Clinical significance of the molecular heterogeneity of gastrointestinal stromal tumors and related research: A systematic review

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Abstract. Gastrointestinal stromal tumors (GISTs) are the most commonly observed mesenchymal tumors of the digestive tract, and they originate from the interstitial cells of Cajal. GISTs can be divided into KIT/PDGFRA-mutant GISTs and wild-type GISTs based on the presence or absence of KIT/PDGFRA mutations. Wild-type GISTs can be divided into succinate dehydrogenase complex (SDH)-deficient GISTs and non-SDH-deficient GISTs. Downstream signaling pathways activated by these mutations serve a pivotal role in the

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Abbreviations: GISTs, gastrointestinal stromal tumors; KIT, a receptor tyrosine kinase; PDGFRA, platelet derived growth factor receptor a; JAK2, Janus kinase 2; STAT3, signal transducer and activator of transcription 3; GDP, guanosine diphosphate; GTP, guanosine triphosphate; RAF, RAF proto-oncogene serine/threonine-protein kinase; MEK, mitogen-activated protein kinase; MAPK, mitogen-activated protein kinase; PI3K, phosphoinositide 3-kinase; AKT, protein kinase B; mTOR, mammalian target of rapamycin; PIP3, phosphatidylinositol-3,4,5-triphosphate; PIP2, phosphatidylinositol-4,5-bisphosphate; PTEN, phosphatase and tensin homolog; BAD, BCL2 associated agonist of cell death; SDH, succinate dehydrogenase; HIF1, hypoxia-inducible factor; IGF, insulin-like growth factor; VEGF, vascular endothelial growth factor; JM, juxtamembrane; EC, extracellular domain; TKI, TKI domain (ATP-binding pocket); TKII, TKII domain (activation loop); NF1, Neurofibromatosis type 1; GI, Gastrointestinal; cfDNA, cell free DNA; ctDNA, circulating DNA

Key words: gastrointestinal stromal tumors, KIT, PDGFRA, RAS, SDH, neurofibromin 1, signal transducers and activators of ttranscription 3, non-coding RNAs, ctDNA

development of GISTs and are associated with the biological behavior, including risk stratification, clinical prognosis and drug resistance. Accurate medical care requires accurate molecular diagnosis, which in turn prolongs the survival of patients with GISTs and makes GIST a chronic disease. At present, there is a lack of effective treatment for imatinib/sunitinib/regorafenib resistant patients and KIT/PDGFRA-WT GISTs, which is undoubtedly a major challenge for future research. The present review summarizes the molecular pathogenesis of GISTs and the progress of related research.

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1. Introduction

Gastrointestinal stromal tumors (GISTs) are found in the stomach (56%), small intestine (32%), colon and rectum (6%), esophagus (0.7%), and other areas, such as the omentum, intestinal membrane, pelvis and retroperitoneum (5.5%) (1). The symptoms of GISTs are often non-specific, and dependent on the size and location of the mass. Many small GISTs (<2 cm) are frequently found by endoscopy or radiographic examination, and these patients typically have no symptoms. The most common symptom observed is gastrointestinal bleeding, which is observed in ~50% of patients, followed by abdominal pain (20-50% of patients) and gastrointestinal obstruction (10-30% of patients). Other symptoms include melena, hematemesis, feeling satiated and a palpable abdominal mass.

Proximal gastric stromal tumors may cause difficulty in swallowing, while tumors located in the pylorus may present as a gastric outlet obstruction (2,3). At initial diagnosis, ~20% of patients present with metastases (4), which typically occur in the abdominal cavity or liver, whereas lung, bone or brain metastases are rare. Lymph node metastasis occurs in 20-60% of children with GISTs and Carney's triad, whereas other types are rare (<10%) (5,6). In addition, GIST-induced expendable hypothyroidism and IGF-II production-related non-islet cell tumor hypoglycemia have also been reported. Therefore, patients with endocrine and metabolic symptoms should also be included in differential diagnosis (7,8).

There are numerous molecular subtypes of GISTs (Fig. 1). In ~85-90% of patients with GISTs, KIT (KIT proto-oncogene, receptor tyrosine kinase) or PDGFRA (platelet derived growth factor receptor α) gene mutations are present which alter cell proliferation, adhesion, apoptosis, survival and differentiation by regulating downstream signaling pathways, including the RAS/RAF/mitogen-activated protein kinase (MAPK) and PI3K/AKT/mTOR signaling pathways (Fig. 3A and B) (9). The remaining 10-15% of GISTs, which do not possess KIT or PDGFRA gene mutations, are referred to as wild-type GISTs (10).

Studies have shown that non-coding RNAs [long non-coding RNAs (lncRNA) and microRNAs (miRNAs)] are associated with the invasion, proliferation and drug resistance of GIST cells (11,12). Detection of circulating (ct)DNA may also contribute to the early diagnosis of GISTs (13).

The global incidence of GISTs (1-1.5 cases/100,000 individuals) and the prevalence rate (13 cases/100,000 individuals) are low (14). Incidence rates in Shanghai, Hong Kong and Norway are relatively higher (1.9-2.1 cases/100,000 individuals), whereas the incidence in the Shanxi Province is relatively lower (4.3 cases/1,000,000 individuals). The median age of diagnosis is 60 years (range, 10-100), but may be diagnosed at any age; ~50% of cases are identified in individuals aged 30-59, there is no significant difference in occurrence between males and females, and the incidence in individuals <20 years is rare (<0.5% of all cases) (15,16).

