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Comparative analysis of gene expression profiles of gastric cardia adenocarcinoma and gastric non-cardia adenocarcinoma

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Abstract. In the present study, gene expression profiles were analyzed to identify the molecular mechanisms underlying gastric cardia adenocarcinoma (GCA) and gastric non-cardia adenocarcinoma (GNCA). A gene expression dataset (accession number GSE29272) was downloaded from Gene Expression Omnibus, and consisted of 62 GCA samples and 62 normal controls, as well as 72 GNCA samples and 72 normal controls. The two groups of differentially-expressed genes (DEGs) were compared to obtain common and unique DEGs. A differential analysis was performed using the Linear Models for Microarray Data package in R. Functional enrichment analysis was conducted for the DEGs using the Database for Annotation, Visualization and Integrated Discovery. Protein-protein interaction (PPI) networks were constructed for the DEGs with information from the Search Tool for the Retrieval of Interacting Genes. Subnetworks were extracted from the whole network with Cytoscape. Compared with the control, 284 and 268 genes were differentially-expressed in GCA and GNCA, respectively, of which 194 DEGs were common between GCA and GNCA. Common DEGs [e.g., claudin (CLDN)7, CLDN4 and CLDN3] were associated with cell adhesion and digestion. GCA-unique DEGs [e.g., MAD1 mitotic arrest deficient like 1, cyclin (CCN)B1, CCNB2 and CCNE1] were associated with the cell cycle and the regulation of cell proliferation, while GNCA-unique DEGs (e.g., GATA binding protein 6 and hyaluronoglucosaminidase 1) were implicated in cell death. A PPI network with 141 nodes and 446 edges were obtained, from which two subnetworks were extracted. Genes [e.g., fibronectin 1, collagen type I α2 chain (COL1A2) and COL1A1] from the two subnetworks were implicated in extracellular matrix organization. These common DEGs could advance our understanding of the etiology of gastric cancer, while the unique DEGs in GCA and GNCA could better define the properties of specific cancers and provide potential biomarkers for diagnosis, prognosis or therapy.

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Key words: gastric cardia adenocarcinoma, gastric non-cardia adenocarcinoma, gene expression data, differentially-expressed genes, functional enrichment analysis, protein-protein interaction network

Introduction

Gastric cancer is the third leading cause of cancer-associated mortality (1). The most common cause of gastric cancer is infection by the bacteria *Helicobacter pylori*, which accounts for ~60% of cases (1,2). Smoking also increases the risk significantly. The prognosis of stomach cancer is generally poor due to the fact that the tumor has often metastasized by the time of diagnosis (3), which makes it necessary to identify biomarkers for an early diagnosis.

Stomach cancers are overwhelmingly adenocarcinomas. Gastric adenocarcinomas are a heterogeneous group of tumors. The cardia lies between the end of the esophagus and the body of the stomach, and is a small macroscopically indistinct zone that lies immediately distal to the gastroesophageal junction. Gastric cardia adenocarcinoma (GCA) and esophageal squamous cell carcinoma (ESCC) share certain etiological risk factors. Abnet *et al* reported a shared susceptibility locus in PLCE1 at 10q23 for GCA and ESCC (4). GCA may have a distinct etiology. Substantially higher TP53 mutation rates have been detected in cases with GCA than gastric non-cardia adenocarcinoma (GNCA) (5). Kamangar *et al* indicated that *H. pylori* is a strong risk factor for non-cardia gastric cancer, but that it is inversely associated with the risk of gastric cardia cancer (6). Kim *et al* found differences in the clinicopathology and protein expression in cardia carcinoma and non-cardia carcinoma (7).

Although a number of genetic alterations have been identified in gastric cancer, including those in cadherin 1 (CDH1) (8,9), β-catenin (10), CDH17 (11) and Met (12), no study has distinguished these alterations by anatomical subsite. A number of previous gene expression profiling studies have also ignored the differences in diverse anatomical subsite (11,13,14), such as in GCA and GNCA. Therefore, a comparative analysis of the gene expression profiles of GCA and GNCA would provide more accurate and valuable information on GCA.

