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Review

Targeted therapies of gastrointestinal stromal tumors (GIST)—The next frontiers

Stefan Duensing a,b, Anette Duensing a,c,*

- ^a Cancer Virology Program, University of Pittsburgh Cancer Institute, Hillman Cancer Center, Pittsburgh, PA, USA
- ^b Department of Microbiology and Molecular Genetics, University of Pittsburgh School of Medicine, Pittsburgh, PA, USA
- ^c Department of Pathology, University of Pittsburgh School of Medicine, Pittsburgh, PA, USA

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ABSTRACT

Gastrointestinal stromal tumors (GISTs) are the most common mesenchymal tumors of the gastrointestinal (GI) tract and are caused by activating KIT or PDGFRA mutations. GISTs can be successfully treated with the small molecule kinase inhibitor imatinib mesylate (Gleevec®, Novartis) with response rates of up to 85%. However, complete responses are rare, and most patients will develop imatinib resistance over time. Recent results have shown that although imatinib effectively stimulates apoptotic cell death in sensitive GIST cells, a considerable proportion of cells does not undergo apoptosis, but instead enters a state of quiescence. Quiescence is characterized by a reversible withdrawal from the cell division cycle, during which the cells remain alive and metabolically active. It is conceivable that quiescence not only plays a pivotal role in the emergence of residual disease but also in creating a pool of tumor cells that survive continuous small molecule therapy and may hence represent the "seeds" for the outgrowth of resistant clones. This review will summarize the current knowledge about GIST biology and treatment response to imatinib including the induction of cellular quiescence in GIST. In addition, we will highlight future strategies to design more effective treatment options to overcome these problems with an aim towards cure of this hitherto untreatable tumor entity.

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Contents

1.	Introduction	575
2.	KIT and PDGFRA in GISTs	576
3.	Targeting KIT with imatinib mesylate (Gleevec $^{ ext{ iny B}}$)	577
	The mode of action of imatinib mesylate	
5.	Imatinib triggers gist cell quiescence	577
6.	Overcoming imatinib-induced quiescence and imatinib resistance	578
7.	Novel targets in GISTs	580
8.	Summary and outlook	580
	Acknowledgements	580
	References	580

1. Introduction

Gastrointestinal stromal tumors (GISTs) are the most common mesenchymal tumors of the gastrointestinal (GI) tract [1]. They can arise throughout the entire GI tract, however, the most commonly affected sites are the stomach (60%) and the small bowel (jejunum and ileum 30%, duodenum 5%) [2]. GISTs are thought to arise from

E-mail address: aduensin@pitt.edu (A. Duensing).

the interstitial cells of Cajal (ICC) or an ICC precursor cell. ICCs are localized between the two muscular layers of the gastrointestinal tract and are involved in the regulation of peristalsis. It has long been known that ICCs are dependent on expression of the KIT receptor tyrosine kinase (RTK) for their proper development and differentiation [3,4]. GISTs are characterized by not only expressing KIT at high levels, but also by the fact that approximately 85% of GISTs harbor mutations in the *KIT* gene [5,6]. Approximately one third of the remaining cases (5–8% of all GISTs) carry mutations in the related RTK, platelet-derived growth factor receptor alpha (*PDGFRA*) [7,8]. Immunohistochemical staining for the KIT protein has become the most important diagnostic parameter for GISTs although a small percentage of GISTs (2–5%) express KIT at very

^{*} Corresponding author at: University of Pittsburgh Cancer Institute, Hillman Cancer Center, Research Pavilion, Suite 1.8, 5117 Centre Avenue, Pittsburgh, PA 15213, USA. Tel.: +1 412 623 5870; fax: +1 412 623 7715.

low levels or not at all [9–12]. Some, but not all of these tumor are wildtype for *KIT* mutations. Despite these findings, unifying features of most GISTs – irrespective of KIT expression and *KIT/PDGFRA* mutational status – are the expression of PKCtheta and DOG1, markers that were originally identified by mRNA expression profiling [13–21].