2. KIT mutation

There are two types of KIT receptors; the wild-type (145 kDa) and the mutant-type (125 kDa) receptor (17). The human KIT gene is a proto-oncogene located on chromosome 4q12-13. Its products belong to the receptor tyrosine kinase class III family, which also includes PDGFRA, PDGFRB, CSF1R and FLT3 receptor (18). The receptor tyrosine kinase class III family is characterized by an extracellular ligand binding domain, which consists of five immunoglobulin-like regions. In addition, the kinase structure includes a transmembrane domain, a juxtamembrane membrane domain and an intracellular kinase domain (Fig. 2). KIT is associated with many human malignancies, including small cell lung cancer, malignant melanoma, colorectal cancer and GISTs. More than 500 different KIT mutations have been discovered in human tumors but only a few of these are considered driver mutations (19). As a KIT ligand, stem cell factor (SCF) can induce receptor dimerization and activation of intrinsic tyrosine kinase activity after binding to the receptor, thus creating docking sites for signaling molecules containing SRC homologous domain 2 (SH2). The SH2 domain is present in numerous signal transduction molecules and consists of ~100 amino acids. It can regulate cell growth by binding phosphorylated tyrosine residues, including Tyr 568, Tyr 570, Tyr 703, Tyr 721, Tyr 730, Tyr 823, Tyr 900 and Tyr 936. Phosphorylated tyrosine, together with adjacent amino acid residues, forms a specific binding site for downstream signaling molecules and activates specific downstream signaling pathways, including the MAPK and PI3K/AKT pathways. The former results in the upregulation of transcription factors, such as MYC, ELK, CREB and FOS, whereas the latter results in the downregulation of cell cycle inhibitors and the enhancement of anti-apoptotic effects (20). Phosphorylation of Tyr 568 serves an important role in the activation of KIT and downstream signaling pathways. Phosphorylated Tyr 568 activates the SRC family kinase and in turn promotes activation of the KIT gene (21). SRC activity in tumors of patients with GISTs is significantly higher compared with that noted in normal tissues (22). Inhibition of SRC family kinase activity weakens KIT activation, suggesting that the activity of the SRC family kinase is necessary for the complete activation of KIT. In addition, SRC family kinases activate SHC to activate the downstream RAS/RAF/MEK/MAPK signaling pathway, which is involved in KIT-mediated cell proliferation (21). Another important KIT phosphorylation site is Tyr 721, which serves as a docking site for the regulatory subunit p85 of PI3K (23). Tyr 703 and Tyr 936 serve as binding sites of Grb2 which are recruited to activate the downstream PI3K/AKT and RAS/RAF/MEK/MAPK signaling pathways (24).

The signal transducers and activators of transcription (STAT) family of proteins is also associated with KIT signaling (25). Binding of SCF to the KIT receptor results in binding of JAK2 to c-kit, followed by autophosphorylation leading to phosphorylation of STAT1, STAT3 and STAT5. Phosphorylated STAT subsequently translocates to the nucleus where it binds to the promoter region of target genes to regulate transcription (26). At present, it is hypothesized that cell cycle disorders caused by genomic inactivation of cell cycle regulatory genes are a common mechanism during the transition from low-risk to high-risk metastatic GISTs (27).

The majority of GISTs (70-80%) have *KIT* gene mutations, which result in activation of c-Kit without SCF binding, thus increasing the activity of downstream signaling pathways (28). Mutations have been identified in exon 11 (70-80%) which encodes the juxtamembrane domain; exon 9, (10%) which encodes the extracellular domain; exon 13, which encodes the TK I domain (1%); and exon 17 (1%), which encodes the TK II domain (29,30). Mutations in the juxtamembrane domain affects the regulatory function of itself and increases auto-activation of the kinase. Mutations in the extracellular domain may disrupt the anti-dimerization motif and lead to homodimerization of the receptor (31).

Mutations in exon 11 are concentrated in the hot spots of codon 550-560 at the 5' end. The most frequently observed type of mutation is deletion at codon 557-558 at the 5' end, followed by deletion mutations at codon 559 and point mutations resulting in V575A (32). Imatinib has desirable therapeutic effects in the majority of patients with GISTs with mutations of the *KIT* gene. However, exon 11 mutations involving codon 557-558 deletion have also been demonstrated



Figure 1. Classification of GISTs. GISTs, gastrointestinal stromal tumors; KIT, KIT, KIT proto-oncogene, receptor tyrosine kinase; PDGFRA, platelet derived growth factor receptor α; SDH, succinate dehydrogenase BRAF, B-Raf proto-oncogene, serine/threonine kinase; NF1, neurofibromin 1.



Figure 2. Structure of KIT and PDGFRA receptors. The main mutation sites and phosphorylation sites of KIT and PDGFRA in sporadic GISTs. GISTs, gastrointestinal stromal tumors; KIT, KIT, KIT proto-oncogene, receptor tyrosine kinase; PDGFRA, platelet derived growth factor receptor α.

to increase the malignant potential of a tumor and reduce recurrence-free survival (RFS) (33-35). A European multicenter analysis showed that deletion mutations in exon 11 of the *KIT* gene at codon 557-558 may be used as a reference factor predicting a less favorable prognosis (36). In another retrospective study, moderate-risk patients with KIT exon 11 deletion mutations had similar recurrence-free survival (RFS) to those with high-risk diseases, whereas those with no KIT exon 11 deletion mutation exhibited similar clinical manifestations to those of very low-risk and low-risk patients. These findings also help to assess the prognosis of patients at moderate risk with deletion mutations in exon 11 deletion (37). Patients with KIT exon 11 mutations exhibit improved drug responses and higher overall survival compared with patients with KIT exon 9 mutations and those lacking KIT or PDGFRA mutations (31). This was also verified in phase I and phase II trials in Europe (38).

