Abstract. The aim of the present study was to investigate more colon cancer-related genes in different stages. Gene expression profile E-GEOD-62932 was extracted for differentially expressed gene (DEG) screening. Series test of cluster analysis was used to obtain significant trending models. Based on the Gene Ontology and Kyoto Encyclopedia of Genes and Genomes databases, functional and pathway enrichment analysis were processed and a pathway relation network was constructed. Gene co-expression network and gene signal network were constructed for common DEGs. The DEGs with the same trend were clustered and in total, 16 clusters with statistical significance were obtained. The screened DEGs were enriched into small molecule metabolic process and metabolic pathways. The pathway relation network was constructed with 57 nodes. A total of 328 common DEGs were obtained. Gene signal network was constructed with 71 nodes. Gene co-expression network was constructed with 161 nodes and 211 edges. ABCD3, CPT2, AGL and JAM2 are potential biomarkers for the diagnosis of colon cancer.

Introduction

Colon cancer together with lung, prostate and breast cancer constitute a threat to human health worldwide (1). Notably, previous findings showed that surgery had minimal adverse reaction in stage 2 patients (2). In addition, some treatment strategies such as adjuvant chemotherapy, were found to be effective, especially for stage 3 colon cancer (3). Thereby, the known critical genes in different stages of colon cancer was necessary for the diagnosis and treatment of this disease.

Materials and methods

Microarray data. The gene expression profile E-GEOD-62932 was extracted from the ArrayExpress Archive, including 64 colon cancer tissues and 4 healthy control samples (9). The 64 colon cancer tissues included 12 samples in stage 1, 17 in stage 2, 20 in stage 3, and 15 in stage 4. Platform information of this profile was GPL570 [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array.

Data preprocessing and DEGs screening. The obtained probe sets were converted into expression value matrix and background correction, normalization and summarizing were performed using the Robust Multi-chip Average algorithm. Based on the information of Affymetrix (*.transcript.csv), the probe sets were annotated. The annotated data were screened with the threshold of >0.8 median (normalized unscaled standard errors) <1.2 and >0.25 median (relative log expression) <0.25.
DEGs between colon cancer in various stages and normal tissues were identified by significance analysis of microarrays method with the cut-off criteria of P<0.05 (10).

Series test of clusters. The gene expression profiles were always changed with tumor development. In the present study, series test of cluster (STC) analysis was used to obtain the significant trending models related to tumor stage and their involved DEGs (11). Clusters with P<0.05 were regarded as statistically significant.

Functional and pathway enrichment analysis. Gene Ontology (GO) is a cross-species and comprehensive database, which was constructed by the GO Consortium (12). Similarly, the Kyoto Encyclopedia of Genes and Genomes (KEGG) is a powerful tool for analysis of biological metabolism and metabolic network (13). Based on the abovementioned databases, GO functional and KEGG pathway enrichment analysis were processed for identified DEGs with the threshold of P<0.05. The Fisher's exact test and multiple comparisons were used to calculate the significance of GO terms and pathways, and false discovery rate (FDR) was the adjusted P-value.

Construction of pathway relation network. The pathway relation network was constructed with 57 nodes and 158 edges. The hub nodes were glycolysis/gluconeogenesis (Degree=17), apoptosis (Degree=17), citrate cycle (TCA cycle) (Degree=16) and pathways in cancer (Degree=13). Notably, pathways in cancer (Outdegree=13), phenylalanine metabolism (Outdegree=4) and gap junction (Outdegree=4) were upstream pathways, while cytokine-cytokine receptor interaction (Indegree=5) and oxidative phosphorylation (Indegree=4) were downstream pathways (Fig. 2).

Gene signal network and gene co-expression network construction for common DEGs. Based on the same gene symbol, a total of 328 common DEGs were obtained, such as adenylate cyclase 9 (Degree=18), ectonucleoside triphosphate diphosphohydrolase 5 (Degree=18) and protein kinase, cAMP-dependent, catalytic, β (Degree=14).

The gene co-expression network was constructed with 161 nodes and 211 edges (Fig. 4). In this network, the hub nodes with a higher degree were ATP-binding cassette, sub-family D, member 3 (ABCD3, Degree=19), carnitine palmitoyltransferase 2 (CPT2, Degree=17) and amylo-α-1, 6-glucosidase, 4-α-glucanotransferase (AGL., Degree=15). Moreover, this network showed that ABCD3 has a positive relationship with various DEGs, including ankyrin 3, adenylate cyclase 9 and acyl-coA dehydrogenase, and short/branched chain.

Table I. Top 5 GO terms of differentially expressed genes.

| GO ID   | GO Name                              | Diff gene counts in GO | Enrichment Score | P-value | FDR    |
|---------|--------------------------------------|------------------------|------------------|---------|--------|
| GO:0044281 | Small molecule metabolic process           | 129                   | 3.905874858     | 5.67E-40 | 1.57E-36 |
| GO:0051301 | Cell division                           | 56                    | 7.834124719     | 7.24E-33 | 1.00E-29 |
| GO:0000278 | Mitotic cell cycle                      | 59                    | 6.707641713     | 9.84E-31 | 9.07E-28 |
| GO:0000236 | Mitotic prometaphase                    | 28                    | 11.55533996     | 7.75E-22 | 5.36E-19 |
| GO:0000087 | M phase of mitotic cell cycle           | 35                    | 7.295034066     | 7.28E-20 | 4.02E-17 |

GO, Gene Ontology; FDR, false discovery rate.
Table II. The top 5 pathways of differently expressed genes.