2. KIT and PDGFRA in GISTs

KIT (CD117) is a 145 kDa, transmembrane receptor tyrosine kinase that belongs to the type III family of RTKs, which includes PDGFRA and PDGFRB, as well as colony-stimulating factor 1 receptor (CSF1R) and FMS-related tyrosine kinase 3 (FLT-3) [22–24]. All type III RTKs are comprised of five extracellular IgG-like loops that encode the ligand-binding and dimerization domains and an intracellular portion, which is divided into the juxtamembrane (JM) domain and a split kinase domain (Fig. 1). KIT is expressed in hematopoietic stem cells, mast cells, melanocytes, germ cells and ICC [25]. Under physiological conditions, the kinase is activated by its ligand stem cell factor (SCF), which leads to receptor dimerization, autophosphorylation and activation (phosphorylation) of downstream signaling cascades that include most prominently the PI3K/AKT/mTOR and the RAS/RAF/MAPK pathways, but also [AK/STAT signaling [26,27,28,29].

Several types of KIT mutations can be found in GISTs, eventually affecting different domains of the protein. However, all oncogenic KIT mutations cause a constitutive, ligandindependent activation of the kinase thereby driving tumorigenesis [30,31]. Despite the fact that different KIT mutations generally lead to the same outcome (constitutive KIT activation). it is likely that downstream signaling pathways that are being activated by different KIT genotypes are not exactly the same [29]. Moreover, the type of KIT mutation correlates with therapeutic outcome (see below). The most common KIT mutations in GIST are detected in KIT exon 11 (Table 1), followed by mutations in exons 9, 13 and 17 [1]. Interestingly, a range of various types of mutations can be found in KIT exon 11 (insertions, deletions and single base substitutions), whereas exon 9 mutations always comprise of a six-base pair insertion leading to duplication of amino acids 502-503. Mutations in exons 13 and 17 always consist of single base substitutions leading to various missense mutations. Approximately 5-8% of GISTs that do not carry KIT mutations harbor activating mutations in the related RTK PDGFRA (Table 1) [7,8]. Interestingly, similar types of mutations are found in PDGFRA as are in KIT-eventually affecting corresponding domains of the protein. However, the frequency distribution of the domains affected differs between KIT and PDGFRA mutations

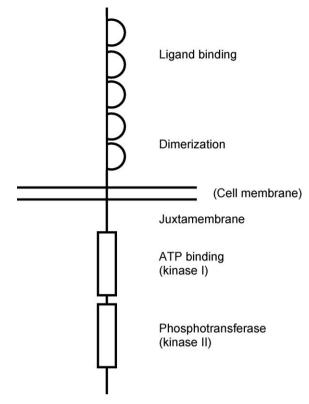


Fig. 1. Stucture of type III receptor tyrosine kinases (RTK). All type III RTKs are comprised of five extracellular IgG-like repeats that are involved in ligand-binding and dimerization. The juxtamembrane domain, just inside the cell membrane, has autoinhibitory function. The kinase domain is split into two parts separating the ATP binding pocket (kinase I) from the activation loop/phosphotransferase domain (kinase II).

[32]. The juxtamembrane domain is most frequently affected by mutations in *KIT*, whereas *PDGFRA* mutations most frequently affect the activation loop of the kinase domain (Table 1). Interestingly, several *KIT/PDGFRA* mutation types have a certain predilection with respect to tumor location. For example, GISTs with *KIT* exon 9 mutations are predominantly seen in the small bowel and have been associated with a more aggressive clinical behavior [33,34], whereas an internal tandem duplication in *KIT* exon 11 most frequently occurs in gastric tumors with spindle-cell morphology [35,36]. On the other hand, most gastric GISTs with epithelioid morphology lack *KIT* mutations [34,37,38] and GISTs with *PDGFRA* mutations arise almost exclusively in the stomach [8,39,40].

Table 1 Primary mutations in GIST.

