IGH and TCRgamma Gene Rearrangement

CERNER ORDERABLE
Order through Molecular Lab, please call 317.491.6654

CPT CODE
81261, 81342

CLINICAL UTILITY
Leukemia and lymphoma of B lymphoid lineages have clonal DNA rearrangements from the original tumor cell. This is in contrast to normal, functional cells of B lineage which demonstrate patterns of extreme diversity of antigen specificity and DNA rearrangement. Clonal immunoglobulin heavy chain (IGH) gene rearrangements are diagnostic for leukemias and lymphomas derived from B lymphoid hematopoietic cell precursors.
The T-cell receptor (TCR) genes (alpha, beta, delta, and gamma) are comprised of numerous, discontinuous coding segments that somatically rearrange to produce heterodimeric cell surface T-cell receptors, either alpha/beta (90%-95% of T cells) or gamma/delta (5%-10% of T cells). With rare exceptions (eg, some neoplastic B-lymphoid proliferations), other cell types retain the "germline" configuration of the TCR genes without rearrangement. The marked diversity of somatic TCR-gene rearrangements is important for normal immune functions, but also serves as a valuable marker to distinguish abnormal T-cell proliferations from reactive processes. A monoclonal expansion of a T-cell population will result in the predominance of a single TCR-gene rearrangement pattern. In contrast, reactive T-cell expansions are polyclonal, with no single clonal population predominating in the population of T cells[1].

METHODOLOGY
Fragment Analysis

SPECIMENS
Preferable primary tumor.

- FFPE tissue (Formalin fixative only)
  1 H&E and 5-8 unstained slides
- Flow cell suspension: at least 5 mL obtained in RPMI1640 media.
- Whole Blood and Bone Marrow: Collect in 5 mL lavender top tube

SPECIMEN STABILITY and SHIPPING

- Transport/Storage of slides at room temperature.
- Flow cell suspension, blood and bone marrow refrigerated between 2-8° C.

CAUSES FOR REJECTION
Excess necrosis for slides. Flow cell suspensions, blood and bone marrow not refrigerated.

SPECIFICITY
Several master mixes are used to test for rearrangements of each targeted gene with each master mix targeting a different conserved region. This comprehensive testing approach improves PCR identification of clonal rearrangements.

ASSAY RANGE

- IGH clonal or polyclonal
- TCRgamma clonal or polyclonal

TURNAROUND TIME
7-10 days

1. Reference information can be found in the Indiana University Health Molecular Assay Procedures.