

Systematic tracking of altered modules identifies the key biomarkers involved in chronic lymphocytic leukemia

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Abstract. Key genes in chronic lymphocytic leukemia (CLL) were investigated through systematically tracking the dysregulated modules from protein-protein interaction (PPI) networks. Microarray data of normal subjects and CLL patients recruited from ArrayExpress database were applied to extract differentially expressed genes (DEGs). Additionally, we re-weighted the PPI network of normal and CLL conditions by means of Pearson's correlation coefficient (PCC). Furthermore, clique-merging method was applied to extract the modules and then the altered modules were screened out. The intersection genes were selected from miss and add genes in the altered modules. The common genes were screened from the intersection genes and DEGs in CLL. A total of 734 DEGs were screened by statistical analysis. In this investigation, there were 1,805 and 703 modules in normal as well as disease PPI network. In addition, 875 altered modules were obtained which included 145 miss genes, 353 add genes and 85 intersection genes. Finally, in-depth analysis revealed 9 mutual genes between the intersection genes and DEGs in CLL. Our analysis revealed several key genes associated with CLL by systematically tracking the dysregulated modules, which might be candidate targets for diagnosis and management of CLL.

Introduction

Fundamental units formed by interacting proteins have been demonstrated to be responsible for implementing important biological processes within cells (1). The identification of protein complexes (modules or pathways) contributes to understanding the complex formation and the higher level organization of cells, and the dysregulation of protein complexes

might be associated with the development of disease. With the advance of microarray techniques, a large number of physical interactions have been cataloged from organisms, fueling the development of computational algorithms for systematically mining protein complexes from the protein-protein interaction (PPI) network. Despite the significant progress in the aspect of extracting protein complexes from the PPI networks over the last few years, computational methods are seriously constrained by noise in current PPI data (2,3). Several computational methods have been developed to predict modules from networks relying on graph clustering, and clique finding, such as MCODE (4), CMC (5) and STM (6). In addition, the identification of dysregulated modules from condition-specific networks will promote the process to reveal the pathogenesis of disease. Recently, a systematic method for uncovering dysregulated modules has been developed by integrating PPI information and condition-specific gene expression profile (7).

Chronic lymphocytic leukemia (CLL) is the most common type of hematopoietic malignancies in adults (8). Nowadays, more and more patients are diagnosed at early-stage, likely because of using routine blood tests as well as the widespread availability of flow cytometry (9-11). However, the treatment of CLL remains a challenge (12). A previous study demonstrated that TL1A could be considered as a negative regulator of leukemic cell proliferation, that may influence the physiopathology and clinical outcome of CLL at an early-stage (13). Moreover, researchers indicated that the inhibition of JAK was a potentially useful new pharmacological approach to CLL treatment (14). However, the underlying mechanisms of CLL have yet to be fully elucidated. Systematic tracking dysregulated module behavior across specific conditions is critical.

In this investigation, we proposed a straightforward but systematic method to identify and compare the modules across normal and CLLs through integrating PPI data and specific gene expression profile of CLL. The results of this study will be critical to reveal the molecular mechanism of this disease and develop promising therapies.

Materials and methods

Data recruitment and preprocessing. Here we selected the microarray expression profile of E-GEOD-2466 (15) CLL from ArrayExpress database to perform our analysis. The gene expression profile numbered E-GEOD-2466 which was based

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on the platform of A-AFFY-1 - Affymetrix GeneChip Human Genome U95Av2 [HG_U95Av2] and A-AFFY-9 - Affymetrix GeneChip Human Genome U95A [HG_U95A] was downloaded. E-GEOD-2466 comprised a total of 111 samples, including 100 genetically well-characterized B-CLL samples and 11 normal control samples. Finally, we obtained the probe annotation data for subsequent analysis.

With the goal of eliminating the influence of non-specific hybridization, the *expresso* function from the *Affy* package was used to obtain the probe data. Moreover, background correction was conducted by means of robust multiarray average (RMA) (16), quantiles (17) was employed to standardize the data, MAS was utilized to implement perfect match (PM) and mismatch (MM) correction (18), medianpolish (16) was performed to summarize the probe data, followed by the filtration of probe data by means of *featureFilter* function. Ultimately, we obtained 20,102 genes from the probe set.

Detection of differentially expressed genes (DEGs). The DEGs between the two groups were extracted relying on *limma* package (19). Empirical Bayes (eBayes) (20) as well as a false discovery rate (FDR) (21) calibration of P-values were implemented using *ImFit* function. The genes were extracted if these genes met the following conditions: $\log_{2}FCI \geq 2$, $P < 0.01$.

PPI network construction. In this study, we downloaded all PPI data with combine-score from the STRING database (22). The protein ID and gene symbols were transformed and then the repeated ones were removed. We selected the interaction relations with combined-score ≥ 0.65 to construct the PPI sub-network.

