



## Review

## Blocking the FGF/FGFR system as a “two-compartment” antiangiogenic/antitumor approach in cancer therapy



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## ABSTRACT

Fibroblast growth factors (FGFs) are a family of pleiotropic factors produced by stromal and parenchymal tumor cells. Even though FGFs have been firstly characterized as angiogenic factors, they exert autocrine and paracrine functions not only on endothelial cells but also on tumor cells and other stromal components. Thus, the FGF/FGF receptor (FGFR) pathway may represent a key player in tumor growth by regulating the complex cross-talk between stromal and tumor compartments.

The ligand dependent or independent activation of the FGF/FGFR system by gene upregulation, oncogenic mutation or amplification occurs in a variety of human tumors and is implicated in various key steps of tumor growth and progression. In addition, FGF/FGFR activation has been described as a mechanism of tumor escape in response to antiangiogenic/anti-VEGF therapies.

Experimental and clinical evidences provide a compelling biologic rationale for the development of anti-FGF/FGFR targeting agents in cancer therapy. However, the development of drugs specifically targeting the FGF/FGFR pathway proved to be difficult, also due to the high redundancy and pleiotropic effects of FGF and FGFR family members. On the other hand, the possibility to develop “two-compartment” targeting agents endowed with both antiangiogenic and antitumor activities remains promising.

Here we will review the preclinical and clinical approaches and potential therapeutics currently available to block the FGF/FGFR system in human cancer.

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## 1. The FGF/FGFR system

### 1.1. Fibroblast growth factors

Fibroblast growth factors (FGFs) are secreted proteins that act as paracrine, autocrine or endocrine factors. The FGF family encompasses 22 members, grouped into seven subfamilies on the basis of phylogenetic analysis and sequence homology [1]. The subfamilies FGF1/2/5, FGF3/4/6, FGF7/10/22, FGF8/17/18 and FGF9/16/20 act as canonical FGFs; FGF11/12/13/14 are intracellular factors acting in an FGF receptor (FGFR) independent manner; FGF19/21/23 subfamily members function as hormones [2].

Canonical FGFs are paracrine factors that mediate their biological responses by binding to and activating tyrosine kinase (TK) FGFRs. The interaction with heparin/heparan sulfate (HS) proteoglycans (HSPGs) plays a pivotal role in mediating the biological activity of FGFs, leading to the formation of signalling FGF/FGFR/HSPG ternary complexes [3]. Moreover, HSPGs sequester FGF molecules near the site of action, providing a reservoir for the growth factor and allowing the formation of extracellular matrix (ECM)-associated FGF gradients [4].

Canonical FGFs mediate a plethora of functions during development. They are involved in patterning of germ cell layers, formation of body axes, induction of organogenesis and morphogenesis. Moreover, FGFs display homeostatic functions in the adult, being involved in tissue repair and remodelling processes. Finally, deregulation of FGF signalling can contribute to pathological diseases, including cancer. In this context, several alterations affecting the FGF/FGFR system have been reported in tumors, including gain- or loss- of function, altered gene expression or changes in binding specificity [2].

Intracellular FGFs act as intracellular signalling molecules in a FGFR-independent manner; they play a major role in neuronal functions at postnatal stages by interacting with intracellular domains of voltage-gate sodium channels and with the neuronal mitogen-activated protein kinase scaffold protein islet-brain-2 [5].

Hormone-like FGFs exhibit poor affinity for HSPGs, resulting in more diffusive properties through blood circulation [6]. These FGFs depend on Klotho co-receptors (see below) to activate intracellular signalling responses [7]. FGF19 (orthologue of murine FGF15) acts as a growth/differentiation factor in the heart and brain at embryonic stages and plays a crucial role in regulating hepatic bile acid production [8]. FGF21 is a metabolic regulator of lipolysis in the white adipose tissue [9] and FGF23 acts as a physiological regulator of phosphate and active vitamin-D blood levels [10].

The wide-ranging biological roles of FGFs, the variety of activated signalling pathways and the complex and dynamic expression of FGF ligands and receptors implies that the FGF/FGFR system must be tightly regulated.

### 1.2. Fibroblast growth factor receptors

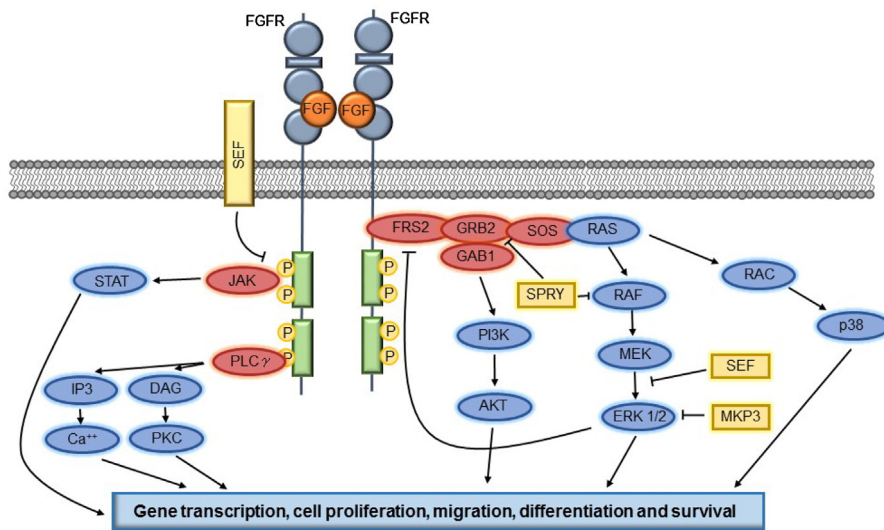
In mammals, FGFRs are encoded by four distinct genes (*FGFR1-4*). FGFRs consist of three extracellular immunoglobulin-like (Ig) domains (D1-3), a single transmembrane helix domain and an intracellular TK domain [11]. D2 and D3 domains are responsible for FGF binding. FGFRs show diverse specificities for FGF ligands. In addition, alternative splicing of the D3 domain that may occur in FGFR1, 2 and 3, but not in FGFR4, generates "IIIb" and "IIIc" isoforms

with additional ligand-binding properties. For instance, FGFR2IIIb binds FGF7 and FGF10, but not FGF2, whereas the FGFR2IIIc isoform binds FGF2 and FGF18, but not FGF7 and FGF10 (see Ref. [12] for further details about the ligand-binding properties of the different FGFRs). Interestingly, FGFR1-3IIIb and FGFR1-3IIIc isoforms often display differential expression in epithelial and mesenchymal tissue, respectively [13].