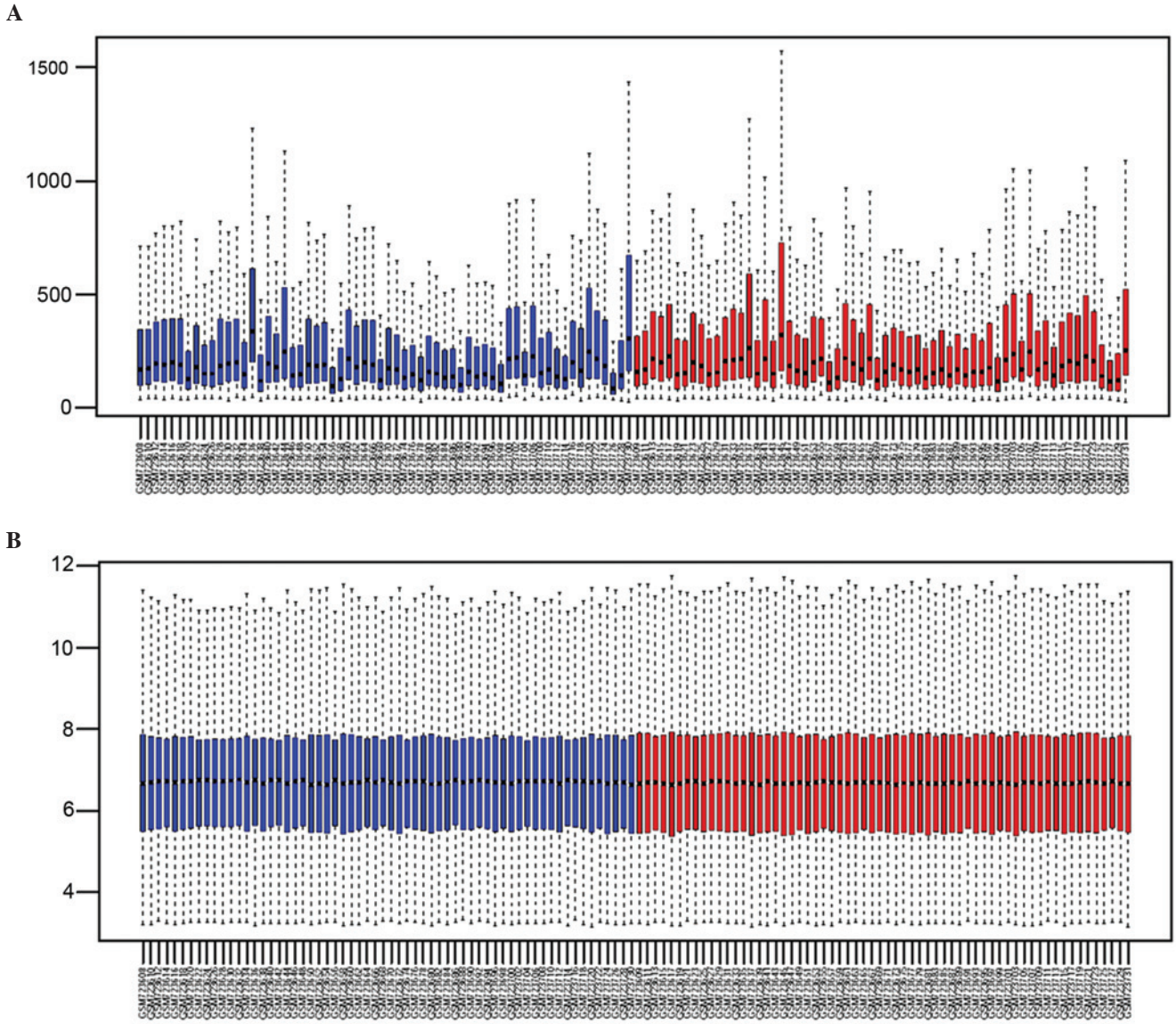

Figure 1. Box plots of gene expression data of GCA and normal control (A) prior to and (B) after normalization. GCA samples are in blue, while normal controls are in red. Black lines in the boxes represent medians. GCA, gastric cardia adenocarcinoma.

Based upon the gene expression data from Wang *et al* (15), the present study adopted functional enrichment analysis and protein-protein interaction (PPI) network analysis to obtain a greater understanding of the common pathogenesis of GCA and GNCA, as well as the unique molecular mechanisms underlying GCA and GNCA, which could facilitate the development of targeted strategies for early detection, prognosis, and therapy.

Materials and methods

Gene expression data. A gene expression dataset (access number GSE29272) (15) was downloaded from Gene Expression Omnibus (http://www.ncbi.nlm.nih.gov/geo/), and consisted of 62 GCA samples and 62 normal controls, as well as 72 GNCA samples and 72 normal controls. Gene expression levels were measured using the Affymetrix Human Genome U133A Array (Affymetrix Inc., Santa Clara, CA, USA).

Pre-treatment and differential analysis. Raw data were treated with the Robust Multi-array Analysis method from the Affy package (16). Values of probes mapping to a same Entrez gene ID were averaged as a final expression level for the specific gene. A total of 22,283 probes and 12,495 genes were obtained.

Differential analysis was performed with the Linear Models for Microarray Data (17) in R to identify DEGs in GCA and GNCA. The cut-offs were set as |log (fold change)|>1 and a P-value of <0.01. Overlapping DEGs of GCA and GNCA, as well as unique DEGs, were further selected out.

Functional enrichment analysis. Gene Ontology (GO; http://www.geneontology.org/) enrichment analysis and Kyoto Encyclopedia of Genes and Genomes (http://www.genome.jp/kegg) pathway enrichment analysis were applied on the overlapping DEGs and unique DEGs using the Database for Annotation, Visualization and Integration Discovery (http://david.abcc.ncifcrf.gov/) online tool (18). P<0.05 was set as the threshold.

