**MatBA®-CLL/SLL Improves Patient Stratification**

**Detects genomic aberrations not assessed by FISH**

**Patient Case 6268:** 65 year old male.

**Clinical History:** New diagnosis.

**Specimen:** Peripheral blood.

**Clinical Question:** What is the risk stratification of the patient?

---

**Initial Prognosis**

**FISH Analysis:** Reported no aberrations.

---

**Clinical Solution**

**INFORM**

- Detected the gain of 3q, gain of 1q, gain of 12q and partial loss of 7q.
- Biomarker not assessed by FISH.

**PREDICT**

- Gain of 3q is detected in 3-5% of CLL cases and has been reported to be associated with shorter overall survival.
- Result from MatBA®-CLL/SLL stratifies the patient into a poor prognostic category.

**DECIDE**

- In this case, the patient would have been mis-prognosed without the data provided by MatBA®-CLL/SLL.
- The genomic aberrations detected are evidence for this patient’s unfavorable prognosis. The clinician may choose to select an aggressive course of treatment.

---

**CLL Risk Stratification Per Prognostic Category**

<table>
<thead>
<tr>
<th>Genomic Aberrations Reported by FISH</th>
<th>Genomic Aberrations Reported by MatBA®-CLL/SLL:</th>
</tr>
</thead>
<tbody>
<tr>
<td>12 gain 11q22 loss (ATM) 13q14 loss 17p13 loss (TP53)</td>
<td>2p25.3-p15 gain 3q26-q27 gain 8p23-p21 loss 8q24 gain 12 gain 11q22 loss (ATM) 13q14 loss 17p13 loss (TP53) [6q21 loss] [7q31 loss] [17q gain] [18q gain] [18p loss] [19 gain]</td>
</tr>
</tbody>
</table>

**Impact on therapy selection & clinical management of CLL patients**

- 38% of cases have a favorable prognosis falling under "watch & wait" approach.
- 3% of cases have an unfavorable prognosis missed by FISH.

**Key:**

- Favorable
- Intermediate
- Unfavorable
- Favorable/Intermediate (no distinction)

[Genomic regions assessed but not currently reported]

**Patients stratified into “Favorable/Intermediate” by FISH will benefit from distinction into proper prognostic categories by:**

- Preventing the selection of “watch and wait” approach for those who would be stratified as intermediate. These patients with early-stage CLL/SLL may benefit from earlier therapy with a lower tumor burden and prior to clonal evolution.
- Delaying therapy for patients with a favorable prognosis, protecting them from toxicity and possible risk of future drug-resistant disease.
- Selecting the proper treatment for patients that initially are mis-prognosed by FISH into the favorable/intermediate category who in fact have an unfavorable prognosis.

**MatBA®-CLL/SLL addresses the need to more accurately determine the prognosis of patients at diagnosis - the greatest opportunity to impact the clinical management of CLL patients.”**
MatBA® - CLL/SLL Array-CGH Report

Results:

<table>
<thead>
<tr>
<th>Genomic Aberration</th>
<th>Result for Aberration</th>
</tr>
</thead>
<tbody>
<tr>
<td>Loss of 8p (8p23.3-p21.3)</td>
<td>Negative</td>
</tr>
<tr>
<td>Loss of 11q (ATM)</td>
<td>Negative</td>
</tr>
<tr>
<td>Loss of 13q (MIR-15A/16.1)</td>
<td>Negative</td>
</tr>
<tr>
<td>Loss of 13q (RB1)</td>
<td>Negative</td>
</tr>
<tr>
<td>Loss of 17p (TP53)</td>
<td>Negative</td>
</tr>
<tr>
<td>Gain of 2p</td>
<td>Negative</td>
</tr>
<tr>
<td>Gain of 3q</td>
<td><strong>Positive</strong></td>
</tr>
<tr>
<td>Gain of 8q</td>
<td>Negative</td>
</tr>
<tr>
<td>Gain of 12</td>
<td>Negative</td>
</tr>
</tbody>
</table>

Interpretation: Positive for the gain of 3q (See comment below). Gain of 3q in CLL patients is associated with an unfavorable prognosis.

Comment: Three additional abnormalities were detected including the partial gain of 1q and 12q, as well as the partial loss of 7q. However, a secondary independent method was not available to confirm these abnormalities.

Description: The gain and loss of specific genomic regions in the monoclonal proliferation of B-cells in chronic lymphocytic leukemia (CLL) are considered to have diagnostic and prognostic value. Loss of 13q at one locus (MIR-15A/16.1) or both loci (MIR-15A/16.1 and RB1) is observed in approximately 50% of CLL patients and as the sole abnormality is associated with a longer overall survival. Those patients with loss of 17p (TP53) or 11q (ATM) in general, have a shorter overall survival. Other aberrations are variously observed in CLL patients with suggested prognostic value.

This assay utilizes microarray-based comparative genomic hybridization (Array CGH) to simultaneously detect the gain and loss of multiple loci in specimen DNA. Quantitative PCR is used to confirm the detected genomic gains and losses. The sensitivity of the assay is 30-40%. Samples in which the monoclonal B-cells are present at less than 30-40%, aberrations may not be detected and will be reported as no aberrations detected.

End of Report

The tests utilizing analyte-specific reagents (ASR) were developed and their performance characteristics determined by Cancer Genetics, Inc. as required by CLIA 88 regulations. They have not been cleared or approved for specific uses by the U.S. Food and Drug Administration (FDA). The FDA has determined that such clearance or approval is not necessary. These tests are used for clinical purposes. Cancer Genetics, Inc., 201 Route 17 North, Rutherford, NJ 07070. Phone number: (888) 334 - 4988 CLIA#: 31D1038733; CAP LAP#: 791652

CPT Codes

81479

Assay Specifications

Sensitivity

Detects genomic gains and losses in up to 85% of CLL. Limit of detection is 30-40 cells in 100 mononuclear cells (assay sensitivity).

Reporting

Results are reported as positive or negative for the gain or loss of each respective alteration. Results of the assay should be interpreted in the context of available clinical, pathologic, and laboratory information. Identification of genomic gain/loss should not be used alone for the diagnosis or prognosis of CLL/SLL.

Specimen Requirements

• One EDTA tube (lavender) of peripheral blood or bone marrow aspirate with minimum: 2-3 ml or 3-5 µm thick formalin-fixed paraffin-embedded (FFPE) sections (10% neutral buffered) on positively coated slides.
• Specimen should be stored & transported at room temp.

Licensure

CAP (Laboratory #: 7191582, AU-ID: 1434060), CLIA (Certificate #: 31D1038733), New Jersey (CLIS ID #: 0002299), New York State (PFI: 8192), Pennsylvania (031978), Florida (800018142), Maryland (1395).

CPT Codes

81479

TAT

10-14 days

MatBA® is a proprietary program developed by CGI to assist physicians in the diagnosis, prognosis and therapy selection for CLL patients. This one-stop-shop solution includes proprietary tests, such as MatBA®-CLL/SLL Array CGH, and the most relevant tests available for the clinical management of CLL patients.