Gene	Exon	Type of mutation	Domain affected	Frequency	
KIT	9	 Insertion (duplication of codons 502/503) 	Extracellular (ligand-binding)	12%	84% (75–90%)
	11	Deletion Insertion Single base substitution	Juxtamembrane (auto-inhibitory)	70%	(73-30%)
	13	 Single base substitution 	Kinase domain I (ATP binding pocket)	1%	
	17	Single base substitution	Kinase domain II (phosphotransferase/activation loop)	1%	
PDGFRA	12	DeletionInsertionSingle base substitution	Juxtamembrane (auto-inhibitory)	0.7%	7% (5–8%)
	14	 Single base substitution 	Kinase domain I (ATP binding pocket)	0.1%	
	18	Single base substitution	Kinase domain II (phosphotransferase/activation loop)	6%	
WILDTYPE	n/a	n/a	n/a	9%	9% (9-15%)

It is widely believed that *KIT* or *PDGFRA* mutations are the tumor-initiating events in GISTs, and it has been shown that *KIT* and *PDGFRA* mutations are mutually exclusive [32]. Nonetheless, the precise molecular mechanism(s) of mutagenesis as well as the tissue preference remains to be elucidated. It seems to be clear, however, that additional oncogenic events are needed for a clinically symptomatic and more rapidly growing tumor to occur, because very small GIST "tumorlets" can be detected in as many as 30% of the population when examining autopsy specimens [41–44]. Most, if not all of these tumors already contain *KIT* or *PDGFRA* mutations.

Nevertheless, strong support for a causative role of KIT/PDGFRA mutations in GIST pathogenesis stems from (i) various in vitro transgenic models [5,45,46], (ii) the existence of a familial GIST syndrome in patients with germline KIT/PDGFRA mutations [47– 55], (iii) mouse models that have been established [56–58] and (iv) the finding that most small, incidental GIST (< 1 cm) already carry KIT mutations [41,43]. Although most GISTs have detectable KIT/ PDGFRA mutations, 9–15% of GISTs are wildtype for both genes, and no other underlying mutation has been detected yet [9,59]. Some of these cases show overexpression of insulin-like growth factor 1 receptor (IGF1R) [60-62]. GISTs in patients with the familial Carney-Stratakis syndrome (paraganglioma and GIST) have germline mutations in the succinate dehydrogenase (SDH) subunits B, C or D leading to enzyme deficiency [63,64]. Although no SDH mutations were detected in non-syndromic pediatric patients with KIT/PDGFRA wildtype tumors, they similarly show a loss of expression and/or function of SDH [65]. Moreover, a few KIT/ PDGFRA wildtype GISTs have been reported to carry activating BRAF V600E mutations [66.67]. However, it has not vet formally been determined whether they are the initiating event in these tumors.

3. Targeting KIT with imatinib mesylate (Gleevec®)

Imatinib mesylate (Gleevec®, Novartis) is a small molecule protein tyrosine kinase inhibitor that was originally identified in a screen for PDGFR inhibitors [68]. It competitively binds to the kinase ATP binding pocket, and also effectively inhibits not only PDGFRA/B, but also the KIT and ABL kinases because of structural similarities of their kinase domains [27,45,46]. Imatinib was first clinically used to target the BCR-ABL fusion kinase, which is the underlying oncogenic stimulus in Philadelphia chromosome-positive chronic myeloid leukemia (CML). It was FDA-approved for this indication in 2000. The same year, the first GIST patient was treated imatinib, and the drug gained FDA approval for GIST in 2002 [69,70]. The use of imatinib for treatment of GIST has reversed an untreatable disease into a tumor entity, in which up to 85% of patients that receive the drug achieve disease control [71-73]. The benefits of imatinib treatment are highlighted by a recent retrospective study that calculated the median overall survival for patients with metastatic GIST in the pre-imatinib era at 19 months [74], whereas the current median overall survival under imatinib therapy is estimated to be more than 50 months [72,75]. As mentioned above, the response of GISTs to imatinib treatment correlates with the type of mutation in the primary tumor [76– 79]. Tumors with KIT exon 11 mutations respond best to imatinib therapy (70-85% objective response-encompassing complete and partial response), whereas KIT exon 9 mutant GISTs only showed an 25-48% overall response rate in a recent study [75,76]. The response rates for tumors with kinase domain mutations (exons 13 and 17) or with no KIT mutation are even below the response rates of exon 9 mutant GIST. This can be explained by the fact that mutations in the KIT kinase domains likely interfere with imatinib binding on one handside, whereas KIT wildtype GISTs may not depend on KIT activation as much as GISTs with KIT mutations. However, the reason for the difference in response rates for exon 9 mutant GISTs is not exactly clear. Notably, these patients significantly benefit from a dose increase from the standard 400 mg imatinib to 800 mg/day [80]. It is also important for the clinical management of PDGFRA mutant GIST that although the most common mutation (D824 V in PDGFRA exon 18) is imatinib-resistant in vitro, most other PDGFRA mutations are imatinib-responsive [77,81,82].

