

Comunicação Oral

CO-01 - MOLECULAR SIGNATURE OF CHOLANGIOCARCINOMA AND HEPATOCELLULAR CARCINOMA: A STEP AHEAD IN DIAGNOSIS AND PROGNOSIS

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Introduction:

Hepatocellular carcinoma (HCC) and cholangiocarcinoma (CC) are the two most common primary hepatic neoplasms. While HCC arises from hepatocytes, the CC is a rare tumor originating from biliary tree and is classified as intra (ICC) and extrahepatic (ECC). The aim of this study was to perform a genomic and epigenetic characterization of HCC, ICC and ECC patients.

Methods:

The molecular characterization was performed by aCGH (45 patients) and MS-MLPA (26 patients) techniques. All samples were collected after surgical resection.

Results:

aCGH results revealed some common alterations between the patients of each group. HCC patients showed gain of 1q, 2q37.2, 8q, 14q32.33 and 17q21.31 and loss of 3q26.1, 6p22.2 and 12p13.31. In the ICC samples we observed gain of 2q37.3 and Xp and loss of 3p, 6p25.3, 11q11, 14q, 16q, Yp and Yq. ECC patients revealed gain of 2q37.3, 6p25.3 and 16p25.3 and loss of 3q26.1, 6p25.3-22.3, 12p13.31, 17p, 18q and Yp. MS-MLPA analysis showed a larger number of copy number gains than losses, being MSH6, VHL, RARB, CHFR, PYCARD, BRCA1 and GATA5 the genes more frequently altered. Furthermore, MSH6, ESR1, WT1, GSTP1, CDH13 and GATA5 were the genes that revealed to be methylated in a larger number of samples.

Conclusion:

When correlated clinical information with the data obtained in this study, it was possible to establish molecular profiles, constituting molecular signatures of different tumoral aggressiveness. This molecular characterization is vital to identify diagnosis and prognosis biomarkers.

