Kinase Mutations and Imatinib Response in Patients With Metastatic Gastrointestinal Stromal Tumor

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**Purpose:** Most gastrointestinal stromal tumors (GISTs) express constitutively activated mutant isoforms of KIT or kinase platelet-derived growth factor receptor alpha (PDGFRα) that are potential therapeutic targets for imatinib mesylate. The relationship between mutations in these kinases and clinical response to imatinib was examined in a group of patients with advanced GIST.

**Patients and Methods:** GISTs from 127 patients enrolled onto a phase II clinical study of imatinib were examined for mutations of KIT or PDGFRα. Mutation types were correlated with clinical outcome.

**Results:** Activating mutations of KIT or PDGFRα were found in 112 (88.2%) and six (4.7%) GISTs, respectively. Most KIT mutations involved exon 9 (n = 23) or exon 11 (n = 85). All KIT mutant isoforms, but only a subset of PDGFRα mutant isoforms, were sensitive to imatinib, in vitro. In patients with GISTs harboring exon 11 KIT mutations, the partial response rate (PR) was 83.5%, whereas patients with tumors containing an exon 9 KIT mutation or no detectable mutation of KIT or PDGFRα had PR rates of 47.8% (P = .0006) and 0.0% (P < .0001), respectively. Patients whose tumors expressed either exon 11 KIT mutations had a longer event-free and overall survival than those whose tumors expressed either exon 9 KIT mutations or had no detectable kinase mutation.

**Conclusion:** Activating mutations of KIT or PDGFRα are found in the vast majority of GISTs, and the mutational status of these oncoproteins is predictive of clinical response to imatinib. PDGFRα mutations can explain response and sensitivity to imatinib in some GISTs lacking KIT mutations.

**GASTROINTESTINAL STROMAL TUMORS** (GISTs) are mesenchymal neoplasms that arise primarily in the gut wall and are typically characterized by the expression of the receptor tyrosine kinase KIT (CD117).1,2 Recent studies have established that activating mutations of KIT are present in up to 92% of GISTs and likely play a fundamental role in the development of these tumors.3-10 The subset of GISTs that lack detectable KIT mutations can be divided into a group that has activating mutations in the related tyrosine kinase platelet-derived growth factor receptor alpha (PDGFRα) and a group without identified kinase mutations.11

Imatinib (formerly STI571; Gleevec in the United States and Glivec in Europe; Novartis Pharma, Basel, Switzerland) is a competitive inhibitor of BCR-ABL, ARG, KIT, PDGFRα, and PDGFRβ tyrosine kinases.12-15 In preclinical studies, imatinib was active against mutant isoforms of KIT commonly found in GIST.13,16 Subsequent treatment of a patient with metastatic GIST resulted in marked clinical, radiologic, and pathologic improvement.17 The clinical activity of imatinib for unresectable, metastatic GISTs has been documented in two clinical studies.18,19

In the present report, pretreatment GIST samples from patients enrolled onto a multicenter, open-label, randomized phase II study of imatinib treatment of metastatic GIST were analyzed for KIT or PDGFRα mutations with the aim of correlating clinical response to imatinib with tumor genotype.19 In addition, the kinase activities of GIST-associated KIT and PDGFRα mutant isoforms were tested for sensitivity to imatinib in vitro in an effort to confirm the relevance of these molecular mechanisms to the observed clinical outcomes.

**PATIENTS AND METHODS**

**Analysis of KIT and PDGFRα Mutations**

Archival pretreatment pathology specimens were obtained from patients enrolled onto a randomized phase II trial of imatinib for metastatic GIST (CSTI571B 2222). The clinical design and primary clinical results have been previously published.19 The study was approved by the local institutional review board of each participating institution, and written informed consent was obtained from each patient. In addition, informed consent for the

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analysis of tumor-associated genetic alterations was obtained independently of patient consent for participation in the clinical study. Sections were prepared from formalin-fixed, paraffin-embedded pretreatment specimens trimmed to enrich for tumor cells. Polymerase chain reaction amplification of genomic DNA for KIT and PDGFRA was performed, and amplicons were analyzed for mutations as previously described. In 15 cases with available frozen material, the entire KIT cDNA was sequenced.

