Interferon α-Inducible Protein 27 Computational Network Construction and Comparison between the Frontal Cortex of HIV Encephalitis (HIVE) and HIVE-Control Patients

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Abstract: Interferon α-inducible protein 27 (IFI27) computational network construction and analysis of frontal cortex of HIV encephalitis (HIVE) is very useful to identify novel markers and potential targets for prognosis and therapy. Based on integrated gene regulatory network infer (GRNInfer) method by linear programming and a decomposition procedure with analysis of the significant function cluster using Kappa statistics and fuzzy heuristic clustering from DAVID, we identified and constructed significant molecular IFI27 networks from 12 frontal cortex of HIVE-control patients and 16 HIVE in the same GEO Dataset GDS1726. Our integrative results reflected an IFI27 membrane module only in the upstream of the frontal cortex of HIVE-control patients (BTN3A2, RASGRP3, ROR1 inhibition), and the frontal cortex of HIVE (DGKG, LY96 activation; RASGRP3 inhibition); IFI27 organelle only in the upstream of HIVE-control patients (CREB5, OAS1, PDCD4 activation), and HIVE (PDCD4 activation; ZC3HAV1, ZNF652 inhibition); IFI27 sequence variant only in the upstream of HIVE-control patients (ISG15_2, OAS1, TNFRSF11B activation; BTN3A2, LCAT, ROR1 inhibition), and HIVE (CFB, DGKG, LCAT, LY96 activation; ISG15_2, TNFRSF11B, ZC3HAV1 inhibition).

Keywords: IFI27, network construction and analysis, the frontal cortex with HIVE, biocomputation.

INTRODUCTION

The neurodegenerative process in HIV encephalitis (HIVE) is associated with cognitive impairment with extensive damage to the dendritic and synaptic structure. Several mechanisms might be involved including release of neurotoxins, oxidative stress and decreased activity of neurotrophic factors [1]. The effect of HIV on the brain has been studied by several researchers. The investigations include decreased brain dopamine transporters associated with cognitive deficits in HIV patients with or without cocaine abuse; Magnetic resonance imaging and spectroscopy of the brain in HIV disease; Analysis of the effects of injecting drug use and HIV-1 infection on 18F-FDG PET brain metabolism [2-4]. IFI27 computational metabolism network construction and analysis of the frontal cortex of HIVE is very useful to identify novel markers and potential targets for prognosis and therapy.

IFI27 is one out of 50 genes identified as high expression in the frontal cortex of HIV encephalitis (HIVE) vs HIVE-control patients. IFI27’s molecular function network contains G-protein coupled receptor, interferon receptor, growth factor, centromere DNA-binding protein, protein phosphatase, phospholipase, metalloprotease, non-receptor tyrosine protein kinase, serine protease inhibitor, non-motor actin binding protein and ubiquitin-protein ligase, and it is relevant to biological process of fatty acid metabolism, mRNA transcription regulation, protein modification, protein phosphorylation, proteolysis, signal transduction, ion transport, immunity and defense and phospholipid metabolism (DAVID database). IFI27's relational study has also been reported previously [5]. However, the molecular mechanism concerning IFI27 network construction in the frontal cortex with HIVE has not been addressed adequately.

This paper is based on our previous publication [6]. Mining larger data sets to get an insight into biological processes at system—wide level has become a challenge for bioinformatics with microarray technologies producing a great deal of gene expression data in the postgenomic era. On the one hand, due to the complexity and distributive nature of biological research, there are several methods for inferring gene regulatory networks but all these methods focus on constructing an entire network calculated from the given microarray data. The large number of genes in those networks makes it is hard to get any clear perception of valuable knowledge from such complicated networks, let alone further study single genes. On the other hand, the wide spread of knowledge from independent databases lowers the study effectiveness. Thus, a novel method of integrating both single molecular network construction and highly centralized gene—functional—annotation analysis is needed for gene network and functional analysis. This paper propose an inte-
grated method, based on linear programming and a decomposition procedure with integrated analysis of the significant function cluster using kappa statistics and fuzzy heuristic clustering. Our method concentrates on and constructs a prioritized single gene knowledge network integrated with DAVID for the prioritised (1,2). We identified IFI27 activation and inhibition networks, (3) upstream and downstream feedback networks, and (4) IFI27 functional module construction. Our construction of IFI27 network may be useful to identify novel markers and potential targets for prognosis and therapy of HIV.