Patients with exon 9 mutations, characterized by codon 502-503 duplication had a higher recurrence and metastasis rate, were significantly associated with larger tumor morphology, tumor growth site (located in the small intestine) and spindle cell type tumor cells (39). There is also a relatively higher incidence of exon 9 mutations in men (40). In a Japanese population-based study, 4 patients with exon 9 mutations were also found to be at high risk and all died of metastasis. These results also suggest that mutation in exon 9 is associated with



Figure 3. Key signaling pathways in GISTs. (A) KIT or PDGFRA oncogenic mutations in GISTs initiate a related signaling pathway leading to activation of STAT, MAPK and PI3K signaling pathways. The NF1 protein regulates the RAS signaling pathway by catalytically activating GTP hydrolysis to inactive GDP. The PTEN tumor-suppressor gene terminates the signaling pathway by dephosphorylation of inositol PIP3 into PIP2. (B and C) SDH deficiency causes the accumulation of succinic acid which inhibits the activity of PHD caused by the accumulation of hypoxia-inducible factor α (HIF1 α). HIF1 α enters the nucleus and binds to HIF1 β to induce overexpression of glycolytic and angiogenic genes (including IGF and VEGF), which in turn acts on the RAS/RAF/MAPK and PI3K/AKT signaling pathways promoting the development of GISTs. GISTs, gastrointestinal stromal tumors; KIT, KIT, proto-oncogene, a receptor tyrosine kinase; PDGFRA, platelet derived growth factor receptor α ; JAK2, Janus kinase 2; STAT3, signal transducer and activator of ttranscription 3; GDP, guanosine triphosphate; RAF, RAF, Proto-oncogene serine/threonine-protein kinase; MEK, mitogen-activated protein kinase; PI3K, phosphoinositide 3-kinase; AKT, protein kinase B; mTOR, mammalian target of rapamycin; PIP3, phosphatidylinositol-3,4,5-triphosphate; PIP2, phosphatidylinositol-4,5-bisphosphate; IGF, insulin-like growth factor; VEGF, vascular endothelial growth factor.

a less favorable prognosis. However, 75% of Japanese patients with exon 9 mutations possessed a GIST located in the stomach, and the conclusion that this mutation type is more common in the small intestine suggested by Losata *et al* (41) was not observed, which may be related to different ethnicities (42). Controversially, no other studies have found any association between exon 9 mutations and a poor prognosis (43). Mutation screening for exon 9 is considered to have guiding significance for GIST treatment since these claim a higher dose of imatinib to be effective, and thus also is of great significance for the treatment. Besides after progression to imatinib resistance, GISTs with KIT mutations at exon 9 and wild-type GISTs seem to respond better to sunitinib (44).

Typically, primary mutations occur in exons 9 and 11, whereas secondary mutations most frequently occur in exon 13 encoding the TK I domain and exon 17 encoding the TK II domain. Most cases of metastatic secondary mutated GISTs have multiple mutations at the same time, both between different metastases and within the same metastatic deposit. Of the secondary mutations in KIT, ~30-40% are secondary KIT exon 17 mutations, accounting for resistance to imatinib or sunitinib in patients with GIST (45,46). In these patients, regorafenib shows therapeutic efficacy (47). Conversely, patients with secondary exon 13 mutations typically respond to sunitinib but not regorafenib (48).

The majority of mutations in exon 13 of KIT in GISTs are K642E mutations caused by base substitution (c.1945A>G; c.1948G>A) (49). These base substitution mutations result in constitutive activation of tyrosine phosphorylation, independent of ligand binding, which activates specific downstream signaling transduction pathways and promotes cell proliferation (50). The majority of mutations in exon 17 of KIT in GISTs are N822K (70%), which also result in maintenance of tyrosine phosphorylation activity (50). Less frequently observed mutations (N822Y, N822K, N822H, D816F, D816Y, D820Y, D820V, D816V and Y823D) have been identified in exon 17 (40,49). D816V has also been found in several other human malignant tumors, including acute myeloid

leukemia (51), mastocytosis (52), germ cell tumors (53), sinus natural killer/T cell lymphoma (54) and intracranial teratoma (55), but is relatively rare in GISTs. Mutations at codon 816 result in constitutive activation of the receptor, which activates the downstream PI3K/AKT signaling pathway. Most KIT exon 13 or exon 17 mutants have spindle-cell morphology, and fewer tumors have epithelioid cell characteristics. Gastric tumors with KIT exon 13 mutations are associated with increased invasiveness, whereas small intestine tumors with KIT exon 13 and exon 17 mutations did not result in any significant differences in behaviors compared with other mutant small intestine GISTs (49).

Furthermore, deletion mutations in chromosomes 14q and 22q are considered early events in the progression of KIT/PDGFRA mutant GISTs. Inactivation of dystrophin is hypothesized to be a late event in the progression of GISTs. Dystrophin is a tumor suppressor which is inactivated in 96% of metastatic GISTs but not in low-risk GISTs (27).