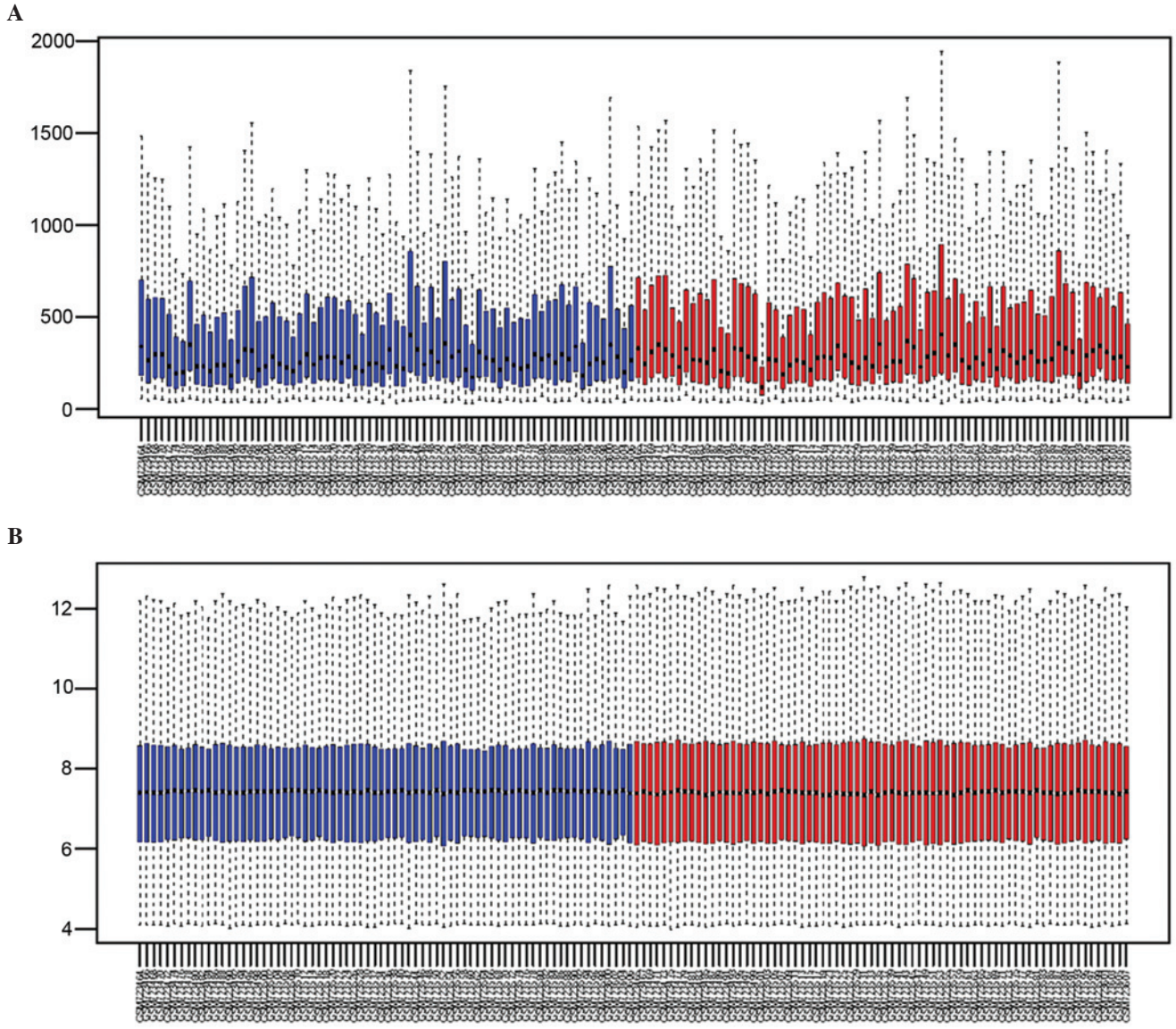

Figure 2. Box plots of gene expression data of GNCA and normal control (A) prior to and (B) after normalization. GNCA samples are in blue, while normal controls are in red. Black lines in the boxes represent medians. GNCA, gastric non-cardia adenocarcinoma.

Construction of the PPI network. A PPI network was constructed for the overlapping DEGs using information from the Search Tool for the Retrieval of Interacting Genes (19). Interactions with a score of >0.4 were retained and then visualized by Cytoscape (20). The proteins in the network serve as the 'nodes', and each pairwise protein interaction is represented by an undirected link and the degree of a node corresponds to the number of interactions of a protein. Degree was calculated for each node. Hub genes were then selected out according to the degree.

Subnetworks were also identified by Cytoscape (20) and its plugin MCODE (21), on which functional enrichment analysis was then applied.

Results

Differentially-expressed genes (DEGs). Gene expression data of GCA and GNCA prior to and after normalization are shown in Figs. 1 and 2. A good performance of normalization was achieved.

A total of 284 DEGs, 151 upregulated and 133 downregulated, were identified in GCA, while 268 DEGs, 126 upregulated and 142 downregulated, were revealed in GNCA. A total of 194 DEGs, 90 upregulated and 104 downregulated, were common between GCA and GNCA (Fig. 3).

Functional enrichment analysis result. Functional enrichment analysis was performed for the overlapping DEGs and unique DEGs. As shown in Table I, upregulated overlapping DEGs were involved in cell adhesion, the response to wounding and the regulation of cell proliferation. Extracellular matrix (ECM)-receptor interaction and focal adhesion were significantly over-represented. As for downregulated overlapping DEGs, digestion, oxidation reduction and the homeostatic process were enriched. The DEGs were associated with the metabolism of xenobiotics by cytochrome P450 and nitrogen metabolism.

