KIT Molecular Testing

Molecular testing for KIT mutations is relevant for various types of cancer and can provide diagnostic, prognostic, and predictive information for systemic mastocytosis (SM), gastrointestinal stromal tumors (GIST), melanoma, and acute myeloid leukemia (AML) associated with inv(16) or t(8;21), also known as core-binding factor (CBF) AML. For GIST and melanoma, PDGFRA testing is also often relevant.

Disease Overview

Core-Binding Factor Acute Myeloid Leukemia

- KIT mutation testing is important for prognostication
- KIT mutations are associated with higher incidence of relapse and lower survival
- KIT mutations may be detected in:
  - inv(16) or t(16;16) AML
  - t(8;21) AML

Mastocytosis

KIT mutation testing is important for:

- Diagnosis (presence of mutation is a minor criteria for SM)
- Prediction of response to targeted therapy

Gastrointestinal Stromal Tumors

- KIT and PDGFRA mutation testing is important for prediction of response to targeted therapy and should be performed in all patients considered for targeted therapy
- Mutation presence and type determine if the patient will benefit from targeted therapy
- Detection of secondary resistance mutations in patient already treated with targeted therapy may guide the use of other therapeutic agents
- Mutation testing may be occasionally used to aid in establishing GIST diagnosis in difficult cases (unusual location, morphology, or immunoprofile)
- Immunohistochemistry for c-kit (CD117) is useful for diagnostic purposes but should not be used to predict response to targeted therapy

Melanoma

- KIT mutation testing is important for prediction of response to targeted therapy
- Immunohistochemistry for c-kit (CD117) should not be used to predict response to targeted therapy

Genetics

Gene

KIT

Structure/Function

- Maps to 4q12
- Receptor tyrosine kinase (type III)
Mutations

A variety of >500 mutations have been described, most commonly in juxtapasmembrane region (exon 11), extracellular region (exons 8, 9), and kinase domain (exons 13, 17). These mutations are commonly detected in patients with:

- **CBF AML**
  - Detected in ~20% of AML with *KIT* mutations, including inv(16)
  - Detected in 20-25% of AML with t(8;21) (particularly the D816V mutation)
- **Mastocytosis**
  - **Adults**
    - D816V mutation detected in 95% of patients with SM
    - Rare juxtapasmembrane mutations
  - **Children**
    - D816V mutation detected in 30-40% of patients with SM
    - ~40% carry *KIT* mutations that reside outside exon 17 (mainly exons 8 and 9)
    - Mutations other than D816V may be detected in SM-associated hematologic neoplasm (AHN)
- **GIST**
  - *KIT* mutations present in ~85% of cases
    - Primary mutations most common in exon 11 (~70% of cases) and exon 9 (~10-15% of cases), much less common in other exons
    - Secondary resistance mutations occur in exons 13, 14, 17, and 18
  - *PDGFRA* mutations present in ~5% of cases
    - Primary mutations most common in exon 18 (~5% of cases)
    - Primary mutations much less common in other exons
- **Melanoma**
  - *KIT* mutations present in 2-8% of cases overall (more common in mucosal and acral melanomas)
    - Most common in:
      - Exon 11 (70% of *KIT* mutated cases)
      - Exon 13 (20% of *KIT* mutated cases)
    - Much less common in other exons

Test Interpretation

**KIT Mutations in AML by Fragment Analysis and Sequencing**

**Analytical Sensitivity**

Detects mutations in:

- Exon 17 in specimens with at least 30% AML cells harboring the mutation
- Exon 8 in specimens with at least 5% AML cells harboring the mutation

**Results**

- Detected: *KIT* exon 8 or 17 mutation
  - Associated with less favorable outcome in in CBF AML
  - TKIs may be useful in conjunction with standard chemotherapy
- Not detected: no detectable mutation in *KIT* exon 8 or 17

**Limitations**

- Not intended to detect minimal residual disease
- Mutations outside of exons 8 and 17 are not detected
- Mutations below analytical sensitivity will not be detected
**KIT (D816V) Mutation by ddPCR, Quantitative**

**Sensitivity**
- Clinical: occurs in >80% of SM cases
- Analytical: 0.03% variant allele frequency (VAF)

**Results**
- Detected VAF: KIT (D816V) point mutation; allele specific amplification of the c.2447 C>T (D816V)
- Results are reported as a percent mutated allele
  - Supports a diagnosis of SM or SM-associated clonal hematologic nonmast cell lineage disease (SM-AHNMD) in the correct clinical context
  - Therapeutic implications
    - Imatinib: ineffective if mutation is present
    - Dasatinib and Nilotinib: uncertain clinical efficacy
- Not detected: no detectable KIT (D816V) point mutation

**Limitations**
- Mutations other than the D816V mutation are not detected, including other D816 variants
- Mutations below analytical sensitivity will not be detected

**Gastrointestinal Stromal Tumor Mutations and KIT Mutations, Melanoma**

<table>
<thead>
<tr>
<th>Variant Class</th>
<th>No. Variant Tested</th>
<th>Positive Percent Agreement (PPA)</th>
<th>PPA, 95% Tolerance at 95% Reliability</th>
</tr>
</thead>
<tbody>
<tr>
<td>SNV</td>
<td>177</td>
<td>100%</td>
<td>98.9-100.0%</td>
</tr>
<tr>
<td>MNVs</td>
<td>42</td>
<td>95%</td>
<td>85.6-99.0%</td>
</tr>
<tr>
<td>Small insertions and duplications&lt;sup&gt;a&lt;/sup&gt;</td>
<td>42</td>
<td>100%</td>
<td>95.6-100.0%</td>
</tr>
<tr>
<td>Medium insertions and duplications&lt;sup&gt;b&lt;/sup&gt;</td>
<td>10</td>
<td>100%</td>
<td>82.9-100.0%</td>
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<tr>
<td>Large insertions&lt;sup&gt;c&lt;/sup&gt;</td>
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<td>100%</td>
<td>22.9-100.0%</td>
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<tr>
<td>Small deletions&lt;sup&gt;a&lt;/sup&gt;</td>
<td>80</td>
<td>100%</td>
<td>97.6-100.0%</td>
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<tr>
<td>Medium deletions&lt;sup&gt;b&lt;/sup&gt;</td>
<td>14</td>
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<td>71.2-99.2%</td>
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<tr>
<td>Large deletions&lt;sup&gt;d&lt;/sup&gt;</td>
<td>22</td>
<td>64%</td>
<td>42.9-81.1%</td>
</tr>
</tbody>
</table>

<sup>a</sup>≤21 bp
<sup>b</sup>22-60 bp
<sup>c</sup>≥61 bp and ≤64bp
<sup>d</sup>≥61 bp and ≥13547bp

bp, base pair; MNVs, multiple nucleotide variants; SNV, single nucleotide variant

**Results**
- Detected: KIT mutation detected in exons 9, 11, 13, 14, 17, 18
- Detected: PDGFRA mutation detected in exons 12, 14, 18
- Not detected: no mutations detected in KIT and PDGFRA

**Limitations**
- Mutations outside of targeted exons are not detected
Test alone cannot be used for diagnosis of malignancy
Variants below the limit of detection (LOD) of 5% VAF may not be detected
10 ng input DNA from extracted tissue sample is minimally required, but 50 ng input DNA is recommended for optimal results
Large variants (>60bp) may not be detected
Not intended to detect minimal residual disease
Does not distinguish between somatic and germline variants

References

Additional Resources