The almost unprecedented success story of the use of a small molecule inhibitor in a solid tumor entity has made the "GIST-imatinib connection" a paradigm for targeted therapy. It has resulted in efforts to find similar therapeutic strategies for other solid tumors to increase remission rates and the quality of positive responses. Unfortunately, the majority of malignancies are not caused by single mutations – but there are nonetheless a plethora of lessons to learn from GISTs and imatinib.

4. The mode of action of imatinib mesylate

Imatinib mesylate binds to the inactivated form of the KIT kinase thereby preventing its activation [27]. It causes a profound and rapid inhibition of active, phosphorylated KIT within minutes, thus underscoring that even the oncogenically activated kinase is in an equilibrium between its active and inactive state, which is merely shifted towards the active conformation. Inhibition of KIT is followed by an equally rapid inhibition of downstream signaling pathways, in particular the PI3K/mTOR/AKT and RAS/RAF/MAPK pathways [29.83]. However, when the dynamics of GIST cell death were analyzed in correlation to the inhibition of KIT kinase activity. it was surprisingly found that apoptosis was considerably delayed and did not peak until approximately 72 h after treatment [29,84]. It is now known that the induction of GIST cell apoptosis is far more complex than a simple shut-down of kinase activity. One example to underscore this notion is the fact that a histone protein of the H2A family, histone H2AX, was found to play an important role in GIST cell death [84,85]. Imatinib causes a massive upregulation of soluble, non-nucleosomal histone H2AX, which drives GIST cells into apoptosis, very likely through an inhibition of ongoing gene transcription. H2AX upregulation was found to correlate with imatinib sensitivity, and depletion of H2AX in GIST cells dampened their apoptotic response to imatinib. Histone H2AX is well known as a key player in the cellular response to DNA damage, but the results obtained from imatinib-treated GIST cells suggest a novel, unexpected function of this protein as a trigger of cell death. Other mechanisms that have been implicated in imatinib-induced GIST cell apoptosis include a downregulation of the protein translation machinery [86] and reduced glucose uptake as evidenced by decreased membrane-bound GLUT4 [87]. In CML, the proapoptotic BH3-only proteins BIM and BAD were found to mediate the apoptotic response after imatinib treatment [88.89] and recently, BIM has also been implicated in imatinib-induced apoptosis in GIST [90]. Further dissection of the pro-apoptotic pathways after imatinib treatment is desirable to identify additional molecules that can be targeted for therapeutic purposes (see below).

5. Imatinib triggers gist cell quiescence

Tumor cell quiescence is a major obstacle to conventional antitumor therapy since most agents specifically target proliferating cells. Quiescent cells remain metabolically active, but are withdrawn from the cell division cycle, which renders them intrinsically resistant to numerous chemotherapeutic agents [91]. Such "dormant" cells can therefore cause refractory disease and/or relapse, if they harbor changes associated with resistance. It was

hence surprising and disconcerting to find that imatinib can induce molecular changes that lead to GIST cell quiescence [92,93]. Specifically, imatinib was found to downregulate the F-box protein SKP2, thereby causing an accumulation of the CDK inhibitor p27^{Kip1}, a major regulator of quiescence. SKP2 itself is regulated by proteolysis, and imatinib was found to disrupt an even higher level of regulation by causing the APC/cyclosome activator CDH1 to relocalize to the nucleus. Here, it may stimulate the degradation of SKP2 and hence initiate the chain of events that ultimately triggers cell cycle exit. The induction of GIST cell quiescence by imatinib reconciles a number of clinical observations including the rarity of complete responses, the fact that some patients remain stable under imatinib therapy in the presence of detectable disease, and, most importantly, the need for continued, long-term drug treatment [94]. Moreover, in the light of the current view that resistance mutations (see below) are pre-existing in most GISTs or evolve during the natural course of the disease even without imatinib treatment [95,96], it is very likely that quiescent cells provide a pool of cells that can lead to resistance at later stages.