GCA-unique DEGs were closely associated with the cell cycle and the regulation of cell proliferation (Table II).

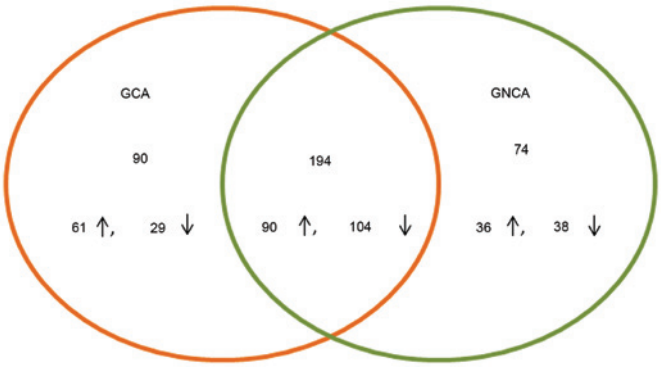

Figure 3. Venn diagram describing the number of differentially-expressed genes in gastric cardia adenocarcinoma (GCA) and gastric non-cardia adenocarcinoma (GNCA). Arrows represent regulation.

Pathways such as the cell cycle, the p53 signaling pathway and the Toll-like receptor signaling pathway were enriched (Table II).

GNCA-unique DEGs were implicated in the regulation of angiogenesis, cell death and small GTPase-mediated signal transduction (Table III). Pathways such as focal adhesion and vascular smooth muscle contraction were enriched (Table III).

PPI network. A PPI network was constructed for the overlapping DEGs (Fig. 4), including 141 nodes and 446 edges.

Subnetwork 1 consisting of nodes with a degree >10 were extracted from the whole network (Fig. 5). The subnetwork contained 14 nodes and 75 edges. Three hub genes with a degree >25 were identified: Fibronectin 1 (FN1), collagen type I α2 (COL1A2) and COL1A1. The degrees of connectivity were 38, 28 and 26, respectively. The 3 hub genes interacted with each other and their neighboring nodes were selected as subnetwork 2, which included 45 nodes and 245 edges (Fig. 5).

Functional enrichment analysis was performed for the genes in the two subnetworks (Tables IV and V). GO enrichment analysis showed that the genes in subnetwork 1 were associated with collagen fibril organization, ECM organization and cell adhesion (Table IV). ECM-receptor interaction and focal adhesion were significantly enriched (Table IV). As for genes from subnetwork 2, they were involved in ECM organization, cell adhesion and extracellular structure organization (Table V). ECM-receptor interaction, focal adhesion, and complement and coagulation cascades were enriched (Table V).

Discussion

A comparative analysis of gene expression data of GCA and GNCA was performed in the present study. A total of 284 DEGs were identified in GCA, while 268 DEGs were revealed in GNCA. As many as 194 DEGs were shared by GCA and GNCA, while 90 DEGs were unique in GCA.

Upregulated common DEGs were involved in cell adhesion and the regulation of cell proliferation. Several members of the claudin family were revealed, including claudin 7 (CLDN7), CLDN4 and CLDN3. CLDN7 expression is an early event in gastric tumorigenesis (22). Zavala-Zendejas *et al* also reported that the overexpression of CLDN7 in the human gastric adenocarcinoma AGS cell line increased its invasiveness, migration and proliferation rate (23). CLDN4 and CLDN3 may also play roles in the pathogenesis of gastric cancer. Cadherin 11 (CDH11) and CDH17 were also found to be upregulated in GCA and GNCA in the present study. CDH17 is reported as a prognostic marker in early-stage gastric cancer (11). Zhang *et al* blocked the proliferation and migration of gastric cancer via targeting CDH17 with an artificial microRNA (24), suggesting that CDH17 is a potential target for the control of gastric cancer progression. In the present study, downregulated common DEGs were associated with digestion and metabolism, suggesting that the function of the stomach was impaired by the cancer. Several enzymes were included in the affected list, such as progastricsin, calpain 9 and aldo-keto reductase family 1 member C2. Mucin 6 (MUC6) and MUC5AC, playing essential roles in epithelial cytoprotection from acids and proteases, were also downregulated.

In the present study, a PPI network, including 141 nodes and 446 edges, was constructed for the common DEGs, from which two subnetworks were disclosed. Genes from the two subnetworks were associated with cell adhesion and ECM organization. The ECM provides a microenvironment for cell proliferation, cell adhesion and cell motion, and thus plays a critical role in cancer development (25) and metastasis (26). FN1, COL1A2 and COL1A1 were the top 3 hub genes in the whole network. FN1 is involved in cell adhesion and migration processes such as metastasis. David *et al* found that fibronectin expression is significantly associated with the expanding growth pattern of the gastric cancer (27). Yang *et al* found that Twist regulates cell motility and invasion in gastric cancer cell lines through N-cadherin and fibronectin production (28).