MATERIALS AND METHODS

Microarray Data

We used microarrays containing 12558 genes from 12 frontal cortex of HIV-control patients and 16 HIV in the same GEO Dataset GDS1726 [1]. HIV-control patients mean normal adjacent frontal cortex tissues of HIV encephalitis (HIVE) and no extensive damage to the dendritic and synaptic structure.

Gene Selection Algorithms

50 molecular markers of the frontal cortex of HIV were identified using significant analysis of microarrays (SAM). SAM is a statistical technique for finding significant genes in a set of microarray experiments. The input to SAM is gene expression measurements from a set of microarray experiments, as well as a response variable from each experiment. The response variable may be a grouping like untreated, treated and so on. SAM computes a statistic \( d_i \), for each gene \( i \), measuring the strength of the relationship between gene expression and the response variable. It uses repeated permutations of the data to determine if the expression of any genes is significantly related to the response. The cutoff for significance is determined by a tuning parameter delta, chosen by the user based on the false positive rate. We normalized data by log2, and selected two class unpaired and minimum fold change =1.52. Here we chose the 50 top-fold significant (high expression genes of HIVE compared with HIV-control patients) genes under the false-discovery rate and \( q \)-value are 9.12%. We identified potential HIV molecular markers and chose the 50 top-fold significant positive genes from 12558 genes from 12 frontal cortex of HIV-control patients and 16 HIV in the same GEO Dataset GDS1726 including interferon alpha-inducible protein 27 (IFI27), complement factor b (CFB), lymphocyte antigen 96 (LY96), programmed cell death 4 (PDCD4), lecithin-cholesterol acyltransferase (LCAT), ras guanyl releasing protein 3 (RASGRP3), zinc finger cccch-type antiviral 1 (ZC3HAV1), tumor necrosis factor receptor superfamily member 11b (TNFRSF11B), zinc finger protein 652 (ZNF652), diacylglycerol kinase gamma (DGKG), etc. (see List of Abbreviations).

IFI27 Up- and Down-Stream Network Construction in the Frontal Cortex of HIV-Control Patients and HIVE

In the frontal cortex of HIV-control patients, IFI27 upstream network appeared that ADH1B, AF075680, CREB5, IFI44L, ISG15_2, OAS1, PDCD4, TNFRSF11B activate IFI27, and BTN3A2, LCAT, RASGRP3, ROR1 inhibit IFI27, as shown in Fig. (1A), whereas in the frontal cortex of HIV, IFI27 upstream network showed that AL080060, CFB, DGKG, LCAT, LY96, M33210, PDCD4 activate IFI27, and ADH1B, AF075680, ISG15_2, RASGRP3, TNFRSF11B, ZC3HAV1, ZNF652 inhibit IFI27, as shown in Fig. (1B). In the frontal cortex of HIV-control patients and in the frontal cortex of HIV, IFI27 downstream network showed no results.

Identification of IFI27 Up- and Down-Stream Modules in the Frontal Cortex of HIV-Control Patients and HIVE by DAVID

In the frontal cortex of HIV-control patients, IFI27 upstream modules mainly include membrane (BTN3A2, RASGRP3, ROR1, IFI27), organelle (CREB5, OAS1, PDCD4,
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IFI27), sequence variant (ISG15_2, OAS1, TNFRSF11B, BTN3A2, LCAT, ROR1, IFI27), etc., as shown in Fig. (2A). In the frontal cortex of HIVE, IFI27 upstream modules mainly cover membrane (DGKG, LY96, RASGRP3, IFI27), organelle (PDCD4, ZC3HAV1, ZNF652, IFI27), sequence variant (CFB, DGKG, LCAT, LY96, ISG15_2, TNFRSF11B, ZC3HAV1, IFI27), etc., as shown in Fig. (2B). In the frontal cortex of HIVE-control patients and in the frontal cortex of HIVE, IFI27 downstream showed no results.