The problem of cellular quiescence after imatinib therapy has been focus of many studies in CML and shows parallels to what has been reported in GIST [97]. Studying quiescence in CML is technically facilitated by the fact that it is possible to isolate G_0 subpopulations with the help of flow cytometry [98]. Similar to GIST patients, a full remission (on a molecular level defined as BCR-ABL mRNA levels below the detection level of quantitative realtime PCR in CML) is rarely achieved after imatinib treatment. Cells not eliminated by anti-leukemic therapy were shown to be part of a primitive CD34⁺ progenitor cell population that has exited the cell division cycle. These CD34⁺. BCR-ABL⁺ CML stem cells are insensitive to imatinib, but also to other apoptotic stimuli [91,99-101]. However, findings using in vitro models of CML cells that proliferate at different rates suggest that their resistance to treatment does not necessarily depend on their cell cycle stage, but rather on "other molecular properties" of these cells [102]. Some of these properties may include high expression levels of ATPbinding cassette transporters (ABC), including the multi-drug resistance protein 1 (P-glycoprotein) and ABCG2 [103,104]. Other mechanisms could consist of differential expression levels of genes that are expressed during cellular differentiation as well as a generally low level of transcriptional activity per se [105]. It is important to note, however, that a certain percentage of the quiescent primitive CD34⁺ progenitor cells already harbors the typical imatinib resistance mutations [106,107]. Attempts to therapeutically target quiescent stem cells in CML have proven to be difficult for the above-mentioned reasons. One approach that yielded promising results in preclinical models included treatment with growth factors like granulocyte-colony stimulating factor (G-CSF) to force quiescent cells to cycle [108]. Future studies are warranted to test whether conceptionally similar approaches can increase the efficiency of targeted therapies in GIST patients.

6. Overcoming imatinib-induced quiescence and imatinib resistance

Besides imatinib-associated quiescence, the development of drug resistance remains one of the biggest hurdles for long-term remission and cure of the disease. Approximately 10% of patients experience primary resistance to imatinib, which is defined as progression within the first three to 6 months of therapy [69,73]. Primary resistance can be seen in all mutation types, but *KIT*/*PDGFRA* wildtype tumors as well as tumors harboring a *KIT* exon 9 or *PDGFRA* D842V mutation are more prone to exhibit primary imatinib resistance. In the case of *PDGFRA* D842V this can be explained by the fact of it being localized in the kinase domain presumably affecting imatinib binding. Secondary, or delayed,

Table 2Secondary (resistance) mutations in GIST.

Gene	Exon	Mutation	Domain affected
KIT	13	• V654A	Kinase domain I (ATP binding pocket)
	14	• T670I	
	17	 D816A/G/H/V 	Kinase domain II
		 D820A/E/G/Y 	(phosphotransferase/
		• N822H/K	activation loop)
		• Y823D	
	18	• A829P	
PDGFRA	18	• D842V	Kinase domain II (phosphotransferase/ activation loop)

resistance to imatinib after showing some initial benefit is seen in 40–50% of patients within 2 years of starting imatinib therapy [32,73]. Although resistant/recurring tumors are most often diagnosed by CT scan, a substantial progress in identifying tumors with secondary resistance has been made by the introduction of 18FDG-PET scans [109,110]. By now, it is well established that the leading cause for imatinib resistance are secondary mutations in the KIT or PDGFRA kinase domain (Table 2) [32,111-120]. Secondary mutations can be detected in two thirds of patients [111–114,121]. They usually occur in the same gene as the primary resistance mutation and have therefore more often been reported in tumors with primary KIT mutation. Within KIT mutated tumors, secondary kinase mutations are more frequently detected in GISTs with a primary exon 11 mutation than GISTs with a primary exon 9 mutation [116]. Amplification of the KIT or PDGFRA genes [111,122,123] seem to play a minor role, especially when compared to what has been reported for BCR-ABL amplifications in CML [95,124]. Furthermore, possible pharmacological reasons for imatinib resistance, such as an increased clearance or binding to plasma proteins, have been reported [125,126].