GCA-unique DEGs were implicated in the cell cycle and the regulation of cell proliferation in the present study. MAD1 mitotic arrest deficient-like 1 (MAD1L1) is a component of the mitotic spindle-assembly checkpoint that prevents the onset of anaphase until all chromosomes are properly aligned at the metaphase plate, and it may play a role in cell cycle control and tumor suppression. Coe *et al* report that MAD1L1 is the most frequent copy number gain in small cell lung cancer cell lines (29). Guo *et al* further suggested that genetic variants in MAD1L1 and MAD2L1 confer a susceptibility to lung cancer, which may result from reduced spindle checkpoint function due to the attenuated function of MAD1L1 and/or MAD2L1 (30). We supposed that MAD1L1 had a similar role in the pathogenesis of GCA. Three members of the cyclin family, CCNB1, CCNB2 and CCNE1, were also found to be upregulated in GCA. The B-type cyclins, CCNB1 and CCNB2, associate with p34cdc2 and are essential components of the cell cycle regulatory machinery. Begnami *et al* found that the expression of cyclin B1 is associated with regional lymph node metastasis and a poor prognosis in gastric cancer (31).

GNCA-unique DEGs were found to be associated with cell death in the present study. Abnormalities in cell death are closely associated with tumorigenesis. The GATA family

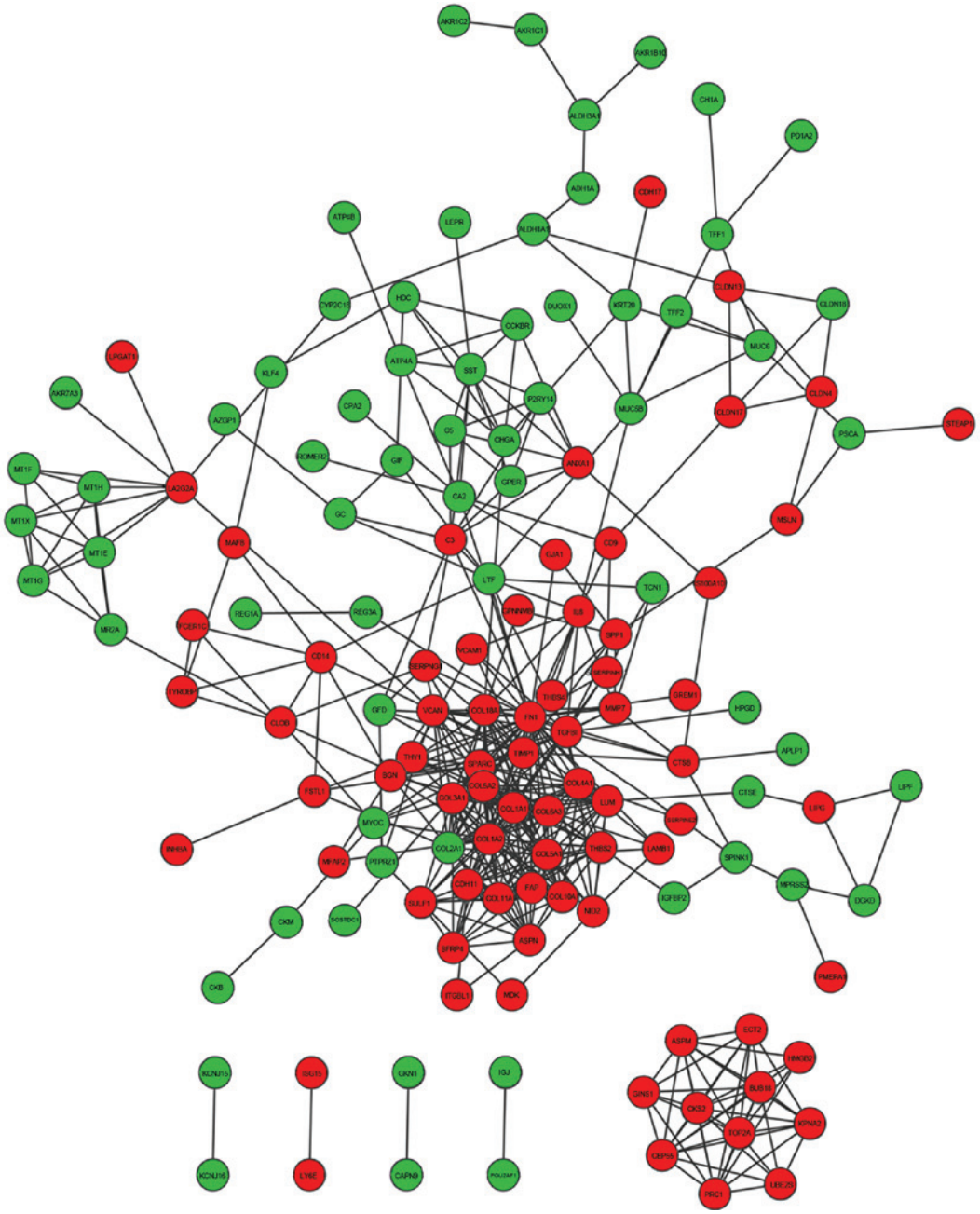

Figure 4. Protein-protein interaction network for the common differentially-expressed genes. Upregulated genes are in red, while downregulated genes are in green.