3. PDGFRA mutations

KIT mutations and PDGFRA mutations are mutually exclusive in GISTs. However, GISTs expressing KIT or PDGFRA oncoprotein exhibit similar mechanisms of tumorigenesis and progression (56). PDGFRA mutations exist in 10-15% of GISTs and are found in exon 12 which encodes the membrane proximal domain (1%), exon 14 which encodes the TK I domain (N659Y, N659K; <1%) and exon 18 which encodes the TK II domain (D824V, D842Y; 5%, I843_del, I843-H845_del, I843_del, I843-H845_del, D842-H845_del, D842-M844_del, D842-H845_del, D842-M844_del; 1%). Secondary mutations associated with secondary resistance occur primarily in exons 14 and 18. The majority of the PDGFRA mutations affect the TK II domain. These mutations alter the activation loop, modulating the ATP binding pocket and causing kinase activation leading to downstream signal transduction pathways that promote cell survival and proliferation (56,57). Protein kinase B (Akt), MAPK, and STAT1 and STAT3 in PDGFRA-mutant GISTs are uniformly activated, resulting in the activation of the same signaling pathways as KIT-mutant GISTs. PDGFRA-mutant GISTs are primarily epithelioid and are predominantly present in the stomach (58). Expression of CD117 in these tumors is weak or absent (56,59). PDGFRA-mutant GISTs are less invasive, accounting for only 2.1% of metastases in patients with GISTs (4,60).

The most common mutation type of PDGFRA in GISTs is D842V mutation in exon 18 (accounting for 9.8% of all mutations and 65% of exon 18 mutations in PDGFRA). The substitution of a valine at codon 842 by aspartic acid leads to resistance to first- and second-line tyrosine kinase inhibitors (TKIs) such as imatinib and sunitinib in patients, and therefore, these patients do not benefit from treatment with TKIs (61). It is also worth noting that in gastric tumors with a PDGFRA mutation, the vast majority of the advanced cases carry the exon 18 PDGFRA D842V mutation (36). Avapratinib (BLU-285) is a novel inhibitor that specifically targets KIT exon 17 and PDGFRA D842 mutations. The results of the phase I NAVIGATOR trial showed that the overall response rate (ORR) of patients with PDGFRA D842V mutation was 84% and treatment caused tumor shrinkage in 98% of cases. The NAVIGATOR phase I trial included four different groups of patients with GISTs: i) GISTs treated with second-line therapeutics; ii) GISTs being treated with third- or fourth-line therapeutics that were regorafenib-naïve; iii) GISTs being treated with fourth-line or more advanced line therapeutics; and iv) PDGFRA D842V-mutated GISTs. In the second-line treatment group, the reported avapritinib ORR was 25%. In patients being treated with third- or fourth-line therapeutics that were regorafenib-naïve, avapritinib was associated with an ORR of 26%. In the patients being treated with fourth-line or more advanced line therapeutics, ORR was 20%. In addition, in vitro studies have shown that crenolanib exhibited improved antiproliferative effects compared with imatinib for patients with this type of mutation. Phase III clinical trials of crenolanib (Randomized Trial of Crenolanib in Subjects with D842V Mutated GIST; clinicaltrials.gov identifier, NCT02847429), and phase III randomized trials of avapritinib and regorafenib (VOYAGER, NCT03465722) are also on-going (62). The majority of GISTs with PDGFRA mutations excluding D842V mutation still respond to imatinib, therefore mutation screening is of great significance for the treatment of GIST (63).

PDGFRA mutations are also found in exon 12 (juxtamembrane domain; JM) and exon 14 (TK I domain), but are relatively rare (64). Among these, exon 12 point mutation V561A is the second most common type of PDGFRA mutation (65). The majority of the exon 14 mutations of PDGFRA are N659K point mutations. Clinical data showed that most tumors with this mutation were located in the stomach, and most of these were epithelioid cells with relatively good prognosis (66).

4. Familial GISTs

The majority of KIT and PDGFRA mutations are sporadic and are only found in GIST tissues. However, there are also patients with rare familial GISTs with autosomal dominant inheritance, and affected family members have a 100% penetrance rate (67). Clinical manifestations include dysphagia, excessive skin pigmentation, urticaria pigmentation and mastocytosis. These patients have the same type of germline KIT and PDGFRA mutations as the somatic mutant GISTs. KIT mutations in familial GIST patients have been found in exon 11 (V559A, W557R, D579 del) (68-70), exon 17 (D820Y) (71) and exon 8 (D419 del) (72). The PDGFRA mutation was also found in exon 18 (D846Y) (73). Histologically, familial GISTs are basically the same as that of patients with sporadic GISTs, but there are multiple lesions, primarily from the proliferation of interstitial cells of Cajal. Identification of patients with familial GISTs is important as the clinical management patterns are different from those of GISTs with somatic mutations. Nevertheless, currently there are no specific treatment options for such patients. Considering the presence of multiple lesions, conservative resection is often adopted in most medical institutions.

5. Wild-type GISTs

Most GISTs are driven by oncogenic KIT or PDGFRA receptor tyrosine kinase activating mutations. However, ~10-15% of GISTs lack KIT and PDGFRA mutations, and are referred

to as wild-type GISTs. Wild-type GISTs can be divided into succinate dehydrogenase complex (SDH)-deficient and non-SDH-deficient GISTs (63). Mutations of any of the four SDH subunits or of members of the RAS pathway [(K/N/H-RAS, BRAF, neurofibromatosis type 1 (NF1)] have been observed in wild-type GISTs.

