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Short Communication

Tropical diseases conference 2019 Differences in autophagy-associated mRNAs in peritoneal fluid of patients with endometriosis and gynecologic cancers

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Endometriosis and gynecologic cancer show similar patterns of invasion. Little is known about the roles of autophagy in endometriosis and, to date, the expression of autophagy-associated mRNAs has not been compared in patients with endometriosis and gynecologic cancers. This study therefore compared the levels of expression of autophagy-associated mRNAs in patients with endometriosis and gynecologic cancers. The levels of autophagy mRNAs, including those encoding mTOR, P13KC3, Beclin-1, Bcl-2, LC3 II, FLIP, Rubicon, BIRC2 and BIRC5, were measured by real time polymerase chain reaction in peritoneal fluid of 27 patients with benign masses (control group), 42 patients with endometriosis, and 43 patients with gynecologic (ovarian, uterine, and cervical) cancers. Findings in the three groups were compared. Autophagy mRNAs were present in all samples from patients with endometriosis and gynecologic cancers. The levels of PI3K, FLIP, and Rubicon mRNAs were significantly higher in the endometriosis than in the control group ($p<0.05$ each). Compared with the gynecologic cancer group, the levels of LC3II and FLIP mRNAs were significantly lower, and the levels of Beclin-1 and Rubicon mRNAs significantly higher, in the endometriosis group ($p<0.05$ each). Levels of PI3K and FLIP mRNA were significantly higher in the endometriosis and gynecologic cancer groups than in the control group ($p<0.05$ each). PI3K, FLIP, and Rubicon mRNAs are closely associated with the pathogenesis of endometriosis. The similar increases in PI3K and FLIP mRNA expression observed in patients with endometriosis and gynecologic cancer suggest that these conditions have similar autophagic characteristics. The lower levels of Beclin-1 mRNA in the gynecologic cancer than in other two groups suggest that lowerBeclin-1 mRNA levels increase the likelihood of developing gynecologic cancer. Recent Publications

Introduction:

Autophagy is a manner of lysosomal self-degradation of cellular components through forming autophagosomes which are conserved in all eukaryotes (1, 2). This is a pivotal manner to maintain mobile homeostasis (three). An autophagosome is a double-membrane vesicle that incorporates sequestered cytoplasmic cargos and transports them to lysosomes (4). Autophagosome formation is an important step in autophagy and is first-rate-tuned by various autophagy-associated gene (ATG) products, inclusive of ATG5, ATG12, and ATG16. During autophagosome formation, ATG5 is conjugated with ATG12 by means of ubiquitin-like conjugation structures and, similarly, forms a homodimer which includes an ATG5-ATG12/ATG16 complicated (five, 6). The complex is localized to autophagy-associated membranes and mediates LC3 conversion (7–nine). LC3 conversion is widely used as a marker of autophagosome formation (10). It has been mentioned that lack of ATG5, ATG12, or ATG16 outcomes in a lower of autophagosome formation, thereby impairing the autophagic system (11–thirteen).

Autophagy is involved in various stress responses, and dysregulation of autophagy has been determined in many sicknesses, such as cardiac ischemia/reperfusion injury, Crohn's sickness, neurodegeneration, myopathy, and diabetes, functioning because the driving or exacerbating aspect inside the pathogenesis of the diseases (3). In addition, autophagy is implicated in cancer development, even though it continues to be debatable whether or not autophagy promotes or suppresses the increase of cancer cells (14). Several reviews have proven that autophagy is a prosurvival process in established most cancers cells, and the inhibition of autophagy is one of the strategies for cancer remedy (14–17). Therefore, elucidation of the quality molecular mechanisms of autophagic procedures is important in expertise the position of autophagy in the pathogenesis of numerous diseases. Several vital regulators had been identified, and their expression mechanisms have been elucidated in numerous models (reviewed in references 4 and 18). Several microRNAs (miRNAs) were suggested to be pivotal regulators of autophagy (19–21). In this have a look at, we investigated the regulatory mechanism of autophagosome formation on the RNA degree.

HuR (human antigen R) (also referred to as HuA or ELAVL1) is a member of the Hu/ELAV (embryonic lethal strange vision)-like RNA binding protein (RBP) family containing three RNA recognition motifs (RRM) (22). HuR binds to AU-rich factors (ARE) inside the untranslated areas (UTRs) of goal mRNAs and regulates gene expression by affecting the stableness or translation of goal mRNAs (22, 23). HuR is ubiquitously expressed and has essential roles in immune reaction, angiogenesis, metastasis, and cancer improvement through regulating cell proliferation, migration, survival, dying, and autophagy (24). HuR is thought to sell cellular increase and survival by using increasing most cancers-re-

lated genes, consisting of the Cox-2, hypoxia-inducible element 1 (HIF-1), and vascular endothelial growth component (VEGF) genes, and augmented expression of HuR is related to cancer progression in a few kinds of most cancers (23, 25–27). Several efforts have been made to validate the capability of HuR as a molecular target for most cancers remedy (28–30).

Here, we look at the role of HuR within the regulation of autophagosome formation and display that HuR silencing reduces autophagosome formation and the autophagic flux of human liver cells. Along with previous studies showing SQSTM1/p62 regulation through HuR (31, 32), we identify ATG5, ATG12, and ATG16 mRNAs as novel objectives of HuR and reveal augmented expression of ATG5, ATG12, ATG16, and HuR in hepatocellular carcinoma (HCC). Our outcomes provide a molecular mechanism of autophagosome formation regulated by HuR and the capacity of HuR concentrated on in cancer development.

Biography :

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