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The Cancer Control Challenge:
Better Understanding It to Better Face It

CYTOGENOMIC CHARACTERIZATION OF THE HCT-8 COLORECTAL ADENOCARCINOMA CELL LINE

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Introduction: Colorectal cancer is the third most common malignant neoplasm in the world, and its development is associated with environmental factors, family history, age, and genetic predisposition. This latter factor has been extensively studied, and numerous genomic alterations associated with the emergence and progression of this type of cancer have been identified. Cancer cell lines are excellent models for in vitro studies that seek to identify altered cellular pathways, mutations in genes critical to/for cancer, and anticancer drug testing, among others. In this sense, the genomic characterization of cancer cell lines by Array Comparative Genomic Hybridization (aCGH) has been used as a resource to evaluate alterations associated with different types of cancer. The HCT-8 cell line, derived from a human colorectal adenocarcinoma, has been used in in vitro studies to evaluate antitumor drugs; however, no genomic characterization has been performed to date. **Objectives:** Characterize and validate cytogenomic alterations in HCT-8 cell line as a potential model in colorectal cancer. **Methods:** HCT-8 cells were thawed, cultured in DMEM supplemented with 10% fetal bovine serum, and maintained until reaching 80–90% confluence. Metaphase chromosomes were obtained using Colcemid treatment for cytogenetic analysis. Genomic DNA was extracted and processed using the SurePrint G3 Human Genome CGH+SNP Microarray Kit for aCGH analysis, allowing the detection of copy number alterations (CNAs) across the genome. **Results:** The analysis revealed that the modal diploid number was $2n = 46$, and a total of 125 CNAs were identified, including 19 gains, 9 losses, 2 deletions, 2 amplifications, and 93 regions of loss of heterozygosity, affecting nearly all chromosomes except 21 and 22. The main gains were observed on chromosomes 14, 18, and X, while the most significant losses occurred on chromosomes 3, 7, and 18. A total of 84 genes were found to be altered in the HCT-8 cell line, many of which have been previously described in tumor samples and are directly associated with the carcinogenesis of colorectal carcinomas, including TP53, KRAS, DCC, SMAD4, and PTEN. Additionally, other altered genes in the cell line may serve as potential biomarkers. **Conclusion:** In conclusion, the cytogenomic characterization of the HCT-8 cell line confirmed that the cell line is a potential model for in vitro studies to understand the carcinogenesis of colorectal adenocarcinoma, as well as for analyzing the effect of drugs, understanding the therapeutic response, and testing compounds with anticancer potential.

Keywords: aCGH; CNAs; *In vitro* model.