Hui Chen, J Cancer Sci Ther 2016, 8:8(Suppl)
http://dx.doi.org/10.4172/1948-5956.C1.081

Clinical opportunities of SNP microarray in breast cancer

Hui Chen
University of Texas, USA

Current advances in single nucleotide polymorphism (SNP) microarray have enabled genome-wide analysis of copy number aberrations and allelic imbalances of oncogenes and tumor suppressor genes in malignant neoplasms. The molecular inversion probe (MIP) technology allows SNP microarray testing on solid tumors with limited (20-80ng) and fragmented DNA from formalin-fixed paraffin-embedded tissue (FFPE). One of the MIP microarray platforms used in OncoScan (Affymetrix) provides genome wide coverage with 220,000 SNP probes and high resolution coverage for approximately 900 cancer genes commonly seen in solid tumors. Cross-laboratory validation has demonstrated reproducibility of OncoScan FFPE assay. In addition, OncoScan shows promise as a quantitative measure of targetable oncogenes such as HER2 in breast cancer. SNP microarray demonstrates potential utility to provide diagnostic, prognostic and therapeutic information beyond conventional biomarker analysis for breast cancer.

Biography

Hui Chen is an Assistant Professor at Department of Pathology, The University of Texas MD Anderson Cancer Center. She received her MD from Peking Union Medical College and PhD in Biochemistry and Molecular Biology from Colorado State University. She had Post-doctoral research training from John Hopkins Medical School and clinical fellowship training in Oncological Surgical Pathology and Molecular and Genetic Pathology from Memorial Sloan Kettering Cancer Center. She is practicing pathologist specialized diagnostic molecular pathology and breast pathology at MD Anderson Cancer Center.

hchen7@mdanderson.org

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