Whole-genome sequencing revealed that the genome of wild-type GISTs exhibit a low mutation frequency, and only ~25% of patients have chromosomal imbalances. Mutations in the 14q23.1 region of KIT/PDGFRA-mutant GISTs result in downregulation of tumor suppressor RTN1, DAAM1 and DACT1, but mutations in the same region in wild-type GISTs does not result in these effects (74). Wild-type GISTs tend to develop in younger patients; ~85% of GISTs in patients <23 years of age are wild-type. Lesions are primarily present in the stomach, and the volume of the tumor is often small, but lymph node metastases are more common. TKIs are often less effective in these cases (75-77).

SDH-deficient GISTs. Succinate dehydrogenase complex (SDH; also known as mitochondrial complex II) deficiency is more common in wild-type GISTs, accounting for ~5% of all GISTs. The lack of SDH is considered to be an important feature of several human tumor subtypes, including GISTs, paraganglioma, renal cell carcinoma and pituitary adenomas (78). SDH is a complex of enzymes located on the mitochondrial inner membrane, and consists of four subunits (SDHA, SDHB, SDHC and SDHD) and two kinds of succinate dehydrogenase assembly factors (SDHAF1 and SDHAF2), which are components of the tricarboxylic acid cycle and the respiratory electron transport chain.

Approximately 50% of subunit mutations are found in SDH-deficient GISTs, and the most frequently observed being SDHA which are primarily germline mutations, accounting for ~30% of all mutations, with mutations in other subunits accounting for the remaining ~20% (79). SDHA-mutant GISTs can be individually identified by SDHA immunohistochemistry. In the other 50% of cases, no subunit mutation is observed, but immunohistochemistry showed a significant decrease or deletion of SDHB protein expression, and the respiratory chain complex II enzyme activity was lost as well. This may be due to epigenetic modifications or related protein defects involved in maintaining stability (80).

Defects in any of the subunits, particularly defects in SDHB, will result in instability of the SDH complex, which in turn affects the function of the complex. When the SDH complex is dysfunctional, there is an accumulation of succinic acid in the cytoplasm which results in the accumulation of hypoxia inducible factor 1 subunit α (HIF1 α). HIF1 α transcriptionally upregulates hypoxia-related tumorigenic processes and angiogenesis. Thus, defects in energy metabolism are key carcinogenic mechanisms (81). Therefore, if any of the SDH subunits are mutated/inactivated, immunohistochemical staining of SDHB is absent, and as such SDHB-negative staining is now considered to be a highly sensitive marker for any SDH subunit germline mutation (80,82).

SDH-deficient GISTs occur primarily in children and patients with Carney-Stratakis syndrome and Carney triad which affects children and younger adults. Patients are usually <40 years of age, while other GISTs are rarely seen in younger individuals. SDH-deficient GISTs account for two-thirds of cases in the 20-29 age group and are more common in females (16). Lesions are almost always located in the stomach, and the antrum is the most common location, followed by the posterior wall of the stomach and the fundus, and they have a tendency for lymphatic invasion and lymph node metastasis compared with other mutant GIST types (83). Immunohistochemically negative SDHA GISTs are rare in children, are more common in males, and lack of SDHA staining is associated with an increased rate of metastasis to the liver; however, there is no difference in tumor size or mitosis rate (79).

The Carney triad includes GISTs, pulmonary chondromas and extra-adrenal paraganglioma. It was first described as a triad of gastric leiomyosarcoma in 1977, and only few patients exhibit a complete Carney triad. In the majority of cases, only two of these tumors are observed (84). Patients with Carney triad are typically younger women who are susceptible to various tumors, including pheochromocytoma and other non-functional bilateral or unilateral adrenal adenomas. Although the Carney triad-associated GISTs lack mutations in any of the SDH subunits, the function of the SDH complex is still impaired and may be associated with hypermethylation of the SDHC promoter (85).

Carney-Stratakis syndrome, first described in 2002, is a rare hereditary syndrome inherited by autosomal dominant inheritance with incomplete penetrance. It is characterized by multifocal gastric GISTs and multicentric paraganglioma (86). Germline mutations in *SDHB*, *SDHC*, *SDHD* have been identified in patients with Carney-Stratakis syndrome (87) and no mutations in the coding sequence of the *SDHA* gene have been identified (88).

Upregulation of insulin like growth factor 1 receptor (IGF1R) expression in SDH-deficient tumors is considered to be a feature of SDH-deficient GISTs (89). IGF1R is part of the insulin-like growth factor family of proteins, which consists of two ligands (IGF1 and IGF2), two receptors (IGF1R and IGF2R) and six IGF binding proteins (IGFBPs). Binding of IGF and IGFR activates downstream signaling, including the RAS/RAF/MAPK and PI3K/AKT pathways (Fig. 3C) (90). Dysfunction of SDH leads to the accumulation of succinic acid, which in turn inhibits the activity of proline hydroxylase, resulting in the accumulation of HIF1a, translocation of HIF1 α to the nucleus and dimerization of HIF1 β to form an active transcription factor that induces expression of glycolytic and angiogenic genes (including IGF and VEGF), which in turn promotes cell proliferation via the RAS/RAF/MAPK and PI3K/AKT signaling pathways (57,91-93). IGF1R expression has been observed in 88.75% of SDH-deficient GISTs, whereas only in 1% of SDHB-positive patients. Thus detection of IGF1R can help to identify SDH defective GISTs. IGF1 has been shown to promote cell proliferation in vitro. Animal experiments have shown that inhibiting IGF signaling reduced tumor growth (94). Epidemiological evidence suggests that IGF1 levels are associated with cancer risk and prognosis (95). At present, upregulation of IGF1R is observed in a number of different types of cancer. Because of its role in the metabolism of cancer cells and its potential correlation with the survival of malignant cells, IGF1R has become a target of anticancer therapy (96-98). In a phase I clinical trial, patients with

