target/pathway/mechanism	Gene expression profiles
Endogenous inhibitors of angiogenesis			
Arresten [12]	<i>COL4A1</i>	Integrin; FAK/c-Raf/MEK/ERK1/2/p38 MAPK [12]	NA
Canstatin [13, 14]	<i>COL4A2</i>	Integrin [14]; apoptosis FLIP [13]	NA
Endorepellin[17]	<i>HSPG2</i>	Integrin alpha2beta1[206]	NA
Endostatin [16]	<i>COL18A1</i>	Wnt [58]; integrin, src [60]; erk [59]	[57]
Fibronectin fragment (Anastellin) [18]	<i>FNI</i>	Erk [207]	NA
Fibulin [208]	<i>FBLN1</i>	Erk, synergy with TGF β [209]	NA
Thrombospondin [19, 20]	<i>TBS1</i>	Phosphoinositide 3-kinase [210], erk [211]; rac [212]	NA
Tumstatin [15]	<i>COL4A3</i>	Alpha v beta 3 integrin, Akt/mTOR [213]	NA
Long Pentraxin 3 [21]	<i>PTX3</i>	FGF2 [214]	NA
Pigment epithelium derived factor (PEDF) [34]	<i>SERPINF1</i>	VEGF [215, 216]	[217]
Angiostatin [25]	<i>PLG</i>	P53, FasL [218], IL12 [52]	NA
Antithrombin III [26]	<i>SERPINC1</i>	NF κ B [219]; perlecan [61]	[61]
Platelet factor 4 [30–32]	<i>PF4</i>	FGF2, VEGF [220]	NA
Tissue inhibitors of metalloproteinases (TIMPs) [24]	<i>TIMP1</i>	MMPs [24]	[65, 66]
	<i>TIMP2</i>		
	<i>TIMP3</i>		
	<i>TIMP4</i>		
PEX [221]	<i>MMP2</i>	MMP2 [221]	NA
Soluble Fms-like tyrosine kinase-1 (S-Flt-1)[33]	<i>FLT1</i>	VEGF [33]	NA
Troponin I [222]	<i>TNNI1</i>	bFGF [223]	NA
Vasostatin [27]	<i>CHGA</i>	TNF α induced gap formation, MAPK [224]	NA
Angiopoietin 2 [35]	<i>ANGPT1</i>	Antagonist of angiopoietin1 for Tie2 binding [35]	NA
TNFSF15 [225]	<i>TNFSF15</i>	NF κ B [226]	NA
VEGF165B [36]	<i>VEGFA</i>	VEGF [36]	NA
VEGI-192 [227]	<i>TNFSF15</i>	NF κ B [226]	NA
Vasohibin [228]	<i>VASH1</i>	VEGF [228]	NA
	<i>VASH2</i>		
TrpRS [229]	<i>WARS2</i>	VE-cadherin [230]	NA
Neutrophil gelatinase-associated lipocalin [231]	<i>LCN2</i>	VEGF [231]	NA
Interferons and cytokines			
Interferons [79, 232]	<i>IFNA1</i>	CXCL10 [233]	[88, 91, 234–238]
	<i>IFNA2</i>		
	<i>IFNB</i>		
	<i>IFNG</i>		
Interleukin 1 [239]	<i>IL1A</i>	Nitric oxide [240]	[241–246]
Interleukin 4 [247]	<i>IL4</i>	IL4R, VCAM1 [248]; vascular permeability factor [249]	[250, 251]
Interleukin 12 [53]	<i>IL12A</i>	CXCL10 [252], VEGF, MMPs [253]	[254–257]
	<i>IL12B</i>		
Interleukin 18 [258]	<i>IL18</i>	TBS1 [259]; CXCL8,9,10 [260]	[261, 262]
Hormones			
2-Methoxyestradiol [67]		Superoxide dismutase [68]	NA
Human chorionic gonadotropin [70]	<i>CGB</i>	MMPs [70]	[71]
Prolactin fragments [74]	<i>PRL</i>	MAPK, type 1 plasminogen activator inhibitor [75]	[76, 263–269]
Somatostatin [72]	<i>SST</i>	Nitric oxide synthase, MAPK [72]	[73]

