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Micro Array-based cytogenomics, gene expression and epigenomics in colorectal Carcinoma

Muhammad G Kibriya, Farzana Jasmine and Habibul Ahsan

University of Chicago, USA

Colorectal carcinoma (CRC) is associated with gross chromosomal instability (CIN) and epigenetic alterations leading to gross differential gene expression. Unlike other groups using aCGH, our group assessed CIN in CRC using a high-density SNP array, which achieves higher resolution and allows simultaneous analysis of copy number (CN) and B-Allele Frequency data. Additionally we studied genome-wide gene expression and methylation profiles using microarrays for comprehensive integrated analyses. We studied paired (tumor and surrounding healthy) fresh frozen tissue from 86 CRC patients using SNP array. We identified a large number of CIN regions in CRC, and were able to assess possible mechanisms of CIN, some of which can not be assessed with other methods. We propose algorithm for interpretation of cytogenetic data obtained from SNP arrays. We identified a number of novel uniparental disomy (UPD) regions. We identified associations between CN abnormalities and different CRC phenotypes, found a large number of novel differentially methylated loci in CRC and integrated genomic and epigenomic (methylation) data for interpretation of gene expression changes. We found commonalities between regions of CN change observed in CRC and other solid cancers. Using Therapeutic Target Database we found relevant drugs, targeted to the genes located in the regions with CN changes, approved or in trials for other cancers and common diseases that may be considered for future therapeutic trials in CRC based on personalized cytogenetic diagnosis. Our study shows the application of micro array-based assays for cytogenetic, genomic and epigenomic studies in CRC and its importance for individualized treatment.

Biography

Dr. Kibriya completed his medical graduation from Institute of Post-Graduate Medicine and Research (IPGMR), Dhaka, Bangladesh and completed his PhD from Medical Academy, Sofia, Bulgaria. He has served as faculty at Columbia University, New York and is currently working at the University of Chicago, Chicago, IL. He has published widely in the field of molecular genomics as it applies to molecular cancer epidemiology.