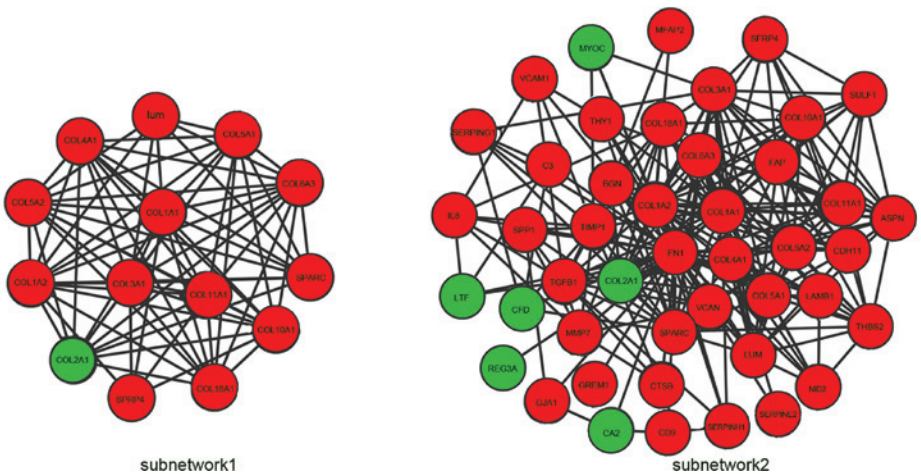

Figure 5. Two subnetworks extracted from the whole protein-protein interaction network.

Table I. Functional enrichment analysis for common differentially-expressed genes.

Group	Category	Term	Count	P-value
Upregulated genes	GOTERM_BP_FAT	GO:0007155, cell adhesion	25	3.75×10^{-13}
	GOTERM_BP_FAT	GO:0022610, biological adhesion	25	3.86×10^{-13}
	GOTERM_BP_FAT	GO:0001501, skeletal system development	12	1.76×10^{-6}
	GOTERM_BP_FAT	GO:0009611, response to wounding	14	8.15×10^{-6}
	GOTERM_BP_FAT	GO:0042127, regulation of cell proliferation	13	1.54×10^{-3}
	GOTERM_CC_FAT	GO:0044421, extracellular region part	40	1.83×10^{-23}
	GOTERM_CC_FAT	GO:0005576, extracellular region	48	6.77×10^{-19}
	GOTERM_CC_FAT	GO:0005578, proteinaceous ECM	23	1.45×10^{-17}
	GOTERM_CC_FAT	GO:0031012, ECM	23	7.16×10^{-17}
	GOTERM_CC_FAT	GO:0005615, extracellular space	24	1.16×10^{-11}
	GOTERM_MF_FAT	GO:0005201, ECM structural constituent	12	1.03×10^{-12}
	GOTERM_MF_FAT	GO:0005539, glycosaminoglycan binding	12	2.27×10^{-10}
	GOTERM_MF_FAT	GO:0001871, pattern binding	12	6.34×10^{-10}
	GOTERM_MF_FAT	GO:0005198, structural molecule activity	18	3.61×10^{-8}
	GOTERM_MF_FAT	GO:0005509, calcium ion binding	14	1.28×10^{-3}
	KEGG_PATHWAY	hsa04512: ECM-receptor interaction	13	5.02×10^{-13}
	KEGG_PATHWAY	hsa04510: Focal adhesion	13	1.60×10^{-8}
	KEGG_PATHWAY	hsa04670: Leukocyte transendothelial migration	5	1.21×10^{-2}
	KEGG_PATHWAY	hsa04514: Cell adhesion molecules	5	1.77×10^{-2}
Downregulated genes	GOTERM_BP_FAT	GO:0007586, digestion	14	1.39×10^{-14}
	GOTERM_BP_FAT	GO:0055114, oxidation reduction	15	4.63×10^{-5}
	GOTERM_BP_FAT	GO:0010035, response to inorganic substance	8	3.23×10^{-4}
	GOTERM_BP_FAT	GO:0010033, response to organic substance	11	1.59×10^{-2}
	GOTERM_BP_FAT	GO:0042592, homeostatic process	11	2.05×10^{-2}
	GOTERM_CC_FAT	GO:0005576, extracellular region	36	1.54×10^{-8}
	GOTERM_CC_FAT	GO:0005615, extracellular space	16	4.01×10^{-5}
	GOTERM_CC_FAT	GO:0044421, extracellular region part	19	4.81×10^{-5}
	GOTERM_CC_FAT	GO:0045177, apical part of cell	6	6.78×10^{-3}
	GOTERM_CC_FAT	GO:0016324, apical plasma membrane	5	1.19×10^{-2}
	GOTERM_MF_FAT	GO:0008289, lipid binding	12	2.71×10^{-4}
	GOTERM_MF_FAT	GO:0048037, cofactor binding	8	1.70×10^{-3}
	GOTERM_MF_FAT	GO:0004175, endopeptidase activity	8	1.52×10^{-2}
	GOTERM_MF_FAT	GO:0070011, peptidase activity, acting on L-amino acid peptides	9	3.64×10^{-4}
	GOTERM_MF_FAT	GO:0008233, peptidase activity	9	4.53×10^{-2}
	KEGG_PATHWAY	hsa00980: Metabolism of xenobiotics by cytochrome P450	5	6.98×10^{-4}
	KEGG_PATHWAY	hsa00982: Drug metabolism	4	8.56×10^{-3}
	KEGG_PATHWAY	hsa00910: Nitrogen metabolism	3	1.06×10^{-2}