FGFRs interact with HSPGs via the D2 domain. The formation of a 2:2:2HSPG/FGF/FGFR ternary complex [14] causes receptor dimerization with conformational shift in receptor structure that leads to *trans*-phosphorylation of multiple residues in the intracellular TK domain. Receptor phosphorylation activates multiple signal transduction pathways that generate distinct cellular responses. As summarized in Fig. 1, major substrates of FGFR TK are the intracellular specific adaptor protein FGFR-substrate-2 (FRS2) and phospholipase-C $\gamma$  (PLC $\gamma$ ) [15]. Activated FRS2 allows the recruitment of the adaptor protein GRB2 that in turn recruits SOS or GAB1 to the signal complex. The recruitment of SOS activates RAS and the downstream RAF/mitogen-activated protein kinase (MAPK) pathway. The downstream effect of this pathway is mainly cell proliferation, even though cell differentiation or cell cycle arrest can also be induced depending on the different cellular context. The recruitment of GAB1 causes the PI3K-mediated activation of the AKT antiapoptotic pathway. PLC $\gamma$  leads to the activation of protein kinase C (PKC) that sustains MAPK and AKT pathways and plays a role in cell migration. Other pathways may be activated in different cell subtypes, including p38 MAPK, JAK-STAT and RSK2 [16].

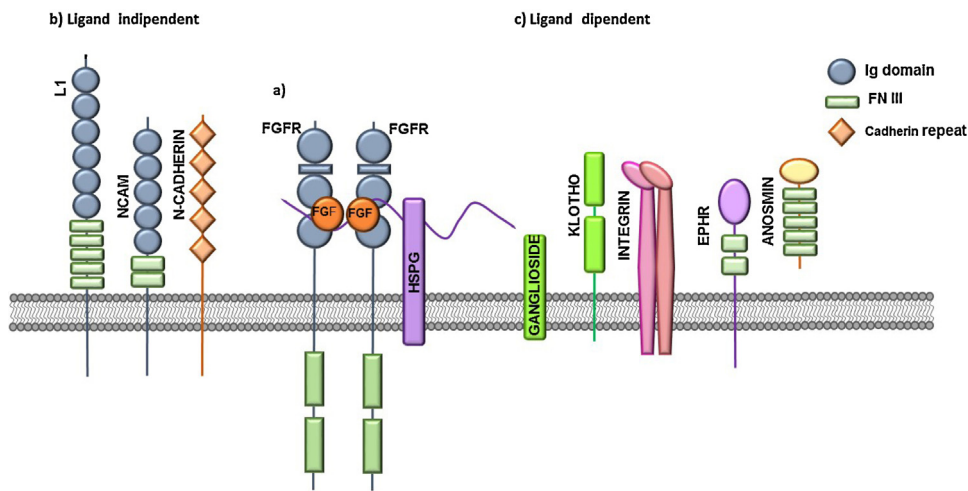
Several extracellular and intracellular mechanisms have been described able to regulate/attenuate FGFR signalling at different levels. FGFRs are internalized upon receptor activation [17], inducing receptor degradation or recycling. Relevant to this point, N-glycosylation of the receptor affects the assembly of the FGF/FGFR1/HSPG complex [18] and internalization of FGFR2 [19]. At intracellular level, MAPK signalling may phosphorylate threonine residues on FRS2, inhibiting the recruitment of GRB2 [20]. Sprouty proteins are negative modulators that compete for GRB2 binding by preventing RAS activation or directly binding RAF and disrupting MAPK signalling [21]. In addition, FGFs can induce the activation of phosphatases, including SEF and MAPK-phosphatase 3 (MKP3). SEF interacts directly with FGFRs, thus preventing their activation, whereas both enzymes can dephosphorylate and inactivate ERK<sub>1/2</sub> [22].

Different molecules can act as cell surface co-receptors for FGFs (Fig. 2). As already mentioned, HSPGs are required for a productive FGF/FGFR interaction that enables FGFR signalling [23]. For this reason, structural modifications of the HS chains deeply affect FGFR signalling and can be responsible for its fine-tuning. As an exception, hormone-like FGFs have reduced affinity for HSPGs and their activity depends on the presence of Klotho proteins as co-receptors. Cell surface  $\beta$ -Klotho and  $\alpha$ -Klotho are co-factors for FGF19/21 and FGF23, respectively, and convert FGFRs into high affinity receptors for endocrine FGFs, limiting nonspecific/off-target signalling. The cell membrane ganglioside GM1 acts as a FGF co-receptor by interacting with FGF2 and promoting its biological activity in endothelial cells [24]. In addition,  $\alpha$ v $\beta$ 3 integrin promotes FGF-mediated endothelial cell proliferation, motility, and FGFR1 recruitment [25], thus contributing to the cross-talk between FGFR and integrin signalling [26]. Neural cell adhesion molecule (N-CAM), neuronal cadherin (N-cadherin) and L1 can activate FGFR1-2



**Fig. 1.** FGFR signalling pathways.

FGFs bind to FGFRs, inducing receptor dimerization and transphosphorylation of their TK domain. This, in turn, leads to the docking of adaptor proteins and consequent activation of downstream signalling pathways. Activated FRS2 recruits and activates RAS-RAF-MEK-ERK1/2 and PI3K-AKT pathways involved in cell proliferation and antiapoptotic activity, respectively. Recruitment and phosphorylation of PLC-γ induces PKC activation and intracellular Ca<sup>2+</sup> release, events that regulate cell motility. The negative regulators MKP3 and SPRY can modulate FGFR signalling whereas SEF may also interfere with ligand binding.



**Fig. 2.** FGFR co-receptors.

(a) FGFs bind to FGFRs and HSPGs, leading to the formation of a ternary complex that induces receptor dimerization and activation. Moreover, various ligand-independent (b) and ligand-dependent (c) cell-surface proteins and glycolipids may act as FGFR co-receptors.

