Molecular profiling of gastrointestinal cancer

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Introduction: Gastro-intestinal cancer (GI) include a variety of cancers that affect esophagus, gallbladder, liver, pancreas, stomach, intestine and other organs involved in digestive system. The above types of cancers appear higher mortality rates in comparison with cancers in other systems. Therefore, it is essential the optimization of treatment management. Even though great achievements have been performed the last years in prediction of cancer therapy, treatment is based in specific markers, avoiding genes that affect or affected through signaling transduction pathways. The present study aimed to analyze the gene expression in cancer cells, representing different GI cancer types and compare them with circulating tumor cells (CTCs) from patients and cells from normal donors.

Methods: RNA was extracted from commercial cell lines representing gastric (MKN45, 231/12/37), liver (Huh 7D-12), colon (CaCO2, HCT116, HCT116) and pancreatic (PANC-1) cancer. Blood was collected from two healthy donors as well as two colon cancer patients. PBMCs in healthy individuals and CTCs in cancer samples were isolated and RNA was extracted. qRT-PCR was performed including reference RNA as positive control. 80 primer pairs were designed for exon-exon amplification of genes involved in signaling pathways, invasion, receptors, cell cycle regulation, resistance etc. ACTB was used as housekeeping genes and DeltaCt analysis was followed. Experiments were performed in triplicates including appropriate controls. Hierarchical clustering was performed to identify gene expression patterns.

Results: The genes ERK1, ERK2, CDC6, JAK1, JAK2, FAS, NRAS, BCL2, NME1 and HSPB1 were not expressed in normal samples, while different expression patterns were observed in commercial cancer cells and cells derived from patients. Regarding the migration-invasion marker NME1, and genes ERK1, BAX, RRM1, ERCC1, ARAF, MET, E2F1, ERBB2, MTOC, TYMS, GART, PNP, RBBP1 and HSPB1, commercial cells had higher expression. On the contrary, patients-derived cells' gene expression was higher for ERK2, PTEN, RPSA, JAK1, JAK2, FAS, Kras, TGFB1 and NANOG. For the rest genes that were studied, there was not observed clear molecular profile. The clustering among samples revealed that cancer cells' gene expression pattern is different than normal, while dissimilar pattern was also observed between commercial cancer cells and CTCs.

Conclusion: Taking everything into consideration it is well understood that personalized treatment is essential, since different expression profiles are observed among samples with the same type of cancer. The more genes that are studied, the more information are collected for the cancer; therefore a treatment with greater success can be achieved. In addition, the study of genes should not limited in receptors and/or pathways, but also to include genes involved in various cell processes. Further studies, in more samples, are imperative to confirm all the above and be able to use at clinical level.