Table 1 continued

Inhibitors of angiogenesis	Gene symbol	Target/pathway/mechanism	Gene expression profiles
“Classic” anti-angiogenic drugs			
Anecortave [110]	–	NA	NA
Combrestatin A4 [111]	–	P38/MAPK [270]	NA
Fumagillin/TNP-470 [112]	–	VEGF [271], FGFR1/PI3 K/AKT [272]	NA
Talidomide [113]	–	VEGF, IGF1, bFGF [114], NFκB [115]	[114]
<i>N</i> -(4-hydroxyphenyl)retinamide [116]	–	BMP1, MCP1 [116]	[116]
Tamoxifen [118]	–	ERα [273]	[119, 120]
Targeted anti-angiogenic drugs			
Axitinib [274]	–	VEGF [274]	NA
Bevacizumab [121]	–	VEGF [121]	[126, 127, 275]
JSM6427 [276]	–	Integrin α5β1 [276]	NA
Sorafenib [122]	–	Tyrosine kinases [277], Raf-MEK-ERK [122]	[129, 130]
αPIGF [124]	–	PIGF [124]	NA
Sunitinib [123]	–	Tyrosine kinases [123]	NA
Pegaptanib [278]	–	VEGF [278]	NA
PTK/ZK [279]	–	VEGF, aromatase [279]	NA
Ranibizumab [280]	–	VEGF [280]	NA
Rapamycin [125]	–	mTOR [281], VEGF [125]	[130–134, 282]
TG100801 [283]	–	VEGF, Src, YES [283]	NA
L19 [284]	–	Fibronectin [284]	NA
Angiopreventive drugs			
α-lipoic acid [155]	–	TRAIL, activin-A [155]	[155]
Artesunate [152, 173]	–	KDR/flk-1 [152]	[174]
Boswellic acid [153]	–	VEGFR2 [153]	NA
Curcumin [172]	–	NFκB [143]	[156, 157, 166–170, 285–288]
Ellagic acid [142, 289]	–	VCAM, ICAM [289], NFκB [142]	[175]
Epigallocatechin gallate[141]	–	MMPs [290, 291], NFκB [77]	[77, 157–165, 292–294]
Gambogic acid [154]	–	VEGFR2 [154]	[176]
Hyperforin [295, 296]	–	MMP9 [297], NFκB [144]	[177]
<i>N</i> -actyl cysteine [140]	–	Nitric oxide [298], MMPs, VEGF [140], NFκB [77, 145]	[77]
Pinitol [146]	–	NFκB [146]	NA
Triterpenoids [178]	–	PPARγ [149], JAK/STAT [150], NFκB [147], Nrf2 [151]	[179]
Thymoquinone [299]	–	Akt, Erk [299]	NA
Xanthohumol [148]	–	NFκB, Akt [148]	NA
Anti-angiogenic phytoestrogens			
Genistein [186]	–	VEGF, PDGF, uPA [300], ERα [301]	[187–201, 302–309]
Quercetin [202]	–	ERα [204, 205]	[310–314]
Resveratrol [202]	–	ERα [203]	[315–319]

A remarkable number of inhibitors of angiogenesis have been described in literature. For each compound the first study indicating an anti-angiogenic effect was cited. For the description of targets, pathways and mechanisms, the first or the most conclusive work is indicated. Gene expression profile studies cited are not necessarily limited to angiogenesis related aspects and have been performed in a variety of biological settings. Every effort was made to include all the publications available. We apologize for any omissions

necrosis were generally reported following implantation of tumor cells engineered with the *IFN-α* gene, a modality that likely favours anti-tumor effects because the cytokine

is released early during tumor formation and in a sustained manner. In general, treatment of established tumors by gene therapy or high-dose cytokine administration led to

less dramatic results, possibly due to resistance of established tumors to anti-angiogenic therapy or to the fact that certain biological activities of IFNs, such as anti-angiogenic effects, could follow a bell-shaped response and are thus not seen following conventional dosage [102, 103].

It is too early to understand whether these discoveries on the transcriptional signature of IFNs will have translational implications. In this regard, however, it is interesting to note that the INTERFEROME database of interferon regulated genes is now available to investigate, among others, the presence of the IFN signature in biological samples [104]. This could be very useful to unravel the endogenous IFN signature in tumor samples (and correlate it to vascularization) or monitor at the transcriptional level the outcome of IFN therapy.