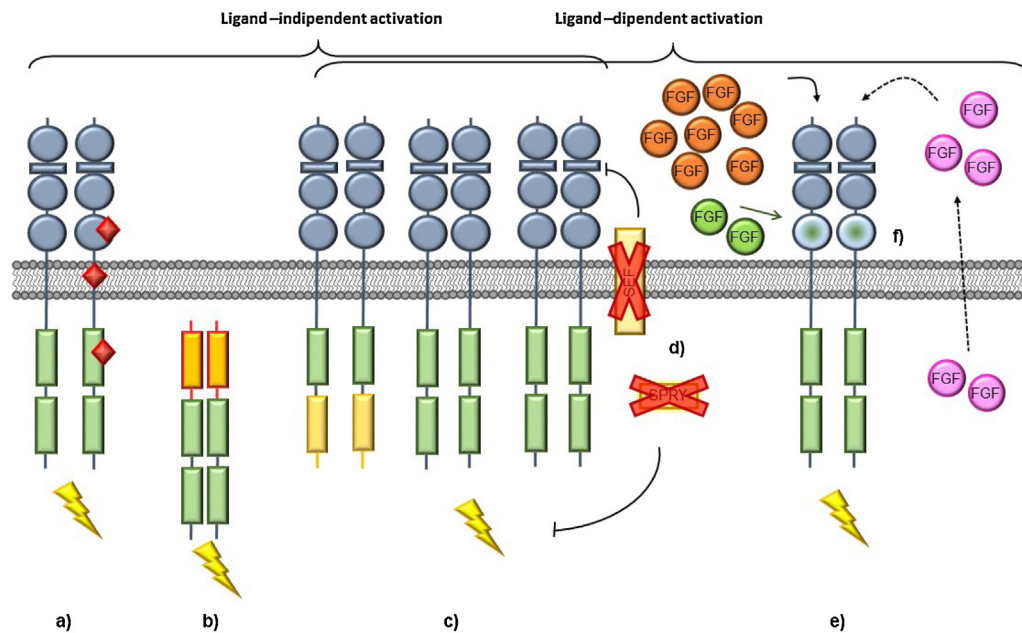
in the absence of canonical FGFR ligands and this interaction is mediated by the acid box motif in the linker region between the D1 and D2 Ig-like loops of the receptor [27]. Therefore, N-CAM and N-cadherin act as a nonconventional FGFR1 ligand, promote receptor stabilization and exert a peculiar control on FGFR intracellular trafficking [28]. Extracellular matrix-associated glycoprotein anosmin-1 binds FGFR1 in a HS-dependent manner, modulating FGFR signalling during development [29]. Finally, EphA4 has been identified as a binding partner for FGFRs. The interaction occurs between the juxtamembrane region of FGFR and the cytoplasmic domain of EphA4 and leads to enhanced level of MAPK signalling and stimulation of cell proliferation [30].

## 2. The FGF/FGFR system in endothelial cells

Angiogenesis is an essential process for tumor growth and progression, since the large-scale growth of a tumor ultimately

requires an adequate blood supply [31]. Indeed, once a tumor lesion exceeds a few millimeters in diameter, hypoxia and nutrient deprivation trigger an 'angiogenic switch' to allow the tumor to progress [32]. In 1980s, the purification to homogeneity of tumor angiogenic proteins led to the first identification of the two heparin-binding angiogenic growth factors FGF1 and FGF2 [33,34]. At present, FGF1 and FGF2 still represent the prototypical and best studied members of the canonical FGF subfamily. *In vivo* they exert a potent pro-angiogenic effect in different experimental models, including the chick embryo chorioallantoic membrane (CAM) [35], rabbit/mouse cornea [36] and murine subcutaneous Matrigel plug [37] assays.

Besides FGF1 and FGF2, only scattered pieces of information indicate that other FGFs show clear pro-angiogenic properties (like FGF4 and FGF8) whereas few or controversial data have been reported for the remaining members of the FGF family (see Ref. [38] for an extensive review). Interestingly, the apparent redundancy of the FGF family may lead to complementary/compensatory actions,



**Fig. 3.** Deregulation of the FGF/FGFR system in cancer.

a) Activating mutations (red diamonds) can occur in the extracellular, transmembrane or TK domain of FGFR, leading to constitutive dimerization and activation of the receptor. b) Chromosomal rearrangements may lead to intragenic translocations that result in the expression of fusion proteins whose dimerization triggers constitutive activation of the FGFR signalling. c) FGFR overexpression can be induced by gene amplification, translocation or aberrant transcriptional regulation. FGFR overexpression can also be accompanied by altered C-terminal splicing (light yellow boxes) that may interfere with receptor internalization with consequent accumulation of the receptor at the cell surface. d) Negative regulators (e.g. SEF) can be down modulated, thus increasing FGFR signalling. e) Cancer cells may induce stromal cells to overexpress FGFs (orange), thus activating a paracrine loop of stimulation. In addition, FGFs (pink) are produced by cancer cells and act in an autocrine fashion. f) Switching between alternatively spliced receptor isoforms may induce imbalanced FGFR signalling with altered specificity for FGF ligands (green).

making difficult the identification of the biological significance of the various FGFs by the gene knockout approach. For instance, FGF2 knockout and FGF1/FGF2 double-knockout mice develop normally with only mild phenotypic defects in their wound healing capacity associated with FGF1/FGF2 deletion [39].

Of note, human umbilical vascular endothelial (HUVE) cells express several canonical FGFs (including FGF1, FGF2, FGF5, FGF7, FGF8, FGF16, FGF18) and two FGF homologous factors (FGF11 and FGF12) [40], thus suggesting that FGFs may also exert autocrine functions in endothelium.

Even though a comprehensive study is still missing, endothelial cells express different members of the FGFR family, FGFR1IIIc being the most represented receptor while FGFR2-IIIc and FGFR3-IIIc are expressed at lower levels [40]. Experiments performed on FGFR1 and FGFR2 null mice in both endothelial and hematopoietic cells indicate that these receptors are not required for vascular homeostasis or physiological functions. However, FGFR signalling in endothelial cells plays a pivotal role in tissue repair and neovascularization following injury, pointing to endothelial cell FGFRs as a target for the therapy of diseases characterized by an aberrant vascular proliferation [41].

The formation of HSPG/FGF/FGFR ternary complexes causes receptor dimerization and *trans*-phosphorylation of multiple residues in the intracellular FGFR TK domain. This leads to the activation of a complex “pro-angiogenic phenotype” in endothelial cells that recapitulates several aspects of the *in vivo* angiogenesis process, including modulation of endothelial cell proliferation, migration, protease production, integrin and cadherin receptor expression, and intercellular gap-junction communication (summarized in Ref. [42]). For instance, FGF1, FGF2, FGF4, FGF7 and FGF8b bind and activate FGFR1 or FGFR2, stimulating endothelial cell proliferation [43]. In addition, FGFs can modulate extracellular matrix degradation, as reported for the capacity of FGF1 and FGF2 to induce the secretion of MMP1 and MMP3 in endothelial cells [44]

and the capacity of FGF2 to stimulate the shedding of endothelial membrane vesicles containing MMP1, MMP9 and metalloprotease inhibitors TIMP-1 and TIMP-2 [45]. Also, various studies demonstrate that FGFs promote endothelial cell migration, as shown by the ability of FGF1, FGF2, FGF7, FGF16 and FGF18 to induce a chemotactic response in endothelium [43,46].

### 3. Deregulation of the FGF/FGFR system in cancer cells

An aberrant regulation of the FGF/FGFR system may occur in human tumors, leading to the deregulated activation of ligand-dependent or ligand-independent FGFR signalling. As summarized in Fig. 3, this may represent the consequence of activating FGFR mutations that occur in the extracellular, transmembrane or TK domain of the receptor; chromosomal rearrangements that result in the expression of FGFR signalling fusion proteins; FGFR overexpression induced by gene amplification, translocation, aberrant transcriptional regulation or down-modulation of negative regulators; FGF overexpression by stromal and/or tumor cell, leading to the activation of autocrine/paracrine loops of stimulation. Clearly, while FGFR mutations are anticipated to impact mainly the tumor cell behavior, FGF overexpression by tumor cells may exert both autocrine and paracrine effects, thus contributing to the epithelial/stroma cross-talk that occurs in the tumor microenvironment. In addition, depending on the molecular mechanism responsible for the ligand-dependent or ligand-independent deregulation of FGFR signaling in a given neoplasm, different approaches can be envisaged aimed at targeting the FGF/FGFR system at the extracellular or intracellular level (see below).

