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Interrelationship among MAPK signaling pathway and lipid metabolism in hepatocellular carcinoma

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The identification of novel biomarkers is of prime importance for the early diagnosis and prognosis of cancer as well as in the implementation of personalized healthcare strategies that offer new therapeutic approaches with optimized and individualized treatment. Hepatocellular carcinoma (HCC) is associated with a high mortality rate and understanding of events leading to HCC pathophysiology is essential for its better management. We performed proteomic analyses to identify differentially expressed proteins and decipher their role in signaling pathways during the progression of HCC. A rodent model for the study of HCC was developed by administration of chemical carcinogens, diethylnitrosamine (DEN) and 2-aminoacetylfluorine (2-AAF), in male Wistar rats. Proteomic approaches such as 2D-Electrophoresis and MALDI-TOF-MS analyses were performed to characterize the differentially expressed proteins in serum. A protein network was constructed that involved the experimentally-identified proteins at an early stage. Histological changes during HCC induction and progression confirmed HCC initiation and hepatotumorigenesis at 1 and 4 months post-carcinogen-treatment, respectively. Analyses identified several differentially expressed serum proteins in animals undergoing tumorigenesis vis-a-vis controls. The study suggests an interrelationship between the MAPK signaling pathway and lipid metabolism through EGFR that leads to continuous proliferation, neoplastic transformation, and hepatotumorigenesis.

Biography

Maryam Ranjpour is a Ph.D. student, sponsored by government of India, at Jamia Hamdard, New Delhi 110062, and India.

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