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Proteome-metabolome profiling of ovarian cancer ascites reveals novel components involved in intercellular communication

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Abstract

© 2014 by The American Society for Biochemistry and Molecular Biology, Inc. Ovarian cancer ascites is a native medium for cancer cells that allows investigation of their secretome in a natural environment. This medium is of interest as a promising source of potential biomarkers, and also as a medium for cell-cell communication. The aim of this study was to elucidate specific features of the malignant ascites metabolome and proteome. In order to omit components of the systemic response to ascites formation, we compared malignant ascites with cirrhosis ascites. Metabolome analysis revealed 41 components that differed significantly between malignant and cirrhosis ascites. Most of the identified cancer-specific metabolites are known to be important signaling molecules. Proteomic analysis identified 2096 and 1855 proteins in the ovarian cancer and cirrhosis ascites, respectively; 424 proteins were specific for the malignant ascites. Functional analysis of the proteome demonstrated that the major differences between cirrhosis and malignant ascites were observed for the cluster of spliceosomal proteins. Additionally, we demonstrate that several splicing RNAs were exclusively detected in malignant ascites, where they probably existed within protein complexes. This result was confirmed in vitro using an ovarian cancer cell line. Identification of spliceosomal proteins and RNAs in an extracellular medium is of particular interest; the finding suggests that they might play a role in the communication between cancer cells. In addition, malignant ascites contains a high number of exosomes that are known to play an important role in signal transduction. Thus our study reveals the specific features of malignant ascites that are associated with its function as a medium of intercellular communication.

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