#### 3.1. Activating mutations

The screening from 210 different human cancers of 1000 somatic mutations in the coding exons of 518 protein kinase genes

**Table 1**  
Chemotherapeutics, other drugs and natural products endowed with antiangiogenic activity. The antiangiogenic activity of these compounds has been demonstrated to be due, at least in part, to their capacity to inhibit FGF production and/or FGFR expression or to interfere with the intracellular signalling triggered by the FGF/FGFR system in endothelial cells (see references for further details).

Chemotherapeutics	Main tumor target(s) (FDA approved)	Ref
6-methylmercaptopurine-riboside	acute lymphatic leukemia	[159]
topoisomerase-I inhibitor topotecan	small cell lung cancer, metastatic ovarian cancer	[160]
medroxyprogesterone-acetate	endometrial cancer, breast cancer in post menopausal women	[161]
Tamoxifen	breast cancer in post menopausal women	[162]
Thalidomide	multiple myeloma	[163]
quinazoline-derived $\alpha$ 1-adrenoreceptor antagonist doxazosin	prostate cancer	[164]
6-thioguanine	acute myelogenous leukemia	[165]
Atiprimod	relapsed acute lymphoblastic and myeloid leukemias	[166]
etoposide	small cell lung cancer, testicular cancer	[167]
combination of tegafur and uracil (UFT)	advanced colorectal cancer, various cancer <sup>a</sup>	[168]
Other drugs	Original therapeutic indication	
Tranilast	anti-allergic drug	[169]
Spironolactone	heart failure	[170]
Zoledronic acid	various skeletal complications	[171]
Cidofovir	cytomegalovirus retinitis in AIDS patients	[172]
Indomethacin	nonsteroidal anti-inflammatory drugs	[173]
Celecoxib		[174]
Cerivastatin	hypercholesterolemia	[175]
Ticlopidine (derivatives)	platelet antiaggregating agent	[176]
Triamcinolone acetonide	intraocular disorders	[177]
HyPE (secretory phospholipase-A2 inhibitor)	asthma	[178]
Natural products	Source	
curcumin	<i>Curcuma longa</i>	[179]
epigallocatechin-3-gallate	green tea	[180]
Gleditsia sinensis	fruit extract	[181]
1,2,3,4,6-penta-O-galloyl-beta-D-glucose	<i>Galla Rhois</i>	[182]
4-O-methylgallic acid	dietary legume <i>Canavalia gladiata</i>	[183]
resveratrol	grapes and wine	[184]
glyceollins	soybean	[185]
alliin	garlic	[186]
stilbene glycosides	<i>Boswellia papyrifera</i>	[187]
salvicine	<i>Salvia prionitis Hance</i>	[188]
polymethoxyflavonoid nobiletin	citrus	[189]
aplidine	marine-derived depsipeptide	[190]
phillinopside A,	sea cucumber <i>Pentacta quadrangulata</i>	[191]
psammaphin A	marine sponge	[192]
carrageenan	edible seaweeds	[193]
carotenoids	marine algae	[194]
epoxydocosapentaenoic acids (EDPs)	omega-3 dietary fatty acids (fish oil)	[195]
1-O-alkylglycerols	fish liver oils	[196]
Neovastat (AE-941)	cartilage	[197]

<sup>a</sup> Approved in UK and Japan.

highlighted various components of the FGF signalling pathways as the most commonly mutated genes in the subset of non-synonymous mutations [47]. For instance, ~50% of bladder cancers have somatic mutations in the *FGFR3*-coding sequence [48], more than half of the mutations occurring at a single position (S249C) in the extracellular domain of the receptor. This mutation leads to the formation of an aberrant intermolecular cysteine bridge that results in ligand-independent constitutive dimerization and activation of the receptor [49]. *FGFR3* mutations have also been identified in many other cancer types, including cervical cancers [50], multiple myeloma (MM) [51,52], prostate cancers [53], spermatocytic seminomas [54] and oral squamous carcinomas [55]. Other mutations located in the TK domain can change the FGFR conformation, leading to a constitutive ligand-independent receptor activation, as observed for *FGFR4* in the childhood rhabdomyosarcoma [56].

At variance with *FGFR* genes, *FGF* mutations are rare in human cancers and their impact on cancer biology is unclear. Indeed, to the best of our knowledge, somatic mutations have been described only for *FGF9* in colorectal and endometrial cancers [57]. They are predicted to result in loss-of-function and it is not known whether these mutations participate in tumor formation.

### 3.2. Gene overexpression and amplification

Elevated *FGFR* levels can be observed in human cancers as the consequence of deregulated gene transcription or amplification. Also in this case, this will lead to the activation of *FGFR* signalling in a ligand-independent manner. At variance with the activation of *FGFR3* by somatic mutations, *FGFR3* gene amplification has been rarely described in cancer [58]. In contrast, both *FGFR1* and *FGFR2* amplifications are more commonly found. For instance, amplification of the chromosomal region 8p11–12, the genomic location of *FGFR1*, is one of the most common focal amplifications in breast cancer [59]. It occurs in approximately 10% of breast tumors and predominantly in estrogen receptor (ER)-positive cancers [59]. Recent studies have demonstrated focal *FGFR1* amplification in non-small cell lung carcinoma cells in 3% of lung adenocarcinomas and 21% of squamous cell carcinomas [60,61]. *FGFR1* amplifications have been observed also in oral squamous carcinomas [62] and are found at a low incidence in ovarian cancer [63], bladder cancer [58] and rhabdomyosarcoma [64]. As to *FGFR2*, approximately 10% of gastric cancers show *FGFR2* amplification, which is associated with poor prognosis in diffuse-type cancers [65]. In addition, *FGFR2* amplification occurs in approximately 2% of breast cancers and breast cancer SUM52PE and MFM-223 cell lines

**Table 2**  
Natural FGF2-trap molecules.

FGF2-trap molecule <sup>a</sup>
TSP-1
fibstatin (fibronectin fragment)
gangliosides
PDGF
α <sub>2</sub> -macroglobulin
PTX3
heparin, free HSPGs
CXCL13
CXCL4
soluble form of the extracellular portion of FGFR1

<sup>a</sup> See [114,198] and references therein.

are sensitive to inhibition of the FGF/FGFR system [66]. Of note, breast and gastric cancer cell lines harbouring *FGFR2* amplifications predominantly express the IIIb isoform of the receptor. Thus, neutralizing FGFR2-IIIb-specific antibodies (like the GP369 antibody) can suppress ligand-induced phosphorylation of the receptor and downstream signalling, leading to the inhibition of tumor cell proliferation *in vitro* and *in vivo* [66].