solid tumors were treated with IGF1R monoclonal antibody R1507 (also known as RO4858696) and chemotherapeutics or targeted drugs. One of these patients did not receive the full treatment, but the partial response to the disease reached 3 years (99). However, the complexity of the IGF1R pathway and its interaction with other signaling pathways has not been fully elucidated. Further preclinical research is required to understand the complex mechanisms to develop improved therapeutic options.

Non-SDH-deficient GISTs. Non-SDH-deficient GISTs include NF1 correlation, BRAF mutation, RAS gene mutation and quadruple wild-type. GISTs with BRAF/RAS or NF1 mutations can be collectively called RAS pathway-mutant GISTs. The demographic characteristics of non-SDH-deficient GISTs are similar to those of KIT/PDGFRA-mutant GISTs, and are more frequently observed in adults and primary exhibit a spindle-cell morphology (100). However, unlike KIT/PDGFRA-mutant GISTs, non-SDH-deficient wild-type GIST are primarily located in the small intestine.

NF1 gene mutation. NF1, also known as von Recklinghausen disease, is an inherited cancer susceptibility syndrome, caused by a biallelic deletion of the NF1 gene and is characterized by neurological, cutaneous and skeletal lesions. It is one of the most common genetic syndromes with an incidence of 1/2,500-3,000 individuals (101). Patients with NF1 type have a higher risk of developing GISTs, and ~7% of NF1 patients have concurrent GISTs, which is considerably higher than the normal population (102). Patients with NF1-related GISTs are usually younger, and the lesions are primarily located in the duodenum and small intestine and exhibit a slower clinical progression. However, 15-20% of patients with NF1-related GISTs exhibit malignant clinical outcomes. The tumors are small in size, with a high positive rate of CD117 and CD34 expression. Tumor tissues are composed of cells with a spindle-cell like morphology, with a low mitotic rate (100,103).

The neurofibromin protein encoded by the *NF1* gene regulates the RAS signaling pathway by catalytically activating Ras-GTP hydrolysis to inactive Ras-GDP. Mutation of the *NF1* gene results in loss of neurofibromin function leading to constitutive activation of RAS, which increases downstream signaling of receptors via the MAPK pathway. This is considered to be an important mechanism for the pathogenesis of NF1-related GISTs (103). Unlike common GISTs, the JAK-STAT3 and PI3K-AKT pathways are less active in NF1-related GISTs (102). NF1-related GISTs do not respond well to imatinib (104); however, there have been reports of therapeutic response to sunitinib (105). Given that NF1-related GISTs increases signaling through the MAPK pathway, this increases the likelihood of treatment with MEK inhibitors.

BRAF gene mutations. The *BRAF* (B-Raf proto-oncogene, serine/threonine kinase) gene encodes serine/threonine protein kinases which belong to the RAF family. These kinases serve a role in regulating the MAPK/ERK signaling pathway and can affect cell cycle progression, cell division and differentiation (106). Pathogenic mutations in the *BRAF* gene cause the

RAF protein to be constitutively activated, resulting in uncontrolled cell growth and proliferation. Additionally, BRAF mutations cooperate with Rac1b, AKT3 and other signaling molecules, which also promote the viability and proliferation of cancer cells (107). BRAF mutations are observed in many benign and malignant tumors, such as benign congenital and acquired melanocytic nevus, malignant melanoma, papillary thyroid cancer, non-small cell lung cancer and colorectal adenoma (108).

BRAF gene mutations account for $\sim 4\%$ of the wild-type GISTs, and the most common mutation is V600E of exon 15, and the BRAF V600E site mutation is considered to be exclusive of KIT and PDGFRA mutations (109). Hostein et al (110) analyzed GIST pathology from the Bergonie Institute from 2004 to 2008 and found that the lesions of GISTs with BRAF mutations were mostly located in the small intestine (5/9; 56%), followed by the stomach (2/9; 22%). There was no significant association between tumor location, tumor size and mitosis between wild-type GISTs with or without BRAF mutations. However, the sample size in this study was too small, thus the results may not be reliable. MEK inhibitors and RAF inhibitors are used to inhibit pathogenic consequences of mutations of BRAF. MEK inhibitors inhibit the downstream MEK protein of BRAF, while RAF inhibitors inhibit the active RAF protein to control the uncontrolled MAPK/ERK signaling pathway. Currently, the FDA approved MEK inhibitors include trametinib and cobimetinib, while RAF inhibitors are dabrafenib and vemurafenib. Patients with BRAF mutations in GISTs have a longer overall survival and a better clinical outcome (111).