A second cytokine whose effects are recurrently associated with angiogenesis inhibition is IL-12, which was initially reported to inhibit new vessel formation induced by the pro-angiogenic factor bFGF in a mouse corneal vascularization assay [105], and in Matrigel plug assays [106]. It has been shown that IFN- γ and, at least in part, CXCL10, appear to play a critical role as mediators of its anti-angiogenic effects [106, 107]. NK cells may contribute to inhibition of angiogenesis by IL-12 not only through the secretion of anti-angiogenic chemokines but apparently also through NK cell-mediated cytotoxicity against endothelial cells [108]. More recently, however, angiogenesis inhibition was observed in IFN- γ ($-/-$) and CXCR3($-/-$) knockout mice treated with IL-12, indicating that NK- and/or T cell-initiated IFN- γ -chemokine cascades were not involved in angiogenesis inhibition in vivo [53, 109]. Whatever the underlying mechanism, results from all these studies agree on the identification of endothelial cells as a major downstream target of the biological effects of IL-12. However, it has been reported that HUVECs do not respond to IL-12 because they lack both subunits of the IL-12 receptor [51]. Microarray data on IL-12 effects on HUVE cells indicates essentially no effects (see above), in line with the lack of receptors on these cells. However, other endothelial cell types could behave differently would be extremely useful to investigate the issue as to whether microvascular endothelial cells express receptors for or respond to IL-12, unfortunately not yet available.

“Classic” anti-angiogenic drugs

The concept of anti-angiogenesis as an anti-cancer strategy has led to the development of many classic drugs such as Anecortave, an angiostatic steroid [110], the tubulin binding agent combretastatin A-4 phosphate [111] and analogues of fumagillin, a naturally secreted antibiotic of *Aspergillus fumigatus fresenius* [112]. No data exist, however, on the effect of these compounds on gene expression profiles. The

anti-angiogenic effects of the sedative thalidomide are apparently linked to its teratogenic actions [113]. Several mechanisms of action involving VEGF, IGF1, bFGF [114] as well as NF κ B [115] have been proposed. The effects of the drug on the transcription profile of endothelial cells have been analyzed using microarrays, however, the expression values have been reported for only six genes (*VEGF*, *bFGF*, *HGF*, *IGF-1*, *IGFBP-3* and *Ang1*) [114]. These data indicate that thalidomide acts on activated endothelial cells such as those present in multiple myelomas. It would be of great interest to further exploit these data for the identification of other anti-angiogenesis related genes that respond to thalidomide.

Ferrari and colleagues reported anti-angiogenic effects of the synthetic retinoid *N*-(4-hydroxyphenyl)retinamide, 4-HPR. These effects were mediated by the member of the TGF β -family members BMP1 and MIC as revealed by gene expression profiling of drug exposed human umbilical endothelial cells followed by functional assays [116]. This is particularly interesting in the light of cancer chemoprevention with 4-HPR [117].

The chemopreventive anti-estrogen, tamoxifen, also has been proposed to exert anti-angiogenic effects [118]. In addition to the abrogation of pro-angiogenic, estrogen receptor α mediated effects, tamoxifen apparently exerts anti-angiogenic effects that do not depend on the receptor [118]. Two studies have applied expression profiling to the analysis of tamoxifen effects, one analyzing breast cancer tissues of pre-surgically treated patients [119] and the other analyzing the estrogen receptor α positive breast cancer cell line MCF7 after over-expression of the aromatase transgene [120]. None of the two studies directly addressed anti-angiogenesis and the models are not suited to distinguish between ER α dependent and independent effects.