### 3.3. Chromosomal translocations

Chromosomal translocations can lead to the expression of fusion proteins with potent oncogenic function. Some of the strongest evidences linking FGFR signalling to oncogenesis derive from the study of haematological malignancies in which FGFR translocations have been observed. Several FGFR intragenic translocations have been identified that typically result in a fusion protein comprising the N-terminus of a transcription factor fused to the TK domain of FGFR1-3 (77), leading to the constitutive dimerization of the fusion protein and TK activation. For example, ZNF198-FGFR1 and BCR-FGFR1 fusion proteins have been found in EMS (8p11 myeloproliferative syndrome) [67] and fusion of ETV6 to FGFR3 has been reported in peripheral T-cell lymphoma with a t(4;12)(p16;p13) chromosomal translocation [68]. A different translocation has been found in MM in which 15% of tumors harbor a t(4;14) translocation that links *FGFR3* at 4p16.3 to the immunoglobulin heavy chain *IGH* locus at 14q32 [52]. This translocation is intergenic, with the breakpoints occurring ~70 kb upstream of *FGFR3*, and brings *FGFR3* under the control of the highly active *IGH* promoter. The ultimate effect of this translocation is the overexpression of FGFR3 out of context, that may result in aberrant hypersensitivity to ligands [69] or to ligand-independent signalling. The t(4;14) translocation is associated with poor prognosis in MM, *FGFR3* representing an attractive therapeutic target for this tumor. Interestingly, oncogenic *FGFR3* gene fusions have been identified also in bladder cancer in which genomic *FGFR3* translocations involve two different fusion partners that generate constitutively activated FGFR3 kinases [70].

### 3.4. Aberrant autocrine and paracrine ligand signalling

Most of the genomic aberrations discussed above lead to constitutive receptor activation and ligand-independent signalling. On the other hand, also the activation of a ligand-dependent signalling may play an important role in the pathogenesis of cancer. This may occur via the activation of autocrine mechanisms of stimulation due to FGF production by cancer cells or may represent the consequence of the paracrine activity exerted on cancer cells by FGF(s) produced by the surrounding stroma. In this context, several murine models have shown that ectopic FGF expression can promote cancer and that FGF overexpression by epithelial cells may induce carcinogenesis through an autocrine loop of stimulation. Examples include: FGF8 expression driven by the *MMTV-LTR* promoter that

causes the occurrence of lobular-type mammary adenocarcinomas in mice at 1 year of age [71]; FGF8 expression in prostate epithelium that initiates prostatic intraepithelial neoplasia and prostatic cancer when occurring in a *Pten* haploinsufficient background [72]; the conditional expression of FGF10 in lung epithelium that induces pulmonary tumors [73].

The first strong evidence for a role of autocrine FGF signalling in driving human tumorigenesis comes from seminal studies on melanomas that express high levels of FGFR1 and FGF2 [74]. Since then, elevated levels of different members of the FGF family have been found in numerous human cancers [38]. Amplification of *FGF1*, resulting in increased FGF1 expression, has been frequently observed in ovarian cancer and is associated with poor survival [75]. An aberrant autocrine FGF2/FGFR1-IIIc feedback loop of stimulation has been found in human non-small-cell lung cancer cell lines resistant to the epidermal growth factor receptor (EGFR) antagonist gefitinib [76]. Similar results were obtained for human head and neck squamous carcinoma cell lines. Indeed, FGF2 and FGFR co-expression frequently occurs in these cells, leading to an autocrine loop of stimulation that may involve also EGFR activation [77]. Several FGFs, including FGF1, FGF2, FGF5, FGF6, FGF7, FGF8, FGF9, FGF10, FGF17, FGF18 and FGF19 are upregulated in human prostate cancer [38] and murine studies have demonstrated the complex FGF/FGFR-dependent interplay between the epithelial and mesenchymal compartments in these tumors [78].

Besides the aberrant activation of autocrine loops of stimulation, paracrine FGF production might also contribute to tumorigenesis. Increased plasma levels of FGF2 and other FGFs are found in multiple cancer types [79]. This partly reflects the increased release of FGFs as tumors invade and degrade the extracellular matrix [80], free FGF molecules acting in turn as paracrine factors. Tumor cells may also induce FGF2 release from the stromal inflammatory infiltrate [81] that may promote tumor survival via a paracrine loop of stimulation and trigger a pro-angiogenic response. Neovascularization can be further augmented by an autocrine production of angiogenic FGF2 by endothelial cells [81].

## 4. The role of the FGF/FGFR system in tumor/stroma cross-talk

Tumors are heterogeneous cellular entities composed of cancer cells and cells of the microenvironment in which they reside [82]. Similar to stromal cells in normal epithelial tissues, stromal cells forming the tumor microenvironment include inflammatory cells (lymphocytes, macrophages and mast cells), fibroblasts and vascular components. The genetic basis of carcinogenesis involves the acquisition of multiple genetic mutations in epithelial cells [83]. Then, tumor cells transform the surrounding stroma into a so-called “activated stroma” that, in turn, can strongly influence/support tumorigenesis and tumor progression [82]. Thus, a reciprocal dynamic interaction occurs between tumor cells and activated stromal cells during cancer initiation and progression. This tumor-host communication interface mediates the proliferation of tumor cells at the primary site, the process of tumor angiogenesis, the migration and survival of cancer cells in the vasculature, and the growth of metastatic lesions at secondary sites through the autocrine/paracrine secretion of ECM proteins and growth factors [84]. Also, emerging evidences emphasize the ability of stromal cells to modulate tumor cell resistance or sensitization to different classes of therapeutics, depending on the specific microenvironmental context [85]. Thus, the tumor microenvironment has become the focus of intense research, with the understanding that the alterations that occur in the tumor stroma might provide important prognostic hints, can affect the

evaluation and selection of candidate drugs, and the generation of new therapeutic targets for various cancers.

As stated above, the FGF/FGFR system may play a critical role during carcinogenesis by regulating the cross-talk between epithelial and stromal compartments. Enhanced FGFR signalling may have myriad effects on tumor biology, including promotion of proliferation, resistance to cell death, augmented motility and invasiveness, increased neovascularization, enhanced metastatic spreading and resistance to chemotherapy and radiation. Several studies have highlighted the importance of FGF/FGFR signalling in mediating epithelial-stromal interactions during prostate carcinogenesis [86,87]. For instance, overexpression of FGF10 in prostatic stroma by lentiviral delivery results in epithelial hyperproliferation that correlates with upregulation of androgen receptor expression [78]. Furthermore, the combination of FGF10 stromal overexpression with the epithelial expression of a constitutively activated form of Akt (myristoylated Akt1) results in cooperative effects on prostate tumorigenesis [78]. However, the translational significance of these murine models for human cancer remains unclear since FGF10 has not been found to be significantly expressed in human prostate cancer [88]. Nonetheless, it is conceivable that other members of the FGF family with receptor-binding specificities similar to FGF10 may be relevant in human prostate cancer, including FGF7 and FGF22. Also, activation of prostate tumor cell growth through androgen-independent stromal growth factor signals, such as FGF7, may occur under conditions of androgen deprivation [89]. These data may help to develop new therapeutic strategies to target the prostate tumor stroma under androgen-manipulated conditions. Interestingly, a recent study has demonstrated that downregulation of the micro-RNAs miR-15 and miR-16 in prostate cancer-associated fibroblasts (CAFs) promotes tumor growth and progression through the reduced post-transcriptional repression of FGF2 and of its receptor FGFR1 [90]. Moreover, reconstitution of miR-15 and miR-16 significantly impaired the tumor-supportive capability of stromal cells *in vitro* and *in vivo*, thus enforcing the therapeutic concept aimed at reconstituting the expression of these micro-RNAs in advanced prostate cancer [90].