In Vitro Studies

KIT and PDGFRA mutations were cloned by site-directed mutagenesis of the respective wild-type cDNA. All mutations were confirmed by bidirectional sequencing. Chinese hamster ovary cells were transiently transfected with plasmids encoding cDNAs for wild-type or mutant proteins. Twenty-four hours after transfection, the cells were treated with control media or media containing various concentrations of imatinib for 90 minutes. The cells were then collected, and protein lysates were prepared and analyzed for KIT or PDGFRA activation as previously described. Experiments involving recombinant DNA were performed using BL2 procedures in accordance with National Institutes of Health Guidelines for Research Involving Recombinant DNA Molecules.

Statistical Analysis

Best clinical response to imatinib were classified as partial responses (PR), stable disease, progressive disease (PD), or nonassessable (NA) determined using standard Southwest Oncology Group response criteria as listed in the report of the primary clinical results of this trial. Response rates were calculated using an intention-to-treat analysis. Seven patients were classified as NA for response. Five of these patients had early adverse events, and therefore clinical response could not be assessed or confirmed (two patients with exon 11 mutations, two patients with exon 9 mutations, and one patient with no mutation). After central radiology review, two patients were deemed to have assessable but not measurable disease (one patient with a KIT exon 11 mutation and one patient with PDGFRA D842V mutation). Patients with NA disease were included in the calculations of event-free survival and survival. Tumor response rates were compared among mutation groups using Fisher’s exact test. Event-free survival and overall survival was estimated using the Kaplan-Meier method and the differences among mutation groups were compared using a log-rank test. For the event-free survival analysis, end point clinical events were defined as PD, patient death from any cause, withdrawal of patient consent, or discontinuation of therapy as a result of toxicity. The current report includes all available patient follow-up data through August 27, 2002.

Logistic and proportional hazards models were fitted to the response, event-free survival, and overall survival data to assess the possible interactions of mutational status and clinical outcome. The following patient characteristics were assessed: daily imatinib dose, sex, Eastern Cooperative Oncology Group performance status at baseline, prior chemotheraphy, age greater than 65 years, presence of liver metastases, decreased pretreatment serum albumin, elevated pretreatment liver transaminases, elevated pretreatment creatinine, presence or absence of exon 9 KIT mutation, presence or absence exon 11 KIT mutation, absence of any KIT or PDGFRA mutation, presence or absence of other genotype (mutation of KIT exon 13 or mutation of KIT exon 17 or any PDGFRA mutation), and no specimen available for genotyping.

RESULTS

Spectrum of Mutations in GIST Patients Enrolled Onto the Phase II Trial

Tumor specimens suitable for genetic analysis were available from 127 (86.4%) of the 147 patients enrolled in this study. In four additional patients, a sample was obtained but proved unsuitable because of an insufficient amount of GIST in the specimen. The results of the genotyping studies are graphically depicted in Fig 1. Overall, 112 (88.2%) of the 127 GISTs evaluated had activating mutations of KIT exon 9, 11, 13, or 17. No GIST had an activating mutation in more than one KIT exon. The most common type of mutation (71 patients) was in-frame deletion of a portion of the juxtamembrane domain (exon 11). These deletion mutations were sometimes accompanied by point mutations or small insertions involving amino acid residues immediately preceding or after the deletion, or both. Isolated point mutations of KIT exon 11 were confined to codons 557 (three cases), 559 (three cases), 560 (six cases), and 576 (two cases). The second most common mutation type was in-frame duplication of nucleotides in KIT exon 9 resulting in the
previously described insertion of AY residues at codon 502 (22 patients) or a novel insertion of FAF residues at position 506 (one patient).4

The entire coding region of KIT mRNA was analyzed in 15 tumors for which frozen tumor was available, using a combination of reverse transcriptase polymerase chain reaction and direct sequencing. In all cases, including one case with no detectable mutation, these results confirmed the genomic DNA analyses; no additional mutations were discovered. In 10 (7.9%) of the 127 cases, no wild-type KIT allele was detected, indicating a homozygous or hemizygous genotype. Because of the presence of normal tissue elements in most of the GIST specimens analyzed, 7.9% represents a minimum estimate of the fraction of GISTS that express only mutant KIT.