Gene interactions re-weighted using Pearson's correlation coefficient (PCC). Gene interactions of the PPI sub-network of CLL and normal subjects were re-weighted by PCC. PCC can evaluate the probability of two co-expressed genes, where value ranged from -1 to +1 (23). Moreover, the absolute value of PCC of each edge was defined as the value of the interaction of the PPI sub-network. In addition, we defined PCC of every gene pair as the weight value of the edge.

Uncovering modules from the sub-network of PPI. Clique-merging, an approach used to identify the modules, is similar to the previous algorithms for detecting complexes from the PPI networks (2,5). Herein, we used the clique-merging to extract the modules from PPI sub-networks. In detail, we discovered all maximal cliques from the network of the normal and disease conditions using fast depth-first approach. Subsequently, the maximal cliques having nodes ≥ 5 were selected. Last we arranged them in descending order according to the score of a clique. This score was its weighted interaction density (WID). According to the WID, we sorted these cliques.

A lot of maximal cliques may be overlapped. Hence, these lapped cliques should be abandoned to decrease size or merged into a bigger sub-graphs. In this study, the weighted inter-connectivity between two cliques was employed to determine whether these two lapped cliques were combined or not. Herein, t_0 (a predefined overlap cut-off criteria) = 0.5 and t_m (a predefined m cut-off criteria) = 0.25 were selected to be the threshold in the current study.

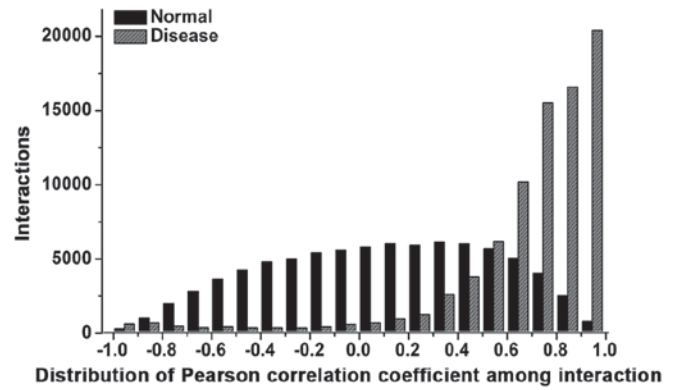


Figure 1. Interaction distribution in normal and CLL groups. CLL, chronic lymphocytic leukemia.

Identification of altered modules. The modules were respectively extracted from the PPI networks of normal controls and CLL. For each module in the normal and disease conditions, we calculated the modules correlation density (MCD) based on the PCC of gene-gene interactions in PPI network. MCD was measured as:

$$d_{cc}(S_i) = \frac{\sum_{p, q \in S_i} PCC(p, q, N)}{\binom{|S_i|}{2}}.$$

The pairs of the disrupted or dysregulated modules were evaluated through determining the module as a maximum weight bipartite matching (24). A similarity graph $M = (V_m, E_m)$ was constructed, where $V_m = \{S_i, T_j\}$, and $E_m = U\{(S_i, T_j) : J(S_i, T_j) \geq t_j, \Delta CC(S_i, T_j) \geq \delta\}$, whereby $J(S_i, T_j) = |S_i \cap T_j| / |S_i \cup T_j|$ was the Jaccard similarity (J) and $\Delta CC(S_i, T_j) = |d_c(S_i) - d_c(T_j)|$ was the differential correlation density (ΔCC) between S_i and T_j (7). In our study, the altered modules with $t_j \geq 2/3$ as well as $\Delta CC \geq 0.05$ were considered as the disrupted modules.

Gene composition of altered modules. With the goal of better understanding the differences of the altered modules in the two groups, we screened out the missed and added genes. Significantly, the common part of the missed as well as added genes was also identified. Moreover, in order to obtain the relevant disease genes, we also took the intersection of the DEGs and the intersection genes.

Results

Detection of DEGs. In our study, a total of 8,630 genes were screened out for subsequent analysis. Using the threshold of $\log_{2}FCI > 2$, and a FDR < 0.01 , a total of 734 genes were identified to be differentially expressed in CLL.

Disruptions in CLL PPI network. Under the combined-score ≥ 0.65 , the PPI sub-networks displayed equal numbers interactions (40,576) and nodes (6,068). Their mean average scores were respectively 0.320 and 0.698 in the normal and disease network. The result of PCC distribution in the two networks is shown in Fig. 1. Differences were observed in the PCC score distribution (-1 to 1) of the two networks. Moreover, the count of the interactions in the normal network was higher than that

Table I. Properties of normal and disease modules.