Besides its autocrine role in human melanoma, FGF2 may exert also paracrine functions in stroma formation during the progression of this tumor. Indeed, FGF2 appears to act on fibroblasts and endothelial cells in order to modulate the tumor microenvironment, thus favoring melanoma growth, neovascularization, invasion, and metastasis [91].

A recent study has identified FGF4 as a growth-promoting and radioprotective factor produced by CAFs in cervical cancer, leading to the activation of a tumor cell/CAF cross-talk that may confer a survival signal to overcome cell death in irradiated cervical cancer cells [92]. In addition, FGF2, FGF7 and FGF10 are implicated as autocrine and paracrine mediators of tumor-stroma interactions in pancreatic ductal adenocarcinomas [93]. In these tumors, mast cells, macrophages, and tumor cells overexpress VEGF-A, VEGF-C, and FGF2 and this was highly correlated to intratumor microvessel density [94].

Interestingly, the FGFR inhibitor PD173074 abrogates the rescue effect exerted by fibroblast supernatant on the cytostatic effects exerted by the TK inhibitor lapatinib on esophageal squamous-cell carcinoma cells [95]. These findings suggest a role for FGF/FGFR signalling in tumor drug resistance induced by stromal fibroblasts and suggest that a combination therapy with lapatinib and a FGF/FGFR inhibitor might be effective in overcoming therapeutic resistance in esophageal squamous-cell carcinoma.

FGF2 is considered a potent angiogenic cytokine in MM. Both MM-derived cell lines and tumor cells isolated from the bone marrow of MM patients express and secrete FGF2, cell sorting studies indicating tumor cells as the predominant source of FGF2 in MM bone marrow [96,97]. Besides its pro-angiogenic functions, FGF2

plays also an important role in mediating tumor-stromal cell interactions in MM [98]. Indeed, bone marrow stromal cells (BMSCs) from MM patients express FGFR1–4 and stimulation of BMSCs with FGF2 induces a time- and dose-dependent increase of interleukin-6 (IL-6), a potent growth and survival factor for MM cells [99]. Accordingly, IL-6 secretion is fully abrogated by anti-FGF2 antibodies, while stimulation with IL-6 enhances FGF2 expression and secretion by MM cell lines as well as by primary MM tumor cells, an effect inhibited by anti-IL-6 antibodies. These findings demonstrate a paracrine interaction between myeloma and bone marrow stromal cells triggered by the mutual stimulation of FGF2 and IL-6.

Finally, FGFs may activate a pro-inflammatory phenotype in endothelium [100], indicating that the FGF/FGFR system may influence also the immune/infiltrate component of tumor milieu.

All these considerations highlight the FGF/FGFR system as a critical player in tumor/stroma cross-talk in several cancer types. Thus, blocking the FGF/FGFR system may represent a “two-compartment” antitumor/antiangiogenic approach in cancer therapy.

## 5. Inhibition of the FGF/FGFR system: therapeutic approaches

Various approaches can be envisaged to neutralize the aberrant activation of the FGF/FGFR system that occurs in cancer, with its consequent effects on both parenchymal and stromal tumor compartments. In particular, we can distinguish between the possibility to prevent/modulate the FGF-FGFR interaction that occurs at the extracellular level or to impair the intracellular signal transduction pathways triggered by the deregulated activation of the receptor.

### 5.1. Inhibition of FGF/FGFR system at the extracellular level

#### 5.1.1. Inhibition of the expression of FGF/FGFR/FGFR co-receptors

A first approach in order to prevent the aberrant activation of the FGF/FGFR system is represented by the possibility to suppress the production of FGFs. To this regard, the capacity to inhibit the production of angiogenic growth factors is a common feature of different chemotherapeutics (like taxane [101] and docetaxel [102]) that downregulate FGF expression by exerting their antiproliferative effect on FGF-producing tumor cells (Table 1). In addition, an interesting antiangiogenic and antitumor activity is exerted *in vivo* by antisense FGF2 oligonucleotides that block FGF production by both tumor and endothelial cells [74,103], as well as by various inhibitors of second messengers involved in FGF expression (*i.e.* PKC, JAK, PI-3K, c-jun, ERK, JNK, STAT1 and STAT3) [104]. Finally, natural products, including genistein, fumagillin, curcumin, salivicine and the green tea component epigallocatechin-3-gallate (Table 1), oxidized low-density lipoproteins [105] and some endogenous cytokines [106] have been reported to negatively regulate the expression of FGFs.

Besides FGFs, also the expression of FGFRs and their co-receptors can be suppressed for therapeutic purposes. To this regard, IFN- $\gamma$  and IL-1 can down-regulate FGFR expression [107]. In addition, transfection with FGFR1 antisense cDNAs, as well as reduction of FGFR2 expression by the synthetic retinoid fenretinide, impaired FGF2-dependent proliferation and migration of endothelial cells *in vitro* [108] and tumor angiogenesis *in vivo* [109].

Examples of how modulation of cell surface FGFR co-receptors can be exploited as an antiangiogenic/antitumor strategy are represented by antithrombin, that inhibits endothelial cell proliferation by down-regulating the surface expression of perlecan [110], and specific inhibitors of the synthesis of complex gangliosides, including fumonisins B<sub>1</sub>, D-threo-1-phenyl-2-decanoylamino-3-morpholino-1-propanol, and

