

TITOLO: Monitoring liver alterations during hepatic tumorigenesis by NMR profiling and pattern recognition

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Monitoring liver alterations during hepatic tumorigenesis by NMR profiling and pattern recognition

Debora Paris¹, Dominique Melck¹, Matteo Stocchero², Oceania D'Apollito³, Rosa Calemma⁴, Giuseppe Castello⁴, Francesco Izzo⁴, Giuseppe Palmieri⁵, Gaetano Corso³ and Andrea Motta¹

(1) Istituto di Chimica Biomolecolare, Consiglio Nazionale delle Ricerche, 80078 Pozzuoli, NA, Italy

(2) S-IN Soluzioni Informatiche, Via G. Salvemini 9, 36100 Vicenza, Italy

(3) Dipartimento di Scienze Biomediche, Università degli Studi di Foggia, 71100 Foggia, Italy

(4) Istituto Nazionale per lo Studio e la Cura dei Tumori, Fondazione G. Pascale, 80131 Naples, Italy

(5) Istituto di Chimica Biomolecolare, Consiglio Nazionale delle Ricerche, 07100 Li Punti-Sassari, SS, Italy

ABSTRACT

Human hepatocellular carcinoma (HCC) is the most recurrent malignancy of the liver and represents one of the main causes of cancer death worldwide. Furthermore, the liver is the most frequent site of metastatic colonization, and hepatic metastases are far more common than primary cancers in Western countries. A possible way of investigating liver diseases is to study the tissue metabolic profiles. High-resolution nuclear magnetic resonance (NMR) spectroscopy of hepatic tissue extracts was combined with pattern-recognition and visualization techniques to uncover metabolic differences among analyzed tissue types. Extracts were from primary HCC, chronic hepatitis-C-virus related cirrhotic tissues, hepatic metastases from colorectal carcinomas, and non-cirrhotic normal liver tissues adjacent to metastases as controls. We identified all metabolites present in the NMR spectra, and after statistical evaluation of all spectral classes, we were able to define the metabolic changes underlying the different liver conditions and diseases. In particular, the lactate and the glucose tissue signals were found to primarily discriminate the different histological samples. We followed the biochemical changes of human hepatic lesions through primary (HCC) and secondary (metastases from colorectal carcinoma) liver tumors, cirrhotic tissues, and non-cirrhotic histologically-confirmed normal liver tissues adjacent to metastases, achieving a metabolic differentiation of the various pathological states based upon the variation of the intracellular lactate/glucose ratio. It is suggested that such a signal pattern may act as a potential marker for assessing pathological hepatic lesions.