RAS gene mutation. The RAS protein acts as a molecular switch that switches between its active GTP binding state and inactive GDP binding state. The majority of RAS mutations are observed in codons 12, 13 or 61. Mutations of the RAS gene or its regulatory factors cause the RAS protein to remain active, leading to tumorigenesis. Activated alleles of HRAS, NRAS and KRAS have been shown to possess a similar phenotype to activated BRAF, CRAF, MEK1 or MEK2-driven alleles in human tumors (112). Miranda et al (113) identified codon 12 (G12D) and codon 13 (G13D) mutations in the KRAS gene in ~5% of patients with GISTs. G12D-mutant tumors are accompanied by deletion mutations in KIT exon 11 (570-576 and 579), whereas patients with G13D mutations are accompanied by PDGFRA gene D842V mutation. Additionally, KRAS and BRAF mutations may affect the response of imatinib-sensitive KIT mutants to imatinib therapy, thus it was suggested that KRAS and BRAF mutation analysis should be introduced in clinical diagnosis of patients with GISTs.

Quadruple wild-type GISTs. Quadruple wild-type GISTs are not associated with SDH mutations, BRAF mutations or RAS mutations (114). Nannini *et al* (115) analyzed the genome of patients with quadruple wild-type GISTs and found that they had significantly different genome profiles from KIT/PDGFR mutation or SDH-deficient GISTs. Molecular markers CALCRL and COL22A1, and specific oncogenes, including NTRK2 and CDK6, and ETS were found in both small intestine quadruple wild-type GISTs. Brenca *et al* (116) found an ETV6-NTRK3 fusion in a patient with rectal

Subtype	Genetic alteration	Mutation	Frequency	Localization	Features
KIT (70-80%)	Exon 11 (JM)	W557-K558_del V559_del V575A	70-80%	Whole GI tract	Malignant potential Imatinib (responsive)
	Exon 9 (EC)	Insertion AY502-503	10%	Small intestine and colon	Higher recurrence and metastasis rates; Imatinib (partially resistant) Sunitinib (responsive)
	Exon1 3 (TK I)	K642E	1%	Whole GI tract	Secondary mutations; Imatinib (responsive)
	Exon 17 (TK II)	N822K D816V	1%	Whole GI tract	Secondary mutations (30-40%); Imatinib or sunitinib resistant; Regorafenib (responsive)
PDGFRA (10-15%)	Exon 12 (JM)	V561A		Stomach	Imatinib (responsive)
	Exon 14 (TK I)	N659Y N659K	<1%		Imatinib (responsive) Relatively good prognosis:
	Exon 18 (TK II)	D824V, D842Y (I843_del I843-H845_del I843_del I843-H845_del	5%	Whole GI tract	Imatinib resistant; avapratinib, crenolanib responsive;
		D842-H845_del D842-M844_del D842-H845_del D842-M844_del)	1%		
SDH-deficient GISTs		SDHx mutation	≈5%	Stomach	Children and young adults Female predilection; High rate of liver metastasis; Overexpression of IGF1R; Imatinib resistant
Non-SDH-deficient GISTs		NF1	<1%	Generally duodenum and small intestine	Younger age; High positive rates of CD117 and CD34; Imatinib resistant
	Exon 15	BRAF (V600E)	≈4%	Unknown	Longer overall survival and better clinical outcome; Imatinib resistant
	KRAS	G12D G13D	≈5%	Unknown	May affect the response of imatinib-sensitive KIT mutants to imatinib therapy
Quadruple wild-type GISTs		ETV6-NTRK3 FGFR1-HOOK3 FGFR1-TACC1 Somatic gene mutations (TP53, MEN1, MAX, FGFR1, CTNND2, CHD4)	Unknown	Unknown	Activation of IGF1R signaling

Table I. Characteristics of each molecular subtype of GISTs.

GISTs, gastrointestinal stromal tumors; KIT, KIT proto-oncogene, receptor tyrosine kinase; PDGFRA, platelet derived growth factor receptor α; JM, juxtamembrane; EC, extracellular domain; TK, TKI domain (ATP-binding pocket); TKII, TKII domain (activation loop); SDH, succinate dehydrogenase; NF1, neurofibromatosis type 1; GI, gastrointestinal.

quadruple wild-type GISTs. Shi et al (117) found a fusion of the FGFR1 gene (FGFR1-HOOK3 and FGFR1-TACC1) in quadruple wild-type GISTs. NF1 gene inactivation was also observed in quadruple wild-type GISTs, but the patient did not show neurofibromatosis type 1 symptoms (118). In addition, somatic gene mutations such as TP53, MEN1, MAX, FGFR1, CTNND2 and CHD4 were found in quadruple wild-type GISTs (119). These findings may assist in the identification of new therapeutic targets. In vitro experiments indicate that ETV6-NTRK3 fusion is associated with activation of downstream IGF1R signaling and that tumor cells are susceptible to IGF1R inhibition. In addition, ALK inhibitors, a target drug for ETV6-NTRK3 gene fusion, have shown therapeutic potential (116). The Murine double-minute 2 inhibitor can inhibit the growth of TP53 wild-type GIST cells and enhance the therapeutic response of GIST cells to TKI. This suggests that the regulation of the p53 gene may be a potential effective therapeutic strategy (120).