Fifteen of 127 cases had no detectable KIT mutation (KIT wild-type [WT]). Given our recent finding of gain-of-function PDGFRA mutations in KIT-WT GISTS, we tested these cases for PDGFRA mutations in the proximal extracellular (exon 10), juxtamembrane (exon 12), TK1 (exon 14), and activation loop (exon 18) domains. Six of the KIT-WT tumors had a PDGFRA mutation (40.0% of KIT-WT). Five of these mutations were in the kinase activation loop, including the previously described point mutation D842V (three patients) and deletion DIMH842–845 (one patient), as well as a novel deletion of I843 (one patient).11 The remaining tumor contained the previously described point mutation V561D in the PDGFRA juxtamembrane domain. None of these cases was included in our original report of PDGFRA mutations in GISTS.11 Screening of 97 cases from this study that had a documented KIT mutations failed to yield any PDGFRA exon 18 mutations, supporting our previous observation that gain-of-function mutations in KIT and PDGFRA are mutually exclusive in GISTS.11

In Vitro Activity of Imatinib Against Representative KIT and PDGFRA Oncoproteins Associated With GISTS

Imatinib binds reversibly to the ATP-binding pocket of ABL, ARG, KIT, PDGFRA, and PDGFRB but not other tyrosine kinases.9,12,15 To assess the drug sensitivity of KIT oncoproteins associated with GISTS, the mutant isoforms were expressed in Chinese hamster ovary cells, and inhibition of autophosphorylation was examined using varying concentrations of imatinib.

The KIT isoforms that were tested included the most commonly identified codons altered by point mutation (V560G) or deletion mutation (del 557 to 558 WK) in exon 11, the exon 9 insertion (ins AY at codon 503), and the point mutations observed in exon 13 (K642E) and exon 17 (N822H, N822K). As shown in Fig 2A, all of these mutant isoforms were as sensitive to imatinib as wild-type KIT (concentration that inhibits phosphorylation by 50% [IC_{50}], 100 to 200 nmol/L). In contrast, and as previously described,28 the mastocytosis-associated D816V isoform was resistant to imatinib up to 10 μmol/L.28 The sensitivity of another exon 11 deletion (del codon 579) was similar to that of the other GIST-associated KIT mutations (data not shown).

Similar assays were performed to test the potency of imatinib against wild-type and mutant isoforms of PDGFRA. In contrast to native PDGFRA, the mutant PDGFRA isoforms were strongly phosphorylated in the absence of PDGF-AA ligand (Fig 2B). Phosphorylation of ligand-stimulated native PDGFRA was positively inhibited by imatinib (IC_{50}, 100 to 200 nmol/L), consistent with earlier reports.12 Imatinib was similarly effective against the V561D, del DIMH842–845, and delI843 PDGFRA isoforms (IC_{50}, 100 to 200 nmol/L), whereas inhibition of the D842V mutant required 10- to 20-fold higher drug levels (IC_{50}, approximately 1 to 2 μmol/L).