| Pathway ID | Pathway name                        | Diff gene counts in pathway | Enrichment score | P-value    | FDR        |
|------------|-------------------------------------|----------------------------|------------------|------------|------------|
| 1,100      | Metabolic pathways                 | 95                         | 3.297358904      | 6.37E-24   | 1.57E-21   |
| 4,110      | Cell cycle                          | 23                         | 7.654743119      | 6.66E-14   | 8.23E-12   |
| 4,914      | Progesterone-mediated oocyte maturation | 17                                         | 8.157835437      | 5.00E-11   | 3.56E-09   |
| 4,114      | Oocyte meiosis                      | 19                         | 7.00099953       | 5.76E-11   | 3.56E-09   |
| 5,200      | Pathways in cancer                  | 29                         | 3.659946318      | 5.29E-09   | 2.61E-07   |

FDR, false discovery rate.

Figure 1. Cluster of the screened differentially expressed genes. The red profiles are statistically significant, but the blue profiles have no statistical significance.
Discussion

Over 75% of colon cancer occurs in individuals with little or no genetic risk (15). However, various gene expressions and their related functions and pathways were altered with the increasing of grade of the tumor. These genes provided the biomarkers for colon cancer of each stage and also suggest effective treatment targets. In the present study, several significant DEGs were screened and resulted in participation in the pathogenesis of colon cancer, including ABCD3, CPT2, AGL and (Junctional adhesion molecule B) JAM2.

ABCD3 encoded a protein of a member of ATP-binding cassette (ABC) transporters, which is involved in peroxisomal import of fatty acids or fatty acyl-CoAs in the organelle (16). Previous findings showed by targeting the expression of the multidrug resistance (MDR)-related ABC transporters, that reversal of MDR could be realized and MDR in cancer could be solved (17). Various ABC transporters such as Ped3p, were confirmed to provide substrates for fatty acid β-oxidation (18). In addition, there was evidence that colorectal cancer cells could be induced to apoptosis by the inhibition of fatty acid oxidation (19,20). Similar to the results in this study, ABCD3 was found to participate in ABC transporters, transmembrane transport, fatty acid β-oxidation and ATP catabolic process. In addition, the results in this study have shown that ABCD3 belong to profile 5 in series test of cluster. The expression of this gene was significantly decreased in stage 1 and 2 of colon cancer samples. Thus, we inferred that ABCD3 may be used as a biomarker for the early detection of colon cancer.

Moreover, CPT2 was a key DEG in profile 5, which was involved in small molecule metabolic process, cellular lipid metabolic process, carnitine shuttle, fatty acid degradation and peroxisome proliferator-activated receptor (PPAR) signaling pathway in the present study. As known, this gene mainly existed...
in mitochondrion and nucleus and was closely associated with mitochondrial long-chain fatty-acid oxidation disorders (21). In tumor-bearing rat models, Seelaender et al found that the expression of mitochondrial inner-membrane CPT2 was markedly decreased (22). Additionally, previous bioinformatic findings showed that the pathway of fatty acid metabolism involved various altered expressed genes and was confirmed to have a close link with colorectal carcinogenesis (23). Furthermore, Wang and Dubois found that the PPAR signaling pathway could promote the emergence of chronic colonic inflammation and colitis-related tumors (24). Of note, the results in the present study showed that the PPAR signaling pathway was the upstream pathway of fatty acid degradation. The abovementioned information shows that CPT2 is a potentially critical biomarker for colon cancer by participating in the fatty acid metabolic process and PPAR signaling pathway.

Another critical DEG, AGL was found to have a positive relationship with CPT2 in the present study. AGL encodes the glycogen debrancher enzyme, which is involved in glycogen degradation (25). In bladder tumor, AGL was confirmed to participate in the induction of hyaluronic acid synthesis and further regulate tumor growth (26). To the best of our knowledge, there is currently no correlative literature showing the relevance between AGL and colon. However, AGL was significantly altered and involved in the carbohydrate metabolic process, response to glucocorticoid stimulus and glucose metabolic process. In 1984, Holroyde et al showed that diverse abnormalities of the carbohydrate metabolic process often occurred in cancer cachexia, such as colorectal cancer (27). In addition, aerobic glycolysis was ensured to be a metabolic adaptation that promotes the proliferation of colorectal cancer cells (28). Based on the abovementioned information, we
hypothesized that AGL was a potential biomarker for the diagnosis of colon cancer.

JAM2 encodes a type I membrane protein that functions as an adhesive ligand for interacting with the number of immune cell types (29). The findings of a previous study revealed that JAM2 played an important role in motility and its adhesion process of colon cancer cells (30). In addition, Royse et al found that JAM2 altered the expression in early- and late-stage colon tumors, and is also closely associated with PTEN, which is a tumor suppressor (31). In the present study, JAM2 was gathered into tight junction, cell adhesion molecules and in blood coagulation. Consistent with previous studies, the indexes of blood coagulation were closely associated with the progression of colon cancer (32). Moreover, various blood coagulation inhibitors were found to be beneficial for colon cancer patients (33). Thus, JAM2 may be involved in the pathogenesis of colon cancer by participating in cell adhesion molecules and blood coagulation.

In summary, the identified DEGs including ABCD3, CPT2, AGL and JAM2 constitute potential biomarkers for the diagnosis of colon cancer by participating in various functions and pathways. The validation of these biomarkers identified is to be conducted in future studies.

Competing interests

Authors declare they have no competing interests.

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