6. ctDNA and GISTs

Extracellular DNA fragments in different body fluids (plasma, serum, urine, and saliva) are referred to as cell free DNA (cfDNA). The primary part of cfDNA in the blood is adsorbed to the surface of white blood cells or red blood cells, and its half-life is short because it is easily degraded by nucleases (121,122). Among these, cfDNA derived from tumor cells is called ctDNA, which may be produced by apoptosis or necrosis of cancer cells (123). cfDNA is primarily composed of ctDNA, and normal extracellular DNA accounts for only a small portion of cfDNA (124,125). The feasibility report of plasma-based ctDNA analysis for tumors in GISTs was first published at the ASCO annual meeting in 2013. The report showed that the consistency of mutations in exon 9 and 11 of KIT between tumor tissue and plasma was 84%. In particular, the consistency of KIT mutations of exon 9 was 100%, whereas that of KIT exon 11 was only 79%. It is also noteworthy that a higher KIT mutation rate (47% vs. 12%) was detected in plasma by BEAMing compared with tumor tissue (13). Maier et al (126) subsequently confirmed the presence of KIT/PDGFRA mutant ctDNA in the plasma, and the quantity of mutant ctDNA was associated with the clinical course of the disease. Namløs et al (127) found that the detection rate of tumor ctDNA mutations in the plasma of high-risk patients or patients with metastatic diseases was higher compared with patients with localized, or moderate- or low-risk GISTs. Jilg et al (128) confirmed that tumor-specific KIT and PDGFRA mutations could be detected in the ctDNA of patients with active GISTs and were positively correlated with disease activity. Other mutations indicating disease progression, including BRAF, NRAS, PIK3CA, PTEN and CTNNB1 mutations, are found in ctDNA, which can influence treatment regimens. All the above studies have demonstrated that ctDNA detection in plasma has important guiding significance for the diagnosis and prognosis of GISTs. However, liquid biopsy technology as a complement to other commonly used clinical techniques still has many limitations, and it is far from ready for use in clinical practice; however, the prospects of this technology is promising.

7. Non-coding RNAs and GISTs

Non-coding RNA refers to RNA that does not encode proteins. It has been found that various miRNAs and lncRNAs are associated with the occurrence and development of GISTs.

MicroRNAs (miRNAs) are small non-coding RNAs which participate in the regulation of post-transcriptional gene expression (129). Dysregulation of various miRNAs has been identified in many different types of cancer, including gastric cancer (130), colorectal cancer (131), pancreatic cancer (132), and childhood glioma (133). miRNAs regulate target gene expression by acting on key molecular pathways and mediate cell invasion, migration, proliferation, apoptosis and drug resistance. A German study found that miR-221 and miR-222 were downregulated in wild-type and mutant GISTs, and in vitro experiments, they confirmed that the expression of these miRNAs induced apoptosis through a KIT/AKT/BCL2 signaling pathway (134). miR-17 (135), miR-20a (135), miR-21 (136), miR-133b (137), miR-137 (138), miR-152 (139), miR-218 (140), miR-494 (141), miR-518a (117), have all been confirmed to be downregulated in GISTs. Overexpression of miR-218 also inhibits the PI3K/AKT pathway and thereby increases the sensitivity of GIST cells to imatinib (140). Conversely, miR-125a and miR-196a were found to be upregulated in GISTs. Overexpression of miR-125a is associated with imatinib resistance (142). Overexpression of miR-196a increases the invasiveness of cancer cells (143), and is associated with high risk classification, a high rate of metastasis and reduced survival rates (144). In addition, studies have shown that circulating miRNAs can be used as biomarkers for detection of various types of malignant tumors, including gastric cancer (145), colorectal cancer (146), and pancreatic cancer (147). Serum circulating miR-518e-5p has been found to be a potential non-invasive biomarker for early detection and diagnosis of secondary imatinib-resistant GISTs (148).

IncRNAs works by interacting with other cellular molecules, including DNA, RNA binding protein and RNA. IncRNAs serve an important role in the diagnosis, monitoring, prognosis and evaluation of therapeutic reactivity of tumors (149). HOTAIR is one of the most widely studied carcinogenic lncRNAs. Overexpression of HOTAIR is associated with an increase in invasiveness of GIST cells and knockdown of HOTAIR can inhibit the invasiveness of GIST cells (143). HOTAIR also regulates the progression of GISTs by inducing methylation of the promoter of the pro-cadherin 10 gene in GIST cells (11). HOTAIR is upregulated in invasive GISTs and mediates gene-specific DNA methylation. This further confirms the role of HOTAIR in GISTs (150). Yan et al (151) confirmed that CCDC26 enhances the sensitivity of imatinib by downregulating IGF-1R expression, and showed that CCDC26 may be used as a therapeutic target to reverse imatinib resistance in patients with GISTs.

8. Conclusion

The progress made in the field of molecular biology in the past 20 years has provided a deeper understanding of the pathogenesis of GISTs. The characteristics of each molecular subtype are summarized in Table I. Receptor TKIs currently used to treat patients with GISTs are based on these subtypes and the use of these drugs significantly prolong life expectancy. Nevertheless, resistance to second-line therapeutics is becoming increasingly common. Additionally, there is no specific treatment for patients with wild-type GISTs. Thus an improved understanding is required to further understand the molecular mechanisms underlying the different subtypes of GISTs to develop improved therapeutic options.

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Availability of data and materials

The datasets used during the present study are available from the corresponding author upon reasonable request.

Authors' contributions

HD and ZY conceived and designed the study and prepared the manuscript. XY, YY, XL and CH were responsible for the literature search, data visualization and analysis. KG and YJ retrieved the relevant literature and revised the manuscript. All authors read and approved the final manuscript.

Ethics approval and consent to participate

Not applicable.

Patient consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

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