**Table 3**  
Inhibitors of FGF/FGFR-mediated intracellular signalling and biological activity.

Targeted second messenger	Inhibitor <sup>a</sup>
Pan-TK	TKI258, tyrphostin 23, genistein, herbimycin A, axitinib, brivanib, cabozantinib, dovotinib, nintedanib, oratinib, pazopamib, ponatinib, regorafenib, sorafenib, sunitinib and vandetanib
FGFR TK	SU5416, SU6668, SU5402, Z24, PD173074, SSR128129E, AZD4547, BGJ398, LY287445, CP-547,632, dominant negative mutant overexpression
FAK	dominant negative mutant overexpression
ERK <sub>1/2</sub>	PD098059, U0126, apigenin, dominant negative mutant overexpression
P38	SB203580
PI3K	LY294002, apigenin, dominant negative mutant overexpression
PKC	Bis I, GO6983, GFX, chelerythrine, H7, NSC 639366, calphostin C, dominant negative mutant overexpression
Rac	dominant negative mutant overexpression
Ras	manumycin A, FTS, FPT inhibitor III, dominant negative mutant overexpression
Raf	dominant negative mutant overexpression
c-Src	PP1, PP2, dominant negative mutant overexpression
SH2	dominant negative mutant overexpression
MEK	dominant negative mutant overexpression
PLC-γ PLC-α	aristolochic acid, ONO-RS-082
AKT	ML-9, dominant negative mutant overexpression
NF-κB	dominant negative mutant overexpression
c-Fyn	dominant negative mutant overexpression
c-jun	antisense oligonucleotide
PAK	dominant negative mutant overexpression
JNK	dominant negative mutant overexpression
P70 <sup>S6K</sup>	Rapamycin
RhoA	C3
c-FES	dominant negative mutant overexpression
Grb2	Grb2–Src homology 2 domain binding antagonist
cAMP	Forskolin, 8-bromo AMPc
Ets-1	dominant negative mutant overexpression
Egr-1	neutralizing single-stranded DNA
Ca <sup>++</sup> influx	CAI
G-proteins	pertussis toxin

<sup>a</sup> See [146,147] and references therein.

D-1-*threo*-1-phenyl-2-hexadecanoylamino-3-pyrrolidino-1-propanol, that affect endothelial cell proliferation triggered by FGF2 [111]. HSPGs can be removed from the cell surface by heparinase treatment that abolishes FGF2-dependent cellular responses [108]. Alternatively, HSPGs can be modified to inhibit their interaction with FGFs, as in the case of sodium chlorate treatment that induces the preferential reduction of trisulfated disaccharide units, thus preventing FGF2 binding, internalization and mitogenic activity [112].

#### 5.1.2. Preventing FGF/FGFR/co-receptor interactions

One of the most exploited approaches for the design of inhibitors of the FGF/FGFR system is based on the production of neutralizing anti-FGF antibodies [103,113] and the search for natural and synthetic FGF binders that sequester the growth factor in the extracellular compartment, thus acting as FGF traps [114,115]. Natural FGF binders (Table 2) have been identified in the ECM and body fluids. Among them, thrombospondin-1 (TSP-1), long pentraxin-3 (PTX3), heparin [87,91,116] and soluble decoy FGFRs [117] have been exploited for therapeutic purposes. For instance, molecular modeling and protein–protein interaction studies were used to map the amino acid residues involved in TSP-1/FGF2 and PTX3/FGF2 binding. The information was translated into pharmacophore models for the screening of small molecule databases. This approach led to identification and characterization of TSP-1 peptidomimetics [116] and PTX3-derived peptides and small molecules [118–120] acting as FGF traps and endowed with antiangiogenic and antitumor properties.

As a component of body fluids, heparin is a negatively charged glycosaminoglycan released in the blood stream during inflammation. It binds almost all the members of the FGF family and acts as an antagonist of the FGF/FGFR system. Unfortunately, its use in the clinics as FGF inhibitor is hindered by its potent anticoagulant activity. This has led to the search and identification of

heparin-like polyanionic molecules acting as FGF traps but with reduced anticoagulant activity. They include, among others, polysulfated/anticoagulant compounds and biotechnological heparins (see Ref. [121] for a comprehensive review about this point). Since heparin binds a variety of angiogenic/mitogenic growth factors besides FGFs [122], heparin-like drugs might have the advantage to sequester various growth factors simultaneously, acting as “multitarget” inhibitors [123]. On the other hand, a too broad binding capacity may lead heparin-like compounds to affect multiple biological processes with consequent undesired side effects and/or toxicity.

Finally, prototypic FGF traps can be represented by soluble forms of the extracellular portion of FGFRs that function as decoy molecules able to bind and sequester FGFs, thus preventing their interaction with the full length transmembrane signalling receptor. To date, the most promising molecule is represented by FP-1039, a soluble FGFR1(IIIc)-Fc fusion protein that binds tightly and inhibits almost all FGFs. This molecule has entered the clinical trial evaluation process [124].

The identification of functional FGF domains responsible for their binding to the different cognate receptors has been exploited for the production of synthetic “masking” peptides. As an example, the peptide comprising the amino acid sequence FGF2(112–155) impaired the interaction of FGF2 with FGFR1 [125] and similar peptides were successfully employed to specifically deliver antitumor drugs to FGFR-overexpressing tumor cells [126]. In addition, vaccination against FGFR1 showed antitumor activity *in vivo* [127] and anti-FGFR neutralizing antibodies blocked FGF2-mediated angiogenesis *in vivo* [113,128–130].

As stated above, FGFR co-receptors deeply influence the ligand/receptor recognition. Thus, interesting approaches have been developed to affect their activity. For instance, FGF2 contains two DGR sequences that are the inverse of the integrin-recognition sequence RGD present in several cell-adhesive proteins. Con-



sistently, both RGD-containing peptides and DGR-containing FGF2-derived peptides inhibit  $\alpha_v\beta_3$  integrin-mediated endothelial cell adhesion to FGF2 and cell proliferation [131,132]. Accordingly, RGD-peptidomimetics inhibit FGF2-dependent neovascularization and tumorigenesis [133]. Relevant to this point, monoclonal anti- $\alpha_v\beta_3$  antibodies prevent FGF2/ $\alpha_v\beta_3$  interaction thus impairing endothelial cell adhesion, proliferation and protease upregulation *in vitro* [132] and FGF2-mediated angiogenesis *in vivo* [134]. A similar mechanism of action may be shared by disintegrins, a class of naturally occurring integrin antagonists that have been demonstrated to inhibit different aspects of FGF2 biology [135].

Besides integrins, also HSPGs can be masked to obtain an antiangiogenic effect. The FGF2-mimicking synthetic peptide F2A4-K-NS binds and masks HSPGs to FGF2 [136]. The LM $\alpha$ 5 (laminin  $\alpha$ 5)-derived peptide A5G27 binds to the glycosaminoglycan chains of CD44, preventing its binding to FGF2 and inhibiting angiogenesis [137]. The heparin-binding lactoferrin fragment LfcinB inhibits the angiogenic activity of FGF2 by binding to HSPGs on endothelial cells [138]. Protamine [139], several CXCL4-derived peptides, the histidine-rich glycoprotein [140] and antithrombin [141] exhibit antiangiogenic properties, whose mechanism of action may rely, at least in part, on their capacity to bind and mask HSPGs to FGFs. Finally, the cholera toxin B subunit inhibits FGF2-dependent proliferation of endothelial cells by hampering the binding of the angiogenic growth factor to cell surface GM<sub>1</sub> ganglioside [111].

