Cytosolic Iron-Sulfur Protein Assembly 1 (CIAO1) Downstream Activation of Phospholipase A2 and Hormone-Mediated Signaling-Induced Cell Death Network in Human Hepatocellular Carcinoma (HCC) by Systems-Theoretical Analysis

Lianxiu Qi1, Lin Wang1,*, Minghu Jiang2, Juxiang Huang1 and Hong Lin1

1Biomedical Center, School of Electronic Engineering, Beijing University of Posts and Telecommunications, Beijing, 100876, China
2Lab of Computational Linguistics, School of Humanities and Social Sciences, Tsinghua University, Beijing, 100084, China

Abstract

We constructed the significant high expression (fold change ≥ 2) cytosolic iron-sulfur protein assembly 1 (CIAO1) downstream activation of phospholipase A2 and hormone-mediated signaling-induced cell death network in human Hepato Cellular Carcinoma (HCC). CIAO1 downstream activation of phospholipase A2 and hormone-mediated signaling-induced cell death network had no result, and downstream CIAO1-activated PL2A2G1B, NUP62 in HCC. By integrative analysis of biological processes simultaneous occurrence between the different CIAO1 activated downstream cell death gene ontology (GO) network of HCC compared with CIAO1 activated downstream cell death GO network of no-tumor hepatitis/cirrhotic tissues, and the same compared CIAO1 inhibited downstream cell death GO network of no-tumor hepatitis/cirrhotic tissues, or the different compared CIAO1 inhibited downstream cell death GO network of HCC, we proposed and verified that CIAO1 activated upstream network had no result; Downstream network consisted of activation of phospholipase A2, cell death, protein kinase cascade, regulation of signal transduction, hormone-mediated signaling, negative regulation of epidermal growth factor receptor signaling pathway, negative regulation of MAPK (Mitogen Activated Protein Kinase) activity, negative regulation of Ras protein signal transduction in HCC, as a result of downstream activation of phospholipase A2 and hormone-mediated signaling-induced cell death in HCC.

Keywords: Cytosolic iron-sulfur protein assembly 1 (CIAO1); Human hepatocellular carcinoma (HCC); Downstream activation of phospholipase A2 and hormone-mediated signaling-induced cell death network; Systems-theoretical analysis

Introduction


We interpreted PL2A2G1B and NUP62 by using gene ontology (GO). PL2A2G1B cellular component, molecular function and biological process are relevant to extracellular region, extracellular space; receptor binding, calcium ion binding, hydrolase activity, bile acid binding, cell surface binding, calcium-dependent phospholipase A2 activity; activation of MAPK activity, neutrophil mediated immunity, fatty acid biosynthesis, phospholipid metabolism, actin filament organization, signal transduction, protein kinase cascade, glucose transport, leucotriene biosynthesis, neutrophil chemotaxis, organismal lipid catabolism, positive regulation of DNA replication, phosphatidylcholine metabolism, positive regulation of fibroblast proliferation, arachidonic acid secretion, positive regulation of protein secretion, positive regulation of immune response, activation of NF-kappaB transcription factor, positive regulation of calcium ion transport into cytosol, positive regulation of specific transcription from RNA polymerase II promoter, activation of phospholipase A2, interleukin-8 production, cellular response to insulin stimulus (GO database). NUP62 cellular component, molecular function and biological process are relevant to nucleus, nuclear pore, nucleolus, cytoplasm, centrosome, nucleocytoplasmic shuttling complex, nuclear membrane; chromatin binding, protein serine/threonine kinase activity, nucleoctytoplasmic transporter activity, protein binding, structural constituent of nuclear pore, receptor signaling complex scaffold activity, transcription regulator activity, SH2 domain binding, ubiquitin binding, thyroid hormone receptor binding, PTB (Phosphorytrosine-binding) domain binding; cell surface receptor linked signal transduction, cell aging, cell death, negative regulation of cell proliferation, hormone-mediated signaling, regulation of signal transduction, protein transport, negative regulation of epidermal growth factor receptor signaling pathway, negative regulation of apoptosis, positive regulation of I-kappaB kinase/NF-kappaB cascade, negative regulation of MAPK activity, positive regulation of epidermal growth factor receptor signaling pathway, positive regulation of transcription, negative regulation of Ras protein signal transduction, mRNA transport, intracellular protein transmembrane transport (GO database).