Targeted anti-angiogenic drugs

One of the key approaches in anti-angiogenesis has been development of targeted agents, which has been successful in the clinic. The classic examples are agents that directly target VEGF, with the most widely known and the first clinically successful anti-angiogenesis agent being Bevacizumab [121], a humanized antibody that recognizes most isoforms of VEGF, thus blocking its capacity to interact with cell surface receptors. Bevacizumab is clinically effective in enhancing disease-free survival in combination with chemotherapy (as monotherapy it is not effective) for a constantly expanding list of cancers, starting with colon. A variant of the same structural components is the use of an antibody fragment of Bevacizumab, known as Ranibizumab, specifically developed for ocular pathologies where it shows notable efficacy in treating

wet age-related macular degeneration. The second key approach has been multi-tyrosine kinase inhibitors that block VEGFR1 and VEGFR2 as well as other tyrosine kinases, the classic examples of these are Sorafenib [122] and Sunitinib [123]. These two molecules have been particularly effective in treating renal cancer, where they are approved and have represented a major therapeutic advance. Recent studies suggest that targeting other components of the VEGF system may be even more effective with fewer side effects, in particular agents targeting PIGF [124] or specifically VEGFR1. Finally, targeting the key intracellular signaling hub, mTOR, with Rapamycin [125] or Rapamycin analogs is intensively under investigation and entering into the clinic.

Transcriptome analyses of the effects of bevacizumab, Sorafenib or Sunitinib on endothelial cells are not available, one would assume that this would be similar to that of VEGF deprivation. However, other effects of these molecules could also be encountered, for example transcriptome analyses of murine models found that bevacizumab treatment up-regulated the Sp1 transcription factor and associated genes [126]. These approaches could also shed light on the source of the hypertension response, which is a common and major collateral effect of this class of drugs. Expression analysis has been done on tumor tissues of bevacizumab treated breast cancer patients with a differential analysis of responders vs non-responders [127]. These data sets show a predominance of genes associated with the tumor microenvironment, including several gene ontology sets related to extracellular matrix and cellular mobility. We had previously noted that the tumor microenvironment signature could be predictive of metastasis [128]. Interestingly, VEGF responses seemed to represent a minor constituent of the response [127].

Transcriptome analysis of the effects of sorafenib in a pulmonary hypertension model indicated a much more complex response was induced by drug therapy [129]. Combinations of sorafenib and rapamycin have been suggested to be effective in preclinical models [130], however, microarray analyses of the effects of rapamycin also show a complex picture. A 12 h exposure of MCF-7 breast cancer cells to rapamycin alone produced relatively modest changes [131], these were enhanced by simultaneous treatment with a differentiating agent, cotylenin A. Interesting up-regulated genes included Transforming growth factor- β -induced gene (TGFBI) and Cyclin G2 and down-regulation of most other cyclins. A similar effect of rapamycin, with up-regulation of Cyclin G2 and down-regulation of cyclins D2 and F, was found in Jurkat T cells [132] and in developing myoblasts [133], although effects on differentiation state were also found in this latter set. The modulation of this group of genes targeted by mTOR inhibitors appears to act as a function of AKT activity

[134]. Interestingly, down-regulation of a probable angiogenic factor, Heparin-binding EGF-like growth factor, was also observed [132].

Angiopreventive drugs

The publication of the first gene expression signatures [135, 136] stimulated a discussion on the validity of the multi-step carcinogenesis model [137, 138]. The possibility to predict the clinical outcome of a tumor through the analysis of the bulk of it has been extensively demonstrated for breast cancer. Yet this is in contrast with the multistep carcinogenesis model that predicts the metastatic subpopulation of the tumor to be very small, hidden in the bulk of the primary tumor. The apparent paradox can be resolved if the steps leading to a metastatic phenotype occur much earlier than so far assumed, long before the tumor becomes clinically overt [139]. Angiogenesis is of paramount importance for the acquisition of the metastatic phenotype inasmuch as it provides the route of dissemination of tumor cells to distant target tissues. Hence, metastasis could be blocked by blocking angiogenesis when the tumor is small, before the actual diagnosis of cancer.

Angiogenesis could therefore become a target of primary prevention in high risk subjects [11]. This means treating healthy people for a long time and compliance will depend on the absence of toxicity or side effects. The discovery of anti-angiogenic effects of the known antioxidant N-acetyl-cysteine [140] and the green tea gallate [141] opened a way to angioprevention [11]. The list of similar compounds with “angiopreventive” activity has considerably grown since (see Table 1). A common theme of their action is inhibition of the inflammation related transcription factor NF κ B that also blocks apoptosis and is active in both, endothelial and tumor cells [77, 142–148] but other pathways play a role at least for triterpenoids [149–151] and artesunate [152] and perhaps for boswellic [153], gambogic [154] and α -lipoic acid [155].