Correlation of KIT Mutational Status With Clinical Response to Imatinib

Best clinical response to imatinib were classified as PR, stable disease, PD, or NA determined using standard Southwest Oncology Group response criteria24 as listed in the report of the primary clinical results of this trial.19 No patient in the study had a complete response.19 Response rates were calculated using an intention-to-treat analysis. Response data for the various tumor genotypes are listed in Table 1. Patients whose tumor expressed an exon 11 mutant KIT protein were much more likely to have a PR with imatinib therapy (83.5%) than patients whose tumor expressed either an exon 9 mutant isoform protein (47.8%; P = .0006) or contained no detectable mutation of KIT or PDGFRA (0.0%; P < .0001). The frequency of a PR was also significantly different between patients with an exon 9 mutation versus no detectable mutation (P = .013). There was no statistically significant difference in the response rates between the group of patients with KIT exon 11 point mutations and the group with exon 11 deletion mutations or between the group with heterozygous tumors and the group with tumors homozygous/hemizygous for exon 11 deletion mutation (data not shown). No statistically significant difference in the response rates between the two doses of imatinib for any of the genotype subgroups was found. A step-wise logistical regression analysis was performed to identify other clinical factors that might predict response to imatinib. The strongest predictor of response was the presence of a KIT exon 11 mutation (hazard ratio, 7.85; 95% CI, 3.55 to 17.37). The only other variable noted in this regression analysis to predict lack of response to imatinib was an elevated creatinine at baseline (hazard ratio, 0.27; 95% CI, 0.08 to 0.92).

The number of PDGFRA-mutant GISTS in the study was too small to define a relationship between PDGFRA mutations and response to imatinib. Nevertheless, none of the patients with the imatinib-resistant D842V mutation responded to drug (two patients with PD, one patient classified as NA as a result of technical difficulties in disease measurement), whereas two of three patients with imatinib-sensitive PDGFRA oncoproteins achieved a PR with imatinib therapy.

Correlation of Tumor Genotype With Event-Free and Overall Survival

Event-free survival for the entire patient population was estimated by Kaplan-Meier analysis. With a median follow-up of approximately 19 months (594 days), 81 (55.1%) of 147 patients had experienced one or more end point clinical events, and the median event-free survival was approximately 17 months (Fig 3A). Event-free survival was also analyzed for the three largest
Fig 2. (A) In vitro sensitivity of wild-type and mutant KIT isoforms to imatinib. All gastrointestinal stromal tumor-associated KIT mutant isoforms were inhibited by imatinib with a similar sensitivity as ligand-activated wild-type KIT. In contrast, the mastocytosis-associated D816V mutant isoform was not inhibited by imatinib. (B) In vitro sensitivity of wild-type and mutant platelet-derived growth factor receptor alpha (PDGFRA) isoforms to imatinib. The V561D, deletion I843, and deletion DIMH 842-845 mutant isoforms had similar sensitivity to imatinib as ligand-activated wild-type PDGFRA. In contrast, the D842V mutant isoform was 10- to 20-fold more resistant to imatinib.
groups of kinase genotypes represented in this study: mutation of KIT exon 11, KIT exon 9, or no detectable mutation of KIT or PDGFRA. As depicted in Fig 3C, patients whose tumors expressed an exon 11 mutant KIT isoform were much less likely to experience treatment failure than patients whose tumors expressed an exon 9 mutant KIT isoform (P < .0001) or were without a detectable mutation in KIT or PDGFRA (P < .0001). There was no significant difference in the rate of treatment failure for the group with KIT exon 9 mutation compared with those with no detectable KIT or PDGFRA mutation (P = .14). In patients without detectable KIT or PDGFRA mutation, the median event-free survival was 82 days. In contrast, the median event-free survival for patients with a KIT mutation of exons 9 or 11 was 200 days and 687 days, respectively.

A proportional hazards model for event-free survival was fitted with the potential prognostic factors described above (Table 2). In the stepwise regression analysis, several variables were noted to be correlated with the risk of experiencing an adverse clinical event; these included exon 11 mutation status, daily imatinib dose, poor baseline Eastern Cooperative Oncology Group performance status, and having no specimen available for genotyping (unknown kinase mutational status). The presence of a KIT exon 11 mutation was the strongest prognostic factor and reduced the risk of adverse clinical events by more than 80%. The protective effect of an unknown mutational status is likely due to the fact that approximately 67% of such patients would be expected to have a KIT exon 11 mutation and are therefore at a reduced risk of adverse clinical events. Clearly, it is better to have a 67% chance of a favorable genotype than to have a documented unfavorable genotype (eg, no kinase mutation of KIT or PDGFRA).