Study of cytosolic iron-sulfur protein assembly 1 (CIAO1) is presented in several papers as follows: Mouse knock-out of IOP1 protein reveals its indispensable role in mammalian cytosolic iron-sulfur protein biogenesis [2]; Tah18 transfers electrons to Dre2 in cytosolic iron-sulfur protein biogenesis [3]; A role for IOP1 in mammalian

*Corresponding author: Lin Wang, Biomedical Center, School of Electronics Engineering, Beijing University of Posts and Telecommunications, Beijing, 100876, China, Tel: 0086-13240981826; Fax: 8610-62785736; E-mail: wanglin98@tsinghua.org.cn

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cytosolic iron-sulfur protein biogenesis [4]; The essential cytosolic iron-sulfur protein Nbp35 acts without Cfd1 partner in the green lineage [5]; Role of human mitochondrial Nfs1 in cytosolic iron-sulfur protein biogenesis and iron regulation [6]; Activation of the iron regulon by the yeast Afh1/Afh2 transcription factors represses mitochondrial but not cytosolic iron-sulfur protein biogenesis [7]; Gene structure and mutation causing X-linked sideroblastic anemia with ataxia with cytosolic iron-sulfur protein maturation disruption [8]. Downstream activation of phospholipase A2 and hormone-mediated signaling-induced cell death is presented in some papers. Such as, Cyttoplasmic phospholipase A2 levels correlate with apoptosis in human colon tumorigenesis [9]; Potentiation by vitamin D analogs of TNFalpha and ceramide-induced apoptosis in MCF-7 cells is related to activation of cytosolic phospholipase A2 [10]; 1,25-Dihydroxyvitamin D3 protects human leukemic cells from tumor necrosis factor-induced apoptosis through inactivation of cytosolic phospholipase A2 [11]; Phospholipase A2-activating protein (PLAA) enhances cisplatin-induced apoptosis in HeLa cells [12]; Alpha-Tocopheryl succinate contributes to apoptosis in erbB2-expressing breast cancer cell via NF-kappaB pathway [13]; Gene network signaling in hormone responsiveness modifies autophagy and apoptosis in breast cancer cells [14]; Rho/ROCK/actin signaling regulates membrane androgen receptor induced apoptosis in prostate cancer cells [15]; Gonadotropin-releasing hormone type II contributes to apoptosis of human endometrial cancer cells by activating GADD45alpha [16]. Yet the distinct high expression Cytosolic Iron-Sulfur Protein Assembly 1 (Gene Network Reconstruction tool) based on linear programming and decomposition procedure.

In this study, we constructed Cytosolic Iron-Sulfur Protein Assembly 1 (Gene Network Reconstruction tool) based on linear programming and decomposition procedure. Here we constructed the high expression Cytosolic Iron-Sulfur Protein Assembly 1 (Gene Network Reconstruction tool) based on linear programming and decomposition procedure.

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Materials and Methods

Microarrays 6,144 genes were used for analyzing Cytosolic Iron-Sulfur Protein Assembly 1 (Gene Network Reconstruction tool) based on linear programming and decomposition procedure. We analyzed Cytosolic Iron-Sulfur Protein Assembly 1 (Gene Network Reconstruction tool) based on linear programming and decomposition procedure. We analyzed Cytosolic Iron-Sulfur Protein Assembly 1 (Gene Network Reconstruction tool) based on linear programming and decomposition procedure. We analyzed Cytosolic Iron-Sulfur Protein Assembly 1 (Gene Network Reconstruction tool) based on linear programming and decomposition procedure. We analyzed Cytosolic Iron-Sulfur Protein Assembly 1 (Gene Network Reconstruction tool) based on linear programming and decomposition procedure. We analyzed Cytosolic Iron-Sulfur Protein Assembly 1 (Gene Network Reconstruction tool) based on linear programming and decomposition procedure.
CIAO1 activated downstream activation of phospholipase A2 and hormone-mediated signaling-induced cell death network in human hepatocellular carcinoma (HCC) by systems-theoretical analysis. Mol Biol 1:105. doi:10.4172/2168-9547.1000105

Table 1: GO Terms and numbers data analysis of the different biological processes of CIAO1 activated downstream cell death network of HCC compared with activated network of no-tumor hepatitis/cirrhotic tissues, the same biological processes of CIAO1 activated downstream cell death network of HCC compared with inhibited network of no-tumor hepatitis/cirrhotic tissues.