### 5.2. Inhibition of signal transduction triggered by FGFR activation

As already mentioned, the first step of the activation of the FGF/FGFR system is represented by the receptor dimerization and autophosphorylation. As for other TK receptors, inhibition of the TK activity of FGFRs by selective or non-selective molecules has been deeply exploited for the discovery of novel antitumor drugs for the treatment of FGF-dependent tumors. Tyrosine kinase inhibitors (TKIs) have been developed as small molecules acting on the ATP-binding pocket of the intracellular TK domain of the receptor. Some of them, like SU5402 and PD173034, are widely used as FGFR inhibitors in the laboratory practice even though clinical applications are limited by their toxicity [142].

A consistent number of wide-spectrum/non-selective TKIs have been shown to block FGFRs and their mechanism of action and therapeutic application have been associated to their capacity to interfere with multiple TK receptor pathways, including FGFRs. Among them, regorafenib is a novel orally active multitarget compound that inhibits a number of pro-angiogenic TK receptors, including FGFR1, VEGFR2, TIE2, and PDGFR [143]; nintedanib (BIBF1120) interferes with VEGFR, PDGFR and FGFR pathways [144]; ponatinib (AP24534), mainly active on BCR-ABL, has been described to exert an anti-FGFR activity *in vitro* [145]. Several other small molecules, including axitinib, brivanib, cabozantinib, dovitinib, oratinib, pazopamib, sorafenib, sunitinib and vandetanib are endowed with this non-selective TKI profile (see Refs. [146,147] for more details).

All these multi-targeting TKIs are endowed with toxicity profiles often related to their anti-VEGFR action, such as cardiovascular or hypertensive drawbacks or proteinuria, or with other side effects, like gastrointestinal disorders or skin reactions. On the other hand, few selective FGFR inhibitors have been characterized and evaluated in clinical trials. AZD4547 (a pan-FGFR inhibitor), BGJ398 (that targets FGFR1, FGFR2 and FGFR3) and LY287445 (a pan-FGFR inhibitor) are under clinical evaluation for different types of cancer characterized by FGFR amplification or activating mutations. These new “FGFR-restricted” drugs show better tolerability in respect to non-selective TKIs, their most relevant side effects (hyperphosphatemia and tissue calcification) being strictly correlated to the inhibition of the FGF23 pathway.

Apart from intracellular-acting TKIs, recent observations have shown that the small molecule SSR128129E can bind the extracellular portion of FGFRs and inhibit FGFR signalling by an allosteric mechanism of action, without affecting the orthosteric binding of FGF to the receptor [148].

The interaction of the different FGFs with the various TK FGFRs leads to the activation of signal transduction pathways that share, at least in part, several intracellular second messengers in stromal and tumor cells, representing potential therapeutic targets. To this aim, synthetic compounds, dominant negative mutants and antisense cDNAs have been tested for their capacity to shut down a deregulated FGF/FGFR system (Table 3). However, as already pointed out for heparin-like FGF inhibitors, the broad spectrum of action of these intracellular inhibitors must be carefully evaluated for their potential multitarget activity and undesired side effects.

## 6. Concluding remarks

The study of the mechanisms of action of FGFs has led to the identification of various molecules that can modulate the aberrant activation of the FGF/FGFR system in different human cancers.

Due to their pleiotropic nature, FGFs may contribute to cancer progression not only by triggering a pro-angiogenic response but also by acting directly on tumor cells via paracrine and autocrine loops of stimulation. Thus, targeting the FGF/FGFR system through “two-compartment” anti-FGF/FGFR agents may provide benefits not only in terms of inhibition of the neovascularization process but also by an oncosuppressive effect on tumor cells, thus hampering the tumor stromal/parenchymal cross-talk.

As described above, a wide array of approaches might be theoretically pursued to develop anti-FGF/FGFR strategies for the treatment of human cancers. For all these approaches, the demonstration of their efficacy has been provided *in vitro* and the antiangiogenic/antitumor potential has been proven *in vivo* in pre-clinical models for many of them. Nevertheless, the search for anti-FGF/FGFR drugs currently under evaluation in cancer clinical trials (<https://clinicaltrials.gov>) indicates that only two major classes of inhibitors of the FGF/FGFR system have been developed so far: FGFR selective and nonselective TKIs and anti-FGFR antibodies, a few studies focusing on FGFR decoy extracellular FGF ligand traps (see Refs. [146,149–153] for a detailed description of FGF/FGFR-targeting agents in phase I, phase II or phase III clinical development). In addition, it is worth noting that FGF/FGFR inhibitors are frequently evaluated in combination with classical chemotherapeutics, in agreement with the notion that, in respect to monotherapies, multidrug regimens may provide better therapeutic benefits in cancer patients. To this respect, the observation that the escape from angiostatic anti-VEGF blockade can be mediated by the upregulation of the FGF/FGFR system [154,155] points to the possibility that the combinatorial or sequential inhibition of VEGF and FGF pathways may translate into improvements in the clinical care of cancer patients. Finally, various compounds like integrin antagonists and heparin, that entered clinical trials for different pharmacologic features, have been evaluated afterwards also for anti-FGF/FGFR potential.

In conclusion, experimental and clinical evidences point to a role for the FGF/FGFR system in tumor neovascularization, growth and metastatic dissemination. However, several challenges are being faced to further develop efficacious FGF/FGFR inhibitors for antiangiogenic/antitumor therapies in cancer. They include, among others; i) identification of cancer patients more likely to benefit from a therapeutic anti-FGF/FGFR approach; ii) identification of prognostic indicators, surrogate markers of angiogenesis and of response to anti-FGF/FGFR therapies in cancer patients; iii) elucidation of the pros and cons about the use of selective

versus nonselective inhibitors; iv) development of drugs specific for individual FGFs or FGFRs that may reduce undesired systemic side-effects related also to alterations of hormone-like FGFs. Relevant to this latter point, blockade of FGFR signalling by selective or broad-spectrum TK inhibitors has been associated with toxicity [146] and a monoclonal antibody directed against FGFR1 has failed because of severe weight loss associated with hypothalamic binding [156]. Interestingly, at variance with the hyperphosphatemic effect of FGFR TK inhibitors in preclinical models [157] and cancer patients [146], long-term administration of the small molecule FGF trap NSC12 does not affect the blood levels of phosphorus, calcium and FGF23 in tumor-bearing mice [120]. These observations are in keeping with the safety profile in murine tumor models of the FGFR1-derived FGF trap FP-1039 [124] and of the allosteric multi-FGFR blocker SSR128129E [148]. Together, these findings suggest that hyperphosphatemia may represent a side effect of FGFR TK inhibitors rather than of extracellular inhibitors of the FGF/FGFR system. Given that both *FGF23* expression and activity are under the control of a complex mechanism of regulation that includes canonical, non-canonical and intracrine FGF/FGFR pathways [158], further studies are required to elucidate this point.

### Conflict of interest

The authors declare that there are no conflicts of interest.

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