Patients who fail to respond to imatinib are currently being treated with sunitinib malate (Sutent[®], Pfizer), a second-line therapy for GIST approved by the FDA in 2006 [127,128]. Sunitinib is a multikinase inhibitor that targets not only KIT and the PDGFRs but also VEGFRs 1-3, FLT3 and RET [129]. The response rate to sunitinib as second-line agent was found to be 65% (7% partial response, 58% stable disease) in a phase III placebo-controlled clinical trial [130]. Patients with wildtype KIT or KIT exon 9 mutations tend to benefit more from sunitinib therapy than patients with KIT exon 11 mutations, but resistance is still a problem with this second-line agent [128,130]. This was not entirely unexpected, since – similar to imatinib – sunitinib has also minimal activity against the KIT exon 17 and PDGFRA exon 18 mutations [131].

These above-mentioned clinical results make it clear that novel approaches to GIST therapy need to focus on (1) making the first line therapy more effective and (2) either avoiding resistance and/ or developing innovative approaches to GIST treatment if resistance has occurred.

One approach to make GIST therapy more effective is the use of improved KIT kinase inhibitors, both in terms of higher affinity binding as well as a more favorable activity spectrum. Some examples of these new kinase inhibitors are being discussed below. However, due to the vast number of compounds that are currently being developed or have already entered clinical trials, only the most prominent compounds are being highlighted (Table 3). Nilotinib (Tasigna®, formerly AMN107, Novartis) shows higher affinity kinase binding (for BCR-ABL) and achieves 7–10-fold greater intracellular concentrations than imatinib in GIST [132,133]. It is currently in clinical trials for GIST, but already

Table 3New therapeutic options for GIST.

Target		Compound	Brand name	Company
Pathway Molecule(s)				
KIT/PDGFRA	KIT, PDGFRs, ABL	Imatinib mesylate (STI571)	Gleevec®	Novartis
	KIT, PDGFRs, VEGFRs 1-3, FLT3, RET	Sunitinib malate (SU11248)	Sutent [®]	Pfizer
		Nilotinib (AMN107)	Tasigna [®]	Novartis
	KIT, PDGFRB, RAF, VEGFR2/3, FLT3, RET	Sorafenib tosylate (BAY 43-9006)	Nexavar [®]	Bayer
	KIT, PDGFRs, SRC, ABL	Dasatinib (BMS-354825)	Sprycel [®]	Bristol-Myers Squibb
PI3K	PI3K	BEZ235	_	Novartis
		XL147	_	Exelixis
		XL765°	_	Exelixis
		SF1126	_	Semafore Pharmaceuticals
		PF-04691502*	_	Pfizer
		GDC-0941	_	Genentech
	AKT	Perifosine	_	Keryx Biopharmaceuticals
		XL418	_	Exelixis
	mTOR	Everolimus (RAD001)	Afinitor®	Novartis
		Sirolimus	Rapamune [®]	Wyeth (now Pfizer)
		Temsirolimus	Torisel [®]	Wyeth (now Pfizer)
MAPK	RAF	XL281	_	Exilixis
	MEK	RDEA119	_	Ardea Biosciences
	MEK1	GDC-0973 (XL518)	-	Genentech (compound acquired from Exilixis)
HSP90	HSP90	Geldanamycin	n/a	n/a
		17-AAG	Tanespimycin [®]	Bristol-Myers Squibb
		IPI-504	=	Infinity Pharmaceuticals
		STA-9090	_	Synta Pharmaceuticals
HDAC	HDAC	Vorinostat (SAHA)	Zolinza®	Merck
		Panobinostat (LBH589)	_	Novartis
		Valproic acid	_	n/a
		Trichostatin A	_	n/a
proteasome	26S subunit	Bortezomib	Velcade [®]	Millennium Pharmaceutical
KIT	KIT (switch pocket)	(Switch pocket kinase inhibitor)	n/a	Deciphera Pharmaceuticals
transcription	KIT promoter	(Quadruplex-DNA binding)	n/a	n/a

also inhibits mTOR.