Gene expression profiling has been performed for many of these compounds yet only very few studies have addressed effects on endothelial cells [77, 155, 156]. The effects of gallates on the transcriptome have been studied for rat liver with the aim to characterize its metabolism that appears to depend on the cytochrome p450 isoform 1A2 (CYP1A2) that also mediates caffeine, melatonin and theophyllin degradation [157]. Long term administration of gallate to rats is well tolerated even at high doses and the transcription of anti-oxidant enzymes, stress related genes as well as energy metabolism related genes is affected [158]. Breast cancer cells respond to the anti-oxidant by blocking ATK expression and phosphorylation and reduced MMP9 expression consistent with the observed inhibition of invasion [159]. Comparing wild-type and Nrf2 knockout

mice, Shen and collaborators identified Nrf2-dependent and -independent effects of the gallate in mice liver and intestine after short term treatments and demonstrated a large number of responding genes [160]. Mammary cancers in carcinogen treated rats have an increased latency after treatment with EGCG, an effect that is apparently mediated by the regulation of the expression of genes involved in nuclear and cytoplasmic transport, transformation, redox signaling, response to hypoxia, and detoxification [161]. Interestingly, the growth inhibition exerted by EGCG on HER2/erbB2 positive mammary tumors is abolished through mutations in the receptor that lead to enhanced NF κ B activity. EGCG resistant tumors show an activation of the MAP-kinase pathway as detected by microarray analyses [162]. Proliferation of normal human neonatal fibroblasts is reversibly blocked by EGCG in correspondence to the repression of transcription of several cell cycle related genes that also resumes after removal of the drug [163]. Endothelial cells, that in contrast to tumor cells do not undergo apoptotic effects at concentrations up to 50 μ M EGCG, respond to the green tea component by the repression of endothelial activation through the reduction of NF κ B translocation to the nucleus [77]. Regulation of NF κ B and downstream genes such as MMPs thus appear to be at the core of the observed anti-angiogenic effects. EGCG transcriptomics has also been addressed in models of auto-immunity [164] and diabetes [165].

In a mouse model of inflammatory bowel disease Nones et al. showed that curcumin acts via an up-regulation of xenobiotic metabolism and a down-regulation of pro-inflammatory pathways, that the authors attribute to the activation of retinoid X receptor (RXR) by pregnane X receptor (Pxr) and peroxisome proliferator-activated receptor alpha (PPAR α) [166]. Curcumin altered the expression of twelve genes in the livers of rats fed with a diet containing the polyphenol indicating a slight peroxisome proliferator activity [157]. In pancreatic tumor cells, curcumin induces miRNA22 leading to an up-regulation of the corresponding target mRNAs coding for the general transcription factor SP1 and the estrogen receptor α [167]. In human colon cancer cells, microarray analyses indicate an effect of curcumin on NF κ B dependent expression of Cox2 and MMP2 in correlation to its effects on invasion [168]. Two studies have addressed the effects of Curcumin on breast cancer cells. Curcumin regulates several apoptosis related genes [169]. Complex microarrays reveal a series of NF κ B downstream targets among the curcumin responsive genes including two pro-inflammatory cytokines, CXCL-1 and -2, that are downregulated by the polyphenol, but other pathways like ERG1 are also affected [170]. Taken together, these effects might well explain the considerable effect on breast cancer metastasis in the mouse model [171]. A single report addressed

effects of the turmeric on endothelial cells analyzing the expression of cell cycle regulators and showing effects on several cell division cycle dependent kinases (CDKs) without an obvious link to the paramount curcumin target NF κ B [156]. Reduced proliferation of endothelial cells could well contribute to the anti-angiogenic effects observed [172]. However, endothelial proliferation can be stimulated by inflammatory cytokines and reduced proliferation can therefore be secondary to NF κ B inhibition [143].