GO, Gene Ontology; BP, biological process; CC, cellular component; MF, molecular function; KEGG, Kyoto Encyclopedia of Genes and Genomes; ECM, extracellular matrix.

of transcription factors participates in gastrointestinal development. GATA binding protein 6 (GATA6) is shown to be expressed in gastric cancer; it activates the expression of gastroprotective trefoil genes, trefoil factor 1 (TFF1) and TFF2 (32). Haveri *et al* further reported that GATA6 expression is altered in neoplastic human gastrointestinal mucosa (33), suggesting that it may play a role in tumor progression. Hyaluronoglucosaminidase 1 (HYAL1) is a lysosomal hyaluronidase. Hyaluronan is believed to be involved in cell proliferation, migration and differentiation. HYAL1 is suggested to exhibit prognostic potential in prostate cancer (34). The study by Lokeshwar *et al* showed that, depending on the concentration,

Table II. Functional enrichment analysis for unique differentially-expressed genes in gastric cardia adenocarcinoma.

Category	Term	Count	P-value
GOTERM_BP_FAT	GO:0022403, cell cycle phase	14	1.66×10^{-7}
GOTERM_BP_FAT	GO:0000279, M phase	12	8.96×10^{-7}
GOTERM_BP_FAT	GO:0022402, cell cycle process	14	5.45×10^{-6}
GOTERM_BP_FAT	GO:0007049, cell cycle	16	7.81×10^{-6}
GOTERM_BP_FAT	GO:0042127, regulation of cell proliferation	14	1.72×10^{-4}
GOTERM_CC_FAT	GO:0044421, extracellular region part	18	2.12×10^{-5}
GOTERM_CC_FAT	GO:0005829, cytosol	18	1.10×10^{-3}
GOTERM_CC_FAT	GO:0005576, extracellular region	23	1.42×10^{-3}
GOTERM_CC_FAT	GO:0043228, non-membrane-bounded organelle	24	1.58×10^{-2}
GOTERM_CC_FAT	GO:0043232, intracellular non-membrane-bounded organelle	24	1.58×10^{-2}
GOTERM_MF_FAT	GO:0008009, chemokine activity	4	1.43×10^{-3}
GOTERM_MF_FAT	GO:0046983, protein dimerization activity	9	4.49×10^{-3}
GOTERM_MF_FAT	GO:0042802, identical protein binding	9	1.18×10^{-2}
GOTERM_MF_FAT	GO:0042803, protein homodimerization activity	6	2.28×10^{-2}
GOTERM_MF_FAT	GO:0008134, transcription factor binding	7	3.76×10^{-2}
KEGG_PATHWAY	hsa04110: Cell cycle	11	8.65×10^{-8}
KEGG_PATHWAY	hsa04115: p53 signaling pathway	6	2.98×10^{-4}
KEGG_PATHWAY	hsa04114: Oocyte meiosis	7	3.66×10^{-4}
KEGG_PATHWAY	hsa04914: Progesterone-mediated oocyte maturation	6	8.83×10^{-4}
KEGG_PATHWAY	hsa04620: Toll-like receptor signaling pathway	5	1.17×10^{-2}

GO, Gene Ontology; BP, biological process; CC, cellular component; MF, molecular function; KEGG, Kyoto Encyclopedia of Genes and Genomes.

Table III. Functional enrichment analysis for unique differentially-expressed genes in gastric non-cardia adenocarcinoma.

Category	Term	Count	P-value
GOTERM_BP_FAT	GO:0045765, regulation of angiogenesis	3	2.99×10^{-2}
GOTERM_BP_FAT	GO:0008219, cell death	8	3.32×10^{-2}
GOTERM_BP_FAT	GO:0016265, death	8	3.43×10^{-2}
GOTERM_BP_FAT	GO:0006937, regulation of muscle contraction	3	3.81×10^{-2}
GOTERM_BP_FAT	GO:0007264, small GTPase mediated signal transduction	5	4.16×10^{-2}
GOTERM_CC_FAT	GO:0015629, actin cytoskeleton	8	2.52×10^{-4}
GOTERM_CC_FAT	GO:0005576, extracellular region	21	5.64×10^{-4}
GOTERM_CC_FAT	GO:0005856, cytoskeleton	16	1.43×10^{-3}
GOTERM_CC_FAT	GO:0044421, extracellular region part	11	1.32×10^{-2}
GOTERM_CC_FAT	GO:0044449, contractile fiber part	4	1.60×10^{-2}
GOTERM_MF_FAT	GO:0008092, cytoskeletal protein binding	9	9.27×10^{-4}
GOTERM_MF_FAT	GO:0003779, actin binding	7	2.04×10^{-3}
GOTERM_MF_FAT	GO:0005198, structural molecule activity	9	3.92×10^{-3}
GOTERM_MF_FAT	GO:0005509, calcium ion binding	10	1.13×10^{-2}
GOTERM_MF_FAT	GO:0005525, GTP binding	6	1.75×10^{-2}
KEGG_PATHWAY	hsa04510: Focal adhesion	6	3.64×10^{-3}
KEGG_PATHWAY	hsa04270: Vascular smooth muscle contraction	4	2.07×10^{-2}

GO, Gene Ontology; BP, biological process; CC, cellular component; MF, molecular function; KEGG, Kyoto Encyclopedia of Genes and Genomes; GTP, guanosine triphosphate.

