

P-023- UNIQUE GENETIC PROFILE OF SPORADIC COLORECTAL CANCER LIVER METASTASIS VERSUS PRIMARY TUMOURS BY SNP-ARRAYS.

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Resumen.

Introduction.

Most genetic studies in colorectal carcinomas (CRC) have focused on those abnormalities that are acquired by primary tumours, particularly in the transition from adenoma to carcinoma, while few studies have compared the genetic abnormalities of primary vs. paired metastatic samples. Material and Methods: In this study we used high-density 500K SNP arrays to map the overall genetic changes present in liver metastases (n=20) from untreated CRC patients studied at diagnosis versus their paired primary tumours (n=20). Results: Overall, metastatic tumours systematically contained those genetic abnormalities observed in the primary tumour sample from the same subject. However, liver metastases from most cases (n=8/20) showed acquisition of genetic aberrations that were not found in their paired primary tumors. These new metastatic aberrations mainly consisted of 1) an increased frequency of genetic lesions of chromosomes that have been associated with metastatic CRC (1p, 7p, 8q, 13q, 17p, 18q, 20q) and, more interestingly, 2) acquisition of new chromosomal abnormalities (e.g. losses of chromosomes 4 and 10q and gains of chromosomes 5p and 6p). Conclusions: These genetic changes acquired by metastatic tumours may be associated with either the metastatic process and/or adaption of metastatic cells to the liver microenvironment. Further studies in larger series of patients are necessary to dissect the specific role of each of the altered genes and chromosomal regions in the metastatic spread of CRC tumours.