α -Lipoic acid (α -LA) is an anti-oxidant in use for the treatment of peripheral neuropathies associated with non-insulin-dependent diabetes. It shows anti-angiogenic activities in vitro and in vivo that translate into a marked reduction of xenograft growth of vascularized tumors [155]. Gene expression studies of α -LA treated endothelial studies identified the pro-apoptotic death receptor ligand TRAIL and activin-A as major candidates for anti-angiogenic effects although a variety of metabolic processes are equally affected [155]. The anti-malaria drug, artesunate, also inhibits angiogenesis [173]. This drug has not been tested itself for effects on the transcriptome although it shows preferential effects on endothelial cells, yet the NCI panel of 60 cell lines has been analyzed with respect to angiogenesis related genes thirty of which significantly correlate with resistance to artesiminin [174].

Expression profiles of colon carcinoma cells that have been treated with ellagic acid, a dietary polyphenol present in berries, show differential expression of several genes of the MAP-kinase pathway including the tyrosine kinase receptors FGFR2 and EGFR [175]. It is not yet clear to which extent this polyphenol exerts effects similar to those of other compounds of the family.

The transcriptome analysis of H22 transplants in mice treated with gambogic acid has led to the hypothesis that the anti-tumor effect observed are indirect and mediated by the immune system since a large portion of the genes induced are classified as immunity related genes [176].

Hyperforin has been demonstrated to be the active compound in St. John's wort inasmuch as the expression profiles elicited by the whole extract and the purified compound in human hepatoma cells are much alike [177]. The anti-angiogenic effects of hyperforin [144] appear to be mediated by the regulation of hypoxia associated genes in addition to mediators of proliferation and apoptosis as well as a series of drug metabolism genes [177].

N-acetyl-cysteine (NAC) is used as a mucolytic drug for many years and its anti-angiogenic effects have been described several years ago [140]. A single study has addressed the effect of the anti-oxidant on global gene expression showing that downstream targets of NF κ B constitute the majority of NAC responsive genes in endothelial cells [77].

The triterpenoids or synthetic oleananes are a novel class of anti-angiogenic chemopreventive drugs [178] acting via PPAR γ [149], JAK/STAT [150], NF κ B [147] and NRF2 [151, 179]. Microarray analyses in wild type and Nrf2 knockout mice confirm the latter pathway to be responsible for the chemopreventive effect against aflatoxin induced DNA-adducts [179]. However, anti-angiogenic effects are most likely mediated by other pathways with NF κ B being an obvious candidate.

For boswellic acid, pinitol, thymoquinone and xanthohumol no gene expression data are available and the data on artesunate are not derived from direct treatments with the drug. Xanthohumol [148] and pinitol [146] act via NF κ B, and the same might hold true for thymoquinone, while similar data are lacking for boswellic acid.

It turns out that most of the angiopreventive drugs act through the inhibition of NF κ B with I κ K being a preferential target, although the mechanism has not always been described in detail. Gene expression studies reflect this mechanistic analogy to a certain extent. A major problem with comparing such data derives from the many different cellular systems analyzed as well as from the fact, that there is no certainty on downstream targets of NF κ B which most likely differ from cell type to cell type. If, for example, gene expression analysis reveals hypoxia as a central process that is targeted by anti-angiogenic drugs, this most probably corresponds to NF κ B mediated effects since most hypoxia related genes are also controlled by NF κ B. A single study analyzed different anti-oxidants in parallel on endothelial cells showing the high similarity of the NF κ B dependent effects elicited by the drugs in endothelial cells [77].

More comparative studies are needed to identify drugs that obtain the desired anti-angiogenic effect at the lowest dosage possible in a specific cellular system. This would also help to identify the drugs best suited for clinical (angio-)prevention trials.

Anti-angiogenic phytoestrogens

There is compelling evidence that endogenous estrogens have pro-angiogenic actions [180–182], which probably participate in the beneficial actions of hormone replacement therapy on the myocardium [183]. Anti-angiogenic activities of estrogens are generally attributed to the estrogen receptor β [184] and the partial antagonist, tamoxifen, shows anti-angiogenic activity in ER α knockout mice [118]. Phytoestrogens are plant derived drugs with a certain affinity for ER α that compete with the endogenous hormone for binding to the receptor and therefore exert a partial antagonistic effect. The effect of the phytoestrogens therefore strongly differs between pre- and post-menopause. Given the wide use of hormone

replacement therapies and the identification of its contribution to the breast cancer risk in postmenopausal women [185] many groups seek safe substitutes for it. This has determined much consideration of phytoestrogens in the hope they might maintain the beneficial effects of estrogens on vascular health without the detrimental pro-carcinogenic effect.