HYAL1 functions as a tumor promoter or as a suppressor in prostate cancer (35). We speculated that it may exert a similar function in the progression of GNCA.

Overall, in the present study, a number of common DEGs were identified in GCA and GNCA, which could advance our understanding of the etiology of gastric cancer. Furthermore,

Table IV. Functional enrichment analysis result for genes from subnetwork 1.

Category	Term	Count	P-value
GOTERM_BP_FAT	GO:0030199, collagen fibril organization	8	7.46×10^{-17}
GOTERM_BP_FAT	GO:0030198, ECM organization	9	4.46×10^{-15}
GOTERM_BP_FAT	GO:0043062, extracellular structure organization	9	1.78×10^{-13}
GOTERM_BP_FAT	GO:0001501, skeletal system development	8	2.72×10^{-9}
GOTERM_BP_FAT	GO:0007155, cell adhesion	6	2.14×10^{-4}
GOTERM_CC_FAT	GO:0044420, ECM part	13	2.50×10^{-24}
GOTERM_CC_FAT	GO:0005578, proteinaceous ECM	13	6.27×10^{-19}
GOTERM_CC_FAT	GO:0031012, ECM	13	1.57×10^{-18}
GOTERM_CC_FAT	GO:0044421, extracellular region part	14	2.24×10^{-15}
GOTERM_CC_FAT	GO:0005576, extracellular region	14	3.48×10^{-11}
GOTERM_MF_FAT	GO:0005201, ECM structural constituent	10	3.45×10^{-18}
GOTERM_MF_FAT	GO:0048407, platelet-derived growth factor binding	6	1.19×10^{-13}
GOTERM_MF_FAT	GO:0005198, structural molecule activity	10	2.88×10^{-10}
GOTERM_MF_FAT	GO:0019838, growth factor binding	6	2.38×10^{-8}
GOTERM_MF_FAT	GO:0046332, SMAD binding	3	7.92×10^{-4}
KEGG_PATHWAY	hsa04512: ECM-receptor interaction	9	3.52×10^{-14}
KEGG_PATHWAY	hsa04510: Focal adhesion	9	4.53×10^{-11}

GO, Gene Ontology; BP, biological process; CC, cellular component; MF, molecular function; KEGG, Kyoto Encyclopedia of Genes and Genomes; ECM, extracellular matrix.

Table V. Functional enrichment analysis result for genes from subnetwork 2.

Category	Term	Count	P-value
GOTERM_BP_FAT	GO:0030198, ECM organization	11	3.24×10^{-13}
GOTERM_BP_FAT	GO:0007155, cell adhesion	18	3.27×10^{-12}
GOTERM_BP_FAT	GO:0022610, biological adhesion	18	3.35×10^{-12}
GOTERM_BP_FAT	GO:0043062, extracellular structure organization	11	3.04×10^{-11}
GOTERM_BP_FAT	GO:0009611, response to wounding	12	2.48×10^{-7}
GOTERM_CC_FAT	GO:0044421, extracellular region part	36	8.96×10^{-32}
GOTERM_CC_FAT	GO:0005576, extracellular region	39	5.65×10^{-25}
GOTERM_CC_FAT	GO:0005578, proteinaceous ECM	23	3.57×10^{-24}
GOTERM_CC_FAT	GO:0031012, ECM	23	1.89×10^{-23}
GOTERM_CC_FAT	GO:0005615, extracellular space	21	1.53×10^{-14}
GOTERM_MF_FAT	GO:0005198, structural molecule activity	15	2.71×10^{-9}
GOTERM_MF_FAT	GO:0005201, ECM structural constituent	13	1.53×10^{-17}
GOTERM_MF_FAT	GO:0048407, platelet-derived growth factor binding	6	9.76×10^{-11}
GOTERM_MF_FAT	GO:0030246, carbohydrate binding	7	6.90×10^{-4}
GOTERM_MF_FAT	GO:0005509, calcium ion binding	8	2.08×10^{-2}
KEGG_PATHWAY	hsa04512: ECM-receptor interaction	13	7.92×10^{-16}
KEGG_PATHWAY	hsa04510: Focal adhesion	13	3.48×10^{-11}
KEGG_PATHWAY	hsa04610: Complement and coagulation cascades	3	4.45×10^{-2}

GO, Gene Ontology; BP, biological process; CC, cellular component; MF, molecular function; KEGG, Kyoto Encyclopedia of Genes and Genomes; ECM, extracellular matrix.

DEGs unique to GCA and to GNCA were identified, which supplemented our knowledge on the pathogenetic mechanisms involved and provided potential biomarkers for the diagnosis, prognosis or treatment of the disease.

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