Module set	No. of modules	Average module size	Correlation		
			Max	Avg	Min
Normal	1,805	19.32798	0.5186083	0.06900261	-0.1587027
Disease	703	43.46373	0.573716	0.0379185	-0.1173073

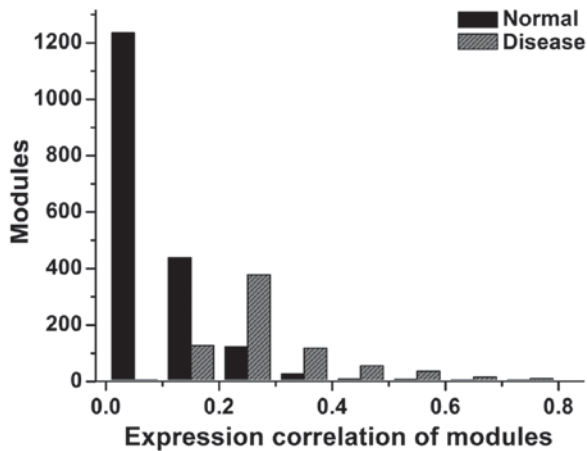


Figure 2. Distribution of the correlation-wise values of modules in normal and CLL group. CLL, chronic lymphocytic leukemia.

in the CLL network when the weight distribution was ranging from -0.9 to -0.4.

Analysis of disruptions in CLL modules. On the basis of the threshold of nodes ≥ 5 , there were 8,773 maximal cliques in the normal and CLL PPI sub-networks, and then, these 8,773 cliques were utilized to conduct module analysis. There were 1,805 and 703 modules from the PPI sub-networks of normal and CLL, respectively (Table I). For the module of CLL, the average module size was higher than that of module of normal. Moreover, for CLL modules, it also showed an overall decrease in average correlation comparing with the normal modules. The connection between the counts of modules and weighted density of modules is shown in Fig. 2. The distribution of modules in normal was higher under 0-0.2, while lower under 0.2-0.8 relative to that in disease condition.

Moreover, there were 646 disrupted module pairs. Relative to the normal group, we found that all altered modules were higher in the disease group based on the module correlation density of the modules.

Gene composition of the altered modules. There were 646 disrupted module pairs in total. Among these module pairs, there were 145 missed genes and 353 added genes in CLL modules relative to normal modules. Of note, 85 genes were the common ones between the added and missed genes. In this investigation, we obtained 9 common genes between the 85 intersection genes and the DEGs, of which were AKT1, UPF3A, SMG7, RPN2, HSPB1, SPCS2, CDC16, COPS5 and PSMB10. Hence, we treated the 9 genes as the key genes involved in CLL.

Discussion

CLL is a variety of chronic lymphoproliferative disorders (24). In our study, we investigated gene profile E-GEOD-2466 and extracted the key genes in CLL on the basis of systematically tracking the disrupted modules of re-weighted PPI networks. In total, 9 key genes were identified through comparing intersection genes in the altered modules and DEGs.

In humans, RAC- α serine/threonine-protein kinase is coded by AKT1 gene. AKT1 has been demonstrated to regulate a large amount of biological processes, for example, cell proliferation, growth, metabolism, survival, and angiogenesis. The AKT1 isoform played a dominant role in the survival and chemoresistance of CLL cells (25). AKT1 gene has been inferred to be related to a variety of diseases. It was familiar in cancer (26,27), tumors (28,29) and insulin resistance (30). Another study has also implicated that the expression of AKT1 was associated with CLL (31,32).

Dolichyl-diphosphooligosaccharide-protein glycosyltransferase subunit 2 is coded by RPN2 in humans. So far there has not been much research on the correlation of RPN2 and a disease, in addition to tumors. For example, it has been verified that RPN2 silencing made breast cells hypersensitive to docetaxel (33). Moreover, RPN2 has also displayed a higher genomic alteration frequency in colorectal cancer (34).

Heat-shock protein 27 (Hsp27) in humans is encoded by HSPB1, which is a chaperone of the small heat-shock protein group (35,36). As known, the common roles of small heat-shock proteins are inhibition of apoptosis, thermotolerance, and cell differentiation. HSPB1 was reported related to breast cancer, shock, Alexander's disease and many kinds of tumors (37-40). Dempsey *et al* (41) have explored that CLL patients expressed significantly higher levels of Hsp27 in lymphocytes than that expressed by lymphocytes from control subjects.

Taken together, we successfully identified a series of key genes for understanding the potential mechanism of gene expression of CLL on the basis of systematically uncovering the altered modules based on the re-weighted PPI networks and DEGs. These results have implications for understanding the mechanisms of gene expression of CLL.

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Availability of data and materials

The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

Authors' contributions

XL and SFK conceived the study and drafted the manuscript. ZW and XYZ acquired the data. CFL and SFK analyzed the data and revised the manuscript. All authors read and approved the final manuscript.

Ethics approval and consent to participate

Not applicable.

Patient consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

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