DISCUSSION
We have previously published work in this field about gene network construction and analysis [6, 11-15] By integration of gene regulatory network infer (GRNInfer) and the database for annotation, visualization and integrated discovery (DAVID 2010 version) we constructed a significant molecular IFI27 network and compared IFI27 up- and downstream gene numbers for activation and inhibition between HIVE-control patients and HIVE (Table 1). Specifically, IFI27 downstream networks showed no results in the frontal cortex of HIVE-control patients and the frontal cortex of HIVE.

In the IFI27 membrane module of the upstream network of frontal cortex of HIVE-control patients, our integrative results suggested that BTN3A2, RASGRP3, ROR1 inhibit IFI27, whereas in that of HIVE, DGKG, LY96 activate IFI27, and RASGRP3 inhibits IFI27. For the IFI27 membrane module of the downstream network there was no result (Fig. 1, 2, Table 2). LY96 is identified by molecular function of CAM family adhesion molecule and transmembrane receptor regulatory/adaptor protein, and it is involved in the biological process of mRNA splicing, protein biosynthesis, endocytosis and immunity and defense (DAVID database). LY96’s relational study has been reported previously [16-20].

DGKG has been reported to be relevant to molecular function of mRNA processing factor, mRNA splicing factor, kinase, nucleotide kinase, epimerase/racemase, complement component, zinc finger transcription factor, KRAB box transcription factor and RNA helicase, and it is involved in biological process of lipid, fatty acid and steroid metabolism, Acr-CoA, cholesterol, purine metabolism, mRNA transcription regulation, pre-mRNA processing, mRNA splicing, MAPK cascade, T-cell and MHCI-mediated immunity, complement-mediated immunity and other neuronal activity (DAVID database). DGKG’s relational study has also been reported [21-24]. RASGRP3’s molecular function consists of select regulatory molecule, G-protein modulator and guanyl-nucleotide exchange factor, and it is concerned with biological process of mRNA transcription regulation, proteolysis, signal transduction, cell adhesion-mediated signaling, ligand-mediated signaling, cell communication and steroid metabolism (DAVID database). RASGRP3’s relational study has also been reported [25-29].

In IFI27 organelle module of upstream network of frontal cortex of HIVE-control patients, our integrative result suggested that CREB5, OAS1, PDCD4 activate IFI27, whereas in that of HIVE, PDCD4 activates IFI27, and ZC3HAV1, ZNF652 inhibits IFI27. In the IFI27 organelle module of downstream network there was no result (Fig. 1, 2, Table 2). PDCD4’s molecular function consists of mitochondrial carrier protein, G-protein, large G-protein, guanyl-nucleotide exchange factor, protein kinase, lipase, non-receptor serine/threonine protein kinase, calmodulin related protein, actin and actin related protein, and it is concerned with the biological processes of amino acid catabolism, mRNA transcription, mRNA transcription elongation, mRNA transcription regulation, mRNA splicing, protein metabolism and modification, protein biosynthesis, proteolysis, cell surface receptor medi-
ated signal transduction, G-protein mediated signaling, calcium mediated signaling, small molecule transport, cell proliferation and differentiation, muscle development, chromatin packaging and remodeling (DAVID database). PDCD4’s relational study has been reported previously [30-35]. ZC3HAV1 has been reported to be relevant to the molecular function of nuclease, mRNA splicing factor, carbohydrate kinase and endoribonuclease, and it is involved in the biological process of nucleoside catalytic and mRNA transcription regulation (DAVID database). ZC3HAV1’s relational study also can be presented in these papers [36-40]. ZNF652 is relevant to molecular function of voltage-gated potassium channel, transcription factor, zinc finger transcription factor, KRB box transcription factor and non-motor microtubule binding protein, and the biological process of nucleoside metabolism, mRNA transcription, mRNA splicing, protein acetylation and spermatogenesis and motility (DAVID database). ZNF652’s relational study has been reported [41-43].