Genistein, however, turned out to be anti-angiogenic [186]. A study on gene expression in endothelial cells revealed that genistein regulates several angiogenesis related genes such as endothelin-converting enzyme-1, endothelin-2, estrogen related receptor alpha and atrial natriuretic peptide receptor A precursor. Genistein also countered the effect of oxidized LDL on VEGFR [187]. Piao and colleagues identified cellular adhesion molecules as a major target for genistein in endothelial cells at concentrations that are, however, likely to induce apoptosis [188]. In PC3 cells that do not express estrogen receptors, Genistein regulates many genes involved in the processes of cell growth, cell cycle, apoptosis, cell signaling transduction, angiogenesis, tumor cell invasion and metastasis [189, 190], most probably consistent with its anti-NF κ B activity [191, 192]. Pancreatic cells showed the involvement of EGFR and the putative NF κ B target EGR1 in the response to the phytoestrogen [193]. Similar effects have been shown in several others cellular systems [194–196] and in mice [197–199]. Genistein effects clearly depend on the dosage with pro-estrogenic activities being dominant at lower and anti-apoptotic activities at higher concentrations [200], similar observations have been reported by Konstantakopoulos et al. [201]. The phytoestrogens resveratrol and quercetin present in the Mediterranean diet have also been reported to exert anti-angiogenic activities through the inhibition of endothelial cell proliferation yet only at high concentrations [202]. Both compounds are believed to act via the ER α [203–205] a fact that sheds some doubt on how much their anti-angiogenic activity can be generalized. Several microarray based studies have been carried out (see Table 1) yet there are no clues to the putative anti-angiogenic activities nor have endothelial cells been considered.

Conclusions

Gene expression profiling has provided important information on the identification of the pathways involved in cellular processes or in the response to external stimuli has not matched reality. Many microarray studies, however, fall short of rigorous experimental and statistical methods, often the simple “fold change” value is used without any statistics or simple t-tests are performed without consideration of the heavily multiparametric nature of global

expression analyses. Only recently has array quality dramatically improved with widespread use of high quality commercial microarrays produced in a highly controlled manner. Yet there is a biological issue in addition to the quality aspect that makes the use of microarrays much less straightforward than expected. Biological systems are complex and variable. The actual state of transcription of a given depends on the number, the type, the position (distance to the transcription start or position relative to other regulatory elements) and the composition of transcription factor binding sites, the long and short range chromatin structure including post-translational histone modifications, the actual sequence, possible cytosine methylation and the availability of transcriptional co-activators and -repressors as well as the presence of specific non coding RNAs that influence mRNA stability. The same drug may therefore elicit very different effects on gene transcription in different cell lines or tissues and the activation of a specific signaling pathway or of a specific transcription factor may result in very different expression profiles depending on the cellular context as well as experimental, physiological or pharmacological concentrations.

In cancer research it is of paramount importance that, in addition to microarray studies on tumor cells and on transcriptional modulation in tumor cells, the influence of drugs on the microenvironment is studied with functional genomics. We have previously shown how breast cancer cells can be classified for their metastatic potential based on expression of genes related to matrix and stroma [128]. In this review we broadly analyze how gene expression of endothelial cells, based on microarray studies, can identify new pathways and explain response behaviour.

In particular, the NF κ B, TNF- α , TGF- β , Akt and MAPK pathways emerge as central targets for anti-angiogenic effects that are shared by many of the drugs tested. Future gene expression studies should therefore study these pathways more systematically eventually choosing very few representative compounds to be studied at a wide range of concentrations and time intervals. Angiogenesis assays in vitro and in vivo may help to select the “best” angiogenesis inhibitor among a list of drugs with similar target specificities and eventually, the knowledge of the precise molecular mechanism may help to identify potentially synergistic drug combinations if, for example, different kinase inhibitory activities can be identified that inhibit NF κ B activation at different steps.

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