FDA-approved for the treatment of imatinib-resistant BCR-ABL-positive CML. Sorafenib tosylate (Nexavar®, formerly BAY 43-9006, Bayer) is an orally available multikinase inhibitor against RAF, VEGFR2/3, PDGFRB, KIT, FLT3 and RET. It is currently in a Phase II clinical trial for GIST [134]. Dasatinib (Sprycel®, BMS-354825, Bristol-Myers Squibb), mainly marketed as a dual SRC/ABL kinase inhibitor and already FDA-approved for imatinib-resistant CML/AML, also potently inhibits KIT and PDGFR kinase activity and has shown preclinical activity against mutant *KIT* D816 V and mutant *PDGFRA* D842 V [135]. So far, the response rates in these clinical trials seem to be varied, and it will be necessary to take the mutation type as well as other factors of the molecular makeup of those tumors into the equation to be able to better predict the response to therapy.

In addition to the classical direct interaction with the ATPbinding pocket and subsequent inhibition of kinase activity, it may be possible to target KIT or PDGFRA through several unrelated mechanisms. This was the rationale to test HSP90 inhibitors as potential therapeutic agents in GIST. Heat shock proteins are chaperone molecules that prevent the degradation of misfolded proteins, such as proteins derived from a mutated gene. In the context of GIST, mutated KIT/PDGFRA is presumably misfolded and would be degraded if not protected by chaperone proteins. Therefore, it was reasoned that inhibition of these chaperones could lead to degradation of the mutated KIT/PDGFRA in GIST (but most likely not the wildtype proteins). This promising strategy has been confirmed in a number of cell line models with several natural (geldanamycin) or synthetic compounds [136]. 17-AAG (Bristol-Myers Squibb) is a geldanamycin-derivative, but is not water-soluble and has hence to be given intravenously [137]. By contrast, IPI-504 (Infinity Pharmaceuticals) was the first water soluble, oral HSP90 inhibitor that entered clinical trials. However, after very promising results in a phase I trial, a phase III clinical trial had to be terminated early because of a higher than anticipated mortality in treated patients versus placebo-treated patients [138]. Nevertheless, new compounds of this class with anticipated less toxicity are in development and/or clinical trials for GIST (for example, STA-9090, Synta Pharmaceuticals).

Other compounds that target KIT by other means than competitive ATP binding include so-called quadruplex-binding small molecules [139] and switch pocket inhibitors (developed by Deciphera). Quadruplex-binding small molecules have initially been developed to target quadruplex DNA structures at telomeres with the aim to inhibit of telomerase and disrupt telomere maintenance thereby selectively inhibiting cancer cell growth. However, the same principle can be applied to targeting quadruplex DNA structures in gene promoter regions with subsequent of inhibition of gene transcription. A first compound (a naphthalene diimide derivative) targeting the KIT promoter region, which harbors potential quadruplex structures, has shown some promise in preclinical studies [139]. By contrast, switch pocket inhibitors make use of the fact that the so-called kinase switch pocket is usually quite unique in a given kinase or kinase sub-family. This is in contrary to the ATP binding pocket, which is very well conserved over a wide range of kinases. The switch pocket is the space, into which the phosphorylated switch binds upon kinase activation. Inhibiting this binding would therefore presumably also inhibit kinase activity. These novel approaches sound very promising, especially if it is possible to overcome potential hurdles of drug toxicity, pharmacodynamics/-kinetics as well as sufficient tumor distribution.

Taken together, future drug development needs to take into considerations that targeting KIT alone may not be sufficient to completely eliminate GIST cells due to entry into a quiescent state (see above). A deeper understanding of GIST cell quiescence [93,140] and identification of potential drug targets relevant for this process will be instrumental to improve the quality of clinical responses. Here, it will be especially important to understand what factors determine whether a cell responds to imatinib therapy by exiting the cell division cycle or by undergoing apoptosis. One possible factor could be the stage of the cell cycle that this cell is in when imatinib treatment is started. Future experiments are needed to determine how cells can be manipulated to achieve a maximum apoptotic response.