Table 1.  

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In the IFI27 sequence variant module of the upstream network of frontal cortex of HIVE-control patients, our integrative result showed that ISG15_2, OAS1, TNFRSF11B activate IFI27, and BTN3A2, LCAT, ROR1 inhibit IFI27, whereas in that of HIVE, CFB, DGKG, LCAT, LY96 activate IFI27, and ISG15_2, TNFRSF11B, ZC3HAV1 inhibit IFI27. In the IFI27 sequence variant module of downstream network there was no result (Fig. 1, 2, Table 2). LCAT is identified by molecular function of interleukin receptor, transferase, acyltransferase, complement component, antibacterial response protein, extracellular matrix structural protein and microtubule binding motor protein, and it is involved in the biological processes of lipid, fatty acid, cholesterol catalytic and synaptic transmission (DAVID database). ISG15_2's relational study has been reported [44-48]. TNFRSF11B has been shown to be concerned with molecular function of receptors including calcium binding protein and tumor necrosis factor receptor, and skeletal and mesoderm development (DAVID database). ISG15_2's relational study has been reported [49-54]. ISG15 is relevant to molecular function of ribosomal protein and annexin, and mRNA transcription regulation, mRNA polyadenylation, protein catalytic and modification, proteolysis and cation transport (DAVID database). ISG15's relational study has been reported [55-59]. CFB's molecular function contains protein kinase, methyltransferase, glycosyltransferase, deacetylase, protease, phosphorylase, non-receptor serine/threonine protein kinase, non-receptor tyrosine protein kinase, zinc finger transcription factor, KRAB box transcription factor and non-motor actin binding protein, and it is relevant to biological processes of purine metabolism, mRNA transcription regulation, protein metabolism and modification, protein biosynthesis, protein modification and glycosylation, proteolysis, electron transport, G-protein mediated signaling and cell structure (DAVID database). CFB's relational study has been reported [60-64].

In conclusion, we first identified the significant molecule IFI27 by SAM, then constructed IFI27 up- and down-stream networks by GRNInfer and further data-mined the main IFI27 modules including membrane, organelle and sequence variant from 12 frontal cortex of no-encephalitis HIV patients and 16 HIV encephalitis (HIVE) and in the same GEO Dataset GDS1726 by using DAVID. Our computation showed the different gene rate of IFI27 network in HIVE as 86% (12/14) compared with no-encephalitis HIV patients considering activation and inhibition relationship. Our integrative results reflected IFI27 membrane module only in the upstream of the frontal cortex of no-encephalitis HIV patients (BTN3A2, RASGRP3, ROR1 inhibition), whereas only in the upstream of the frontal cortex of HIVE (DGKG, LY96 activation; RASGRP3 inhibition); IFI27 organelle only in the upstream of no-encephalitis HIV patients (CREB5, OAS1, PDCD4 activation), whereas only in the upstream of HIVE (PDCD4 activation; ZC3HAV1, ZNF652 inhibition); IFI27 sequence variant only in the upstream of no-encephalitis HIV patients (ISG15_2, OAS1, TNFRSF11B activation; BTN3A2, LCAT, ROR1 inhibition), whereas only in the upstream of HIVE (CFB, DGKG, LCAT, LY96 activation; ISG15_2, TNFRSF11B, ZC3HAV1 inhibition) (Table 2).

ACKNOWLEDGEMENTS

This work was supported by the National Natural Science Foundation in China (No.60871100) and the Teaching and Scientific Research Foundation for the Returned Overseas Chinese Scholars, State Education Ministry. State Key Lab of Pattern Recognition Open Foundation, Major science and technology projects of new transgenic biological breeds (2009ZX08012-001B), Key project of philosophical and social science of MOE (07JZD0005).
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Abbreviations, contd....


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