On the basis of Kaplan-Meier analysis, the overall survival for the entire patient population at 76 weeks was 85% (Fig 3B). As depicted in Fig 3D, patients whose tumors expressed an exon 11 mutant KIT isoform had improved survival compared with patients whose tumor expressed an exon 9 mutant KIT isoform (P = .0034) or whose tumor had no detectable mutation of KIT or PDGFRA (P < .0001). There was also a significant difference in survival in favor of the KIT exon 9 mutation subgroup compared with those patients with no detectable KIT or PDGFRA mutation (P = .0067). As with event-free survival, a proportional hazards model was fitted with the potential prognostic factors described above (Table 2). The presence of a KIT exon 11 mutation was the strongest prognostic factor, reducing the risk of death by more than 95%.

**DISCUSSION**

Therapeutic responses to targeted inhibition of activated tyrosine kinases have been demonstrated in certain types of leukemia, sarcoma, and breast cancer. The mechanisms of kinase activation vary considerably among these cancers, but the influence of these mechanisms on drug response has not been well studied. GISTs, in particular, present a variety of genomic mutations across two different receptor tyrosine kinase genes. We report here that the type of KIT or PDGFRA mutation in clinically advanced GISTs is predictive of the response to imatinib therapy. We show that most GISTs express kinase oncoproteins that are intrinsically sensitive to imatinib, accounting for the excellent overall clinical response to imatinib. Nonetheless, a minority of GISTs express kinase oncoproteins that are either intrinsically resistant to imatinib, or are associated with poor clinical response despite in vitro sensitivity to imatinib. These findings highlight the relevance of molecular oncogenic mechanisms in determining response to targeted therapies in cancer.

Gain-of-function mutations of PDGFRA were only recently discovered in GISTs. The current series of tumors is the largest that has been examined for PDGFRA mutations and confirms that PDGFRA and KIT mutations are mutually exclusive. PDGFRA mutations were demonstrated in 4.7% of the genotyped GISTs in this clinical trial and involved domains homologous to those often mutated in KIT. The data from this study support a mechanistic link between PDGFRA activation and imatinib activity in GIST patients whose disease does not express a mutant KIT protein. Whereas all GIST-associated mutant KIT isoforms examined had in vitro sensitivity to imatinib similar to that of wild-type KIT protein, the PDGFRA D842V mutant was substantially more resistant to the drug. The imatinib-resistant KIT D816V mutation in human mastocytosis and the PDGFRA D842V mutation involve the same conserved aspartic acid residue in the kinase activation loop, suggesting a common basis for imatinib resistance in KIT and PDGFRA oncoproteins activated by this mechanism. On the basis of studies of ABL kinase mutations that are correlated with clinical resistance to imatinib in chronic myelogenous leukemia, the level of in vitro resistance manifested by the PDGFRA D842V isoform

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**Table 1. KIT and PDGFRA Genotype Versus Clinical Response in the CSTI571B 2222 Phase II Trial**

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Partial Response</th>
<th>Stable Disease</th>
<th>Progressive Disease</th>
<th>Nonassessable</th>
</tr>
</thead>
<tbody>
<tr>
<td>KIT exon 11, n = 85</td>
<td>71</td>
<td>83.5</td>
<td>7</td>
<td>8.2</td>
</tr>
<tr>
<td>KIT exon 9, n = 23</td>
<td>11</td>
<td>47.8</td>
<td>6</td>
<td>26.1</td>
</tr>
<tr>
<td>No PDGFRA or KIT mutation, n = 9</td>
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<td>0.0</td>
<td>3</td>
<td>33.3</td>
</tr>
<tr>
<td>PDGFRA-sensitive, n = 3</td>
<td>2</td>
<td>66.7</td>
<td>0</td>
<td>0.0</td>
</tr>
<tr>
<td>PDGFRA-resistant D842V, n = 3</td>
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<td>0.0</td>
<td>0</td>
<td>0.0</td>
</tr>
<tr>
<td>KIT exon 13, n = 2</td>
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<td>100.0</td>
<td>0</td>
<td>0.0</td>
</tr>
<tr>
<td>KIT exon 17, n = 2</td>
<td>1</td>
<td>50.0</td>
<td>0</td>
<td>0.0</td>
</tr>
</tbody>
</table>

**NOTE.** Each of the KIT genotypes is categorized by the exon location of the mutation (all are imatinib-sensitive), whereas PDGFRA genotypes are categorized as either sensitive (PDGFRA-sensitive) or resistant (D842V) to imatinib.