7. Novel targets in GISTs

The search for novel targets outside KIT and PDGFRA is motivated by the fact that most imatinib-resistance mutations occur within the KIT or PDGFRA genes themselves, which may thwart efforts to target these proteins even with improved compounds. In addition, genotype-phenotype studies have shown that multiple resistant tumor nodules within the same patient oftentimes do not carry the same resistance mutations [111,112,122,141,142], which makes a kinase-centric approach difficult. It may hence be promising to target the KIT/PDGFRA downstream signaling pathways, an approach that has shown some promise in preclinical studies [83]. The most critical signaling axis for GIST cell survival seems to be the PI3K/AKT/ mTOR pathway [29,83]. A number of compounds targeting various molecules of these signaling modules are currently in clinical trials including several PI3K inhibitors, AKT inhibitors and mTOR inhibitors (Table 3). Targeting the RAS/RAF/MAPK pathway, for which various compounds are now available (Table 3), may be particularly important for the low percentage of GISTs that present with BRAF mutations [66,67] and GISTs developing in NF1 patients [143–145]. However, it has been shown in various in vitro models that targeting the PI3K pathway holds more promise in most sporadic GISTs [146]. Compounds targeting KIT/PDGFRA downstream pathways may be especially amenable to combination therapy, either with a KIT/PDGFRA inhibitor or with each other.

An emerging family of target proteins that are not involved in signaling pathways related to KIT/PDGFRA are histone deacetylases. The function of these proteins is to deacetylate histones thereby leading to a conformational change of the chromatin. Histones are the components of nucleosomes, which have long been known as mere packaging units to compact DNA. We now know that histones can be post-transcriptionally modified in many ways, e.g. by phosphorylation, methylation and acetylation, thereby regulating the conformation and accessibility of DNA. Acetylated histones are usually found in regions with open chromatin, thus enabling transcription. Therefore, inhibiting histone deacetylases should promote this relaxed chromatin conformation. It has been hypothesized that this leads to increased transcription of cell cycle inhibitory genes, thereby leading to a therapeutic effect. However, recent reports suggest a more complex mechanism of action that involves increased acetylation of heat shock proteins leading to disruption of their chaperone function [146-148]. A number of HDAC inhibitors are already FDAapproved for lymphomas, and some prominent compounds are trichostatin A (a natural compound), valproic acid, suberoylanilide hydroxamic acid (SAHA, vorinostat, Zolinza®, Merck), and panobinostat (LBH589, Novartis). HDAC inhibitors have recently shown promising results in preclinical models for GIST [146,149] and are currently in clinical trials. The idea of using HDAC inhibitors does not seem to be very specific for targeting KIT in GIST, but they have proven to be quite effective in preclinical models, as mentioned above. As novel functions of HDACs are emerging, we may also learn more about the exact mechanisms of action of HDAC inhibitors.

Another promising novel target in GISTs may be the ubiquitinproteasome machinery, which is responsible for the degradation of poly-ubiquitylated proteins and therefore protein stability of various regulatory proteins that play a role in GISTs. In a recent study, it was shown that the FDA-approved proteasome inhibitor bortezomib (Velcade®, Millennium) can effectively induce cell death in imatinib-sensitive as well as imatinib-resistant GIST cell lines [150]. Remarkably, the mode of action was an upregulation of the pro-apoptotic histone H2AX and a simultaneous almost complete loss of expression of the KIT kinase. The latter was caused by a transcriptional shutdown in GIST cells. These results not only highlight that bortezomib may be potentially beneficial in GIST patients but also the exquisite dependency of GIST cells on active gene transcription, another promising target in GIST therapy. Similarly to the HDAC inhibitors described above, targeting the proteasome at first glance looks like a rather unspecific therapeutic approach in GIST. However, dissecting the exact mechanism of action of bortezomib in GIST has shown that this compound is able to target two pathways that are crucial for GIST cell survival at the same time.

8. Summary and outlook

Targeted therapy of GISTs has been an extraordinary success story, and up to 85% of patients benefit from single-agent therapy with imatinib. Insights into the mode of action of imatinib as well as a better understanding of the underlying GIST cell biology have revealed pathways that are extremely rich in potential drug targets. In the future, it can be expected that GISTs remain one of the most useful paradigms and model systems for tumor therapy. A concerted effort of clinical and basic science, pathology, drug development and pharmaceutical industry is very likely to succeed in developing innovative approaches to more complete and longerlasting remissions to improve the quality of life and long-term survival of patients with GISTs.

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