<table>
<thead>
<tr>
<th>Terms</th>
<th>Numbers</th>
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<tr>
<td>protein kinase cascade</td>
<td>1</td>
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<tr>
<td>activation of phospholipase A2</td>
<td>1</td>
</tr>
<tr>
<td>regulation of signal transduction</td>
<td>1</td>
</tr>
<tr>
<td>cell death</td>
<td>1</td>
</tr>
<tr>
<td>hormone-mediated signaling</td>
<td>1</td>
</tr>
<tr>
<td>negative regulation of epidermal growth factor receptor signaling pathway</td>
<td>1</td>
</tr>
<tr>
<td>negative regulation of MAPK activity</td>
<td>1</td>
</tr>
<tr>
<td>negative regulation of Ras protein signal transduction</td>
<td>1</td>
</tr>
<tr>
<td>fatty acid biosynthesis</td>
<td>1</td>
</tr>
<tr>
<td>organismal lipid catabolism</td>
<td>1</td>
</tr>
<tr>
<td>phosphatidylcholine metabolism</td>
<td>1</td>
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<tr>
<td>phospholipid metabolism</td>
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</table>

Table 2: GO Terms and numbers data analysis of the different biological processes of CIAO1 activated downstream cell death network of HCC compared with inhibited network of HCC.

<table>
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<tbody>
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<td>negative regulation of epidermal growth factor receptor signaling pathway</td>
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The biological process and data analysis of the different GO terms and numbers were compared among different databases presented in our articles [19-32]. In this study, we constructed CIAO1 upstream and downstream activated and inhibited downstream activation of phospholipase A2 and hormone-mediated signaling-induced cell death network in no-tumor hepatitis/cirrhotic tissues and HCC. The biological process and data analysis of the low and high expression CIAO1 downstream activation of phospholipase A2 and hormone-mediated signaling-induced cell death network was done in no-tumor hepatitis/cirrhotic tissues (HBV or HCV infection) and HCC by GO database. By comparison with the same and different upstream and downstream GO and numbers of CIAO1 activated and inhibited downstream cell death network between no-tumor hepatitis/cirrhotic tissues and HCC, we put forwards hypothesis of CIAO1 activated downstream cell death network of downstream activation of phospholipase A2 and hormone-mediated signaling-induced cell death in HCC.

We extracted the biological process of GO terms and did numbers data analysis of the different biological processes of CIAO1 activated downstream cell death network in HCC compared with inhibited network of no-tumor hepatitis/cirrhotic tissues (Table 1 and Table 2). We constructed the high expression (fold change ≥ 2) CIAO1 activated downstream activation of phospholipase A2 and hormone-mediated signaling-induced cell death network in human hepatocellular carcinoma (HCC) compared with low expression no-tumor hepatitis/cirrhotic tissues (HBV or HCV infection) in GEO data set using integration of gene regulatory network inference method. Our result showed that CIAO1 downstream activation of phospholipase A2 and hormone-mediated signaling-induced cell death upstream network had no result, and downstream CIAO1-activated PLA2G1B, NUP62 (Figure 1 and Figure 2) in HCC.

By further comparison with the same biological processes of and different gene ontology (GO) of CIAO1 activated and inhibited downstream cell death network between no-tumor hepatitis/cirrhotic tissues and HCC, we found that the different biological processes of CIAO1 activated upstream network had no result; Downstream network consisted of protein kinase cascade, activation of phospholipase A2, regulation of signal transduction, cell death, hormone-mediated signaling, negative regulation of epidermal growth factor receptor signaling pathway, negative regulation of MAPK activity, negative regulation of Ras protein signal transduction in HCC compared with activated network of no-tumor hepatitis/cirrhotic tissues.
The same biological processes of CIAO1 activated upstream network had no result; downstream network had no result in HCC compared with inhibited network of no-tumor hepatitis/cirrhotic tissues.

The different biological processes of CIAO1 activated network had no result; Downstream network included negative regulation of epidermal growth factor receptor signaling pathway, negative regulation of MAPK activity, negative regulation of Ras protein signal transduction, protein kinase cascade, regulation of signal transduction, activation of phospholipase A2, cell death, hormone-mediated signaling compared with inhibited network of HCC.

By integrative analysis of biological processes simultaneous occurrence between the different CIAO1 activated downstream cell death gene ontology (GO) network of HCC compared with CIAO1 activated downstream cell death GO network of no-tumor hepatitis/cirrhotic tissues, and the same compared CIAO1 inhibited downstream cell death GO network of no-tumor hepatitis/cirrhotic tissues, or the different compared CIAO1 inhibited downstream cell death GO network of HCC, we proposed and verified that different compared cell death GO network of no-tumor hepatitis/cirrhotic tissues, or the same compared inhibited downstream cell death GO network of HCC.

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References