Abbreviation: PDGFRA, platelet-derived growth factor receptor alpha.
would be predicted to result in clinical resistance. Consistent with this prediction, none of the three patients whose tumor harbored the D842V mutation showed a clinical response. The other mutant isoforms of PDGFRA were sensitive to imatinib in vitro, and two of three patients bearing tumors with these mutations responded well to therapy. These findings provide a basis for imatinib response in some KIT-WT GISTs and suggest that imatinib can be used successfully in the treatment of GISTs driven by imatinib-sensitive PDGFRA oncoproteins. These data are complementary to the data by Cools et al, who reported the efficacy of imatinib in treating patients with hypereosinophilic syndrome associated with the oncogenic FIP1L1-PDGFRA fusion protein. It remains to be proven whether imatinib will have therapeutic activity against other solid tumors driven by wild-type or oncogenic PDGFRA kinase.

A subset of GIST tumors in this study lacked detectable KIT or PDGFRA mutations. Although such GISTs lack apparent genomic mutations, they can express phosphorylated KIT or PDGFRA proteins that likely contribute to tumor proliferation or survival. In the present study, GISTs lacking a detectable kinase mutation had a lower overall response to imatinib (0.0%) than tumors with an exon 11 mutation (83.5%) or an exon 9 mutation (47.8%). Event-free and overall survival were also significantly shorter in patients whose GISTs lacked a detectable kinase mutation. These results suggest that GISTs lacking a KIT or
**PDGFRA** mutation are biologically distinct and might be less dependent on these kinases than GISTs expressing mutant kinases.

The PR rate and event-free survival also differed between the groups of patients whose GISTs had **KIT** exon 9 versus exon 11 mutations. This finding is notable, because the KIT oncoproteins encoded by exon 9 and exon 11 mutations were equally sensitive to imatinib in vitro (Fig 2A). Preliminary studies suggest differences in downstream signaling in exon 9 versus exon 11 **KIT**-mutant GISTs, and such biologic differences might influence the susceptibility of the tumor cells to apoptosis in response to kinase suppression by imatinib. Alternatively, the activation mechanisms for **KIT** exon 9 mutants might vary between the in vitro and in vivo settings. It is also noteworthy that in many patients, disease progression did not occur until 12 months after initiating treatment with imatinib. Preliminary studies suggest that the molecular mechanisms for late resistance to imatinib in GISTs may be analogous to those described in patients with chronic myelogenous leukemia.

These data provide strong evidence of a mechanistic link between expression of an imatinib-sensitive mutant **KIT** or **PDGFRA** kinase in GISTs and clinical response to imatinib. Overall, the PR rate of patients with an imatinib-sensitive kinase was 75.7% (87 of 115 patients), whereas the PR rate in patients with no kinase mutation or an imatinib-resistant mutation was 0.0% (zero of 12 patients). Expressed differently, 87 of the 87 genotyped patients (100.0%) who achieved a PR during imatinib therapy had GISTs that expressed an imatinib-sensitive mutant kinase.

In conclusion, we provide evidence that **KIT** and **PDGFRA** mutational status predicts clinical response to imatinib in patients with metastatic GIST. In a subset of GISTs lacking **KIT** mutations, gain-of-function **PDGFRA** mutations can account for imatinib clinical response. Therefore, imatinib therapy should not be withheld from patients whose GISTs lack **KIT** mutations or whose GISTs do not express the KIT protein. These findings emphasize that molecular subclassification of GISTs is crucial in the design and interpretation of clinical trials and in identifying patients who are at high risk for early treatment failure.

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The acknowledgment is included in the full-text version of this article, available on-line at www.jco.org. It is not included in the PDF (via Adobe Acrobat Reader®) version.

**AUTHORS’ DISCLOSURES OF POTENTIAL CONFLICTS OF INTEREST**

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