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Shivani Golem

University of Kansas Medical Center, Kansas City, Kansas, USA

Clinical Utility of Chromosomal Microarray in Detecting Cryptic Abnormalities in Myeloid and Lymphoid Malignancies

Chromosomal microarray analysis (CMA) is a high-resolution whole-genome test that detects genetic abnormalities associated with genomic material losses, gains, and a cancer-specific genomic change called copy-neutral loss-of-heterozygosity (CN-LOH). Comprehensive whole genome testing detects additional genetic abnormalities in genes associated with cancer that can be used in the diagnosis, prognosis, and treatment decisions for any given cancer type, whether liquid cancers or solid tumors. CMA testing, especially in new diagnostic myeloid and lymphoid cancer cases with non-informative karyotype or FISH findings, identifies clinically significant gains, losses, and CN-LOH changes in the patient's cancer genome, which helps the clinician in diagnosis, prognostication, and therapy decisions. This presentation will include our institute's experience in processing CMA cases and a review of CMA results, which detected cryptic gene fusions, submicroscopic focal duplications or deletions, disease-defining subtypes, and prognostically significant CN-LOH regions with clinically significant cancer-associated genes. CMA testing helped our clinicians in better patient management.

Keywords: Cryptic rearrangements, Chromosomal microarray, Myeloid malignancies, Lymphoid Malignancies, Cytogenetics, FISH

Biography

Dr. Golem is an associate professor in the Department of Pathology at the University of Kansas Medical Center. Dr. Golem specializes in Cancer Cytogenetics, Molecular Genetics, and Genomics.

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