Identification of differentially expressed genes between primary lung cancer and lymph node metastasis via bioinformatic analysis

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Abstract. Lung cancer (LC), with its high morbidity and mortality rates, is one of the most widespread and malignant neoplasms. Mediastinal lymph node metastasis (MLNM) severely affects postoperative survival of patients with LC. Additionally, the molecular mechanisms of LC with MLNM (MM LC) remain not well understood. To identify the key biomarkers in its carcinogenesis and development, the datasets GSE23822 and GSE13213 were obtained from the Gene Expression Omnibus database. The differentially expressed genes (DEGs) were identified, and the Database for Annotation, Visualization and Integrated Discovery was used to perform functional annotations of DEGs. Search Tool for the Retrieval of Interacting Genes and Cytoscape were utilized to obtain the protein‑protein interaction (PPI) network, and to analyze the most significant module. Subsequently, a Kaplan‑Meier plotter was used to analyze overall survival (OS). Additionally, one co-expression network of the hub genes was obtained from cBioPortal. A total of 308 DEGs were identified in the two microarray datasets, which were mainly enriched during cellular processes, including the Gene Ontology terms ‘cell’, ‘catalytic activity’, ‘molecular function regulator’, ‘signal transducer activity’ and ‘binding’. The PPI network was composed of 315 edges and 167 nodes. Its significant module had 11 hub genes, and high expression of actin β, MYC, arginine vasopressin, vesicle associated membrane protein 2 and integrin subunit β1, and low expression of NOTCH1, synaptojanin 2 and intersectin 2 were significantly associated with poor OS. In summary, hub genes and DEGs presented in the present study may help identify underlying targets for diagnostic and therapeutic methods for MM LC.

Introduction

Lung cancer (LC) is one of the most malignant neoplasms, and increases in its morbidity and mortality rates have made it a main cause of human mortality. In the last 50 years, research has revealed a marked increase in the incidence and mortality rates of LC (1). The incidence and mortality rates of LC in men ranked first among all malignant tumor groups, and the incidence in women ranked second most common worldwide in 2018 (2). The onset of LC is insidious and it has a poor prognosis. Mediastinal lymph node metastasis (MLNM) during treatment is one of the most important factors affecting the postoperative survival of patients (3).

The MLNM process of LC includes the growth of a primary tumor, angiogenesis and exfoliation of tumor cells, which invade the tissue matrix, and make cancer cells survive in the blood circulation and amass into tiny tumor thrombi (4). Previous studies in China have reported that the 5-year survival rate of patients with LC without MLNM could be >60%, but was only 15‑42% with MLNM (5,6). Numerous previous studies (7‑11) have demonstrated that the pathophysiological process of the development of LC with MLNM (MM LC) is associated with the mutation and abnormal expression of genes, including C‑X‑C motif chemokine receptor 4 (CXCR4), vascular endothelial growth factor-C (VEGF-C), vascular endothelial growth factor receptor-3, VEGFR-3, vascular endothelial growth factor receptor-3, VAMEP2, vesicle associated membrane protein 2

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Abbreviations: ACTB, actin β; ADAM, ADAM metallopeptidase domain; AVP, arginine vasopressin; BiNGO, Biological Networks Gene Oncology tool; BP, biological processes; CC, cellular components; CXCR4, C‑X‑C motif chemokine receptor 4; DEGs, differentially expressed genes; ERBB2, Erb‑b2 receptor tyrosine kinase 2; GEO, Gene Expression Omnibus; GEPIA, Gene Expression Profiling Interactive Analysis; GO, Gene Ontology; ITGB1, integrin subunit β1; ITSN2, intersectin 2; KEGG, Kyoto Encyclopedia of Genes and Genomes; LC, lung cancer; MCODE, Molecular Complex Detection; MF, molecular function; MLNM, mediastinal lymph node metastasis; MM LC, lung cancer with mediastinal lymph node metastasis; non‑MM LC, lung cancer samples without mediastinal lymph node metastasis; OS, overall survival; PET, positron emission tomography; PPI, protein‑protein interaction; RAB5B, RAB5B, member RAS oncogene family; SYNJ2, synaptojanin 2; VEGFR‑3, vascular endothelial growth factor receptor-3; VAMP2, vesicle associated membrane protein 2

Key words: LC, PPI, MLNM, DEGs, bioinformatics analysis
VEGFR-3 and VEGF-C (7), high expression levels of ADAM family members (8), downregulation of VEGF-D expression (10), and high expression levels of VEGF-C (11) may be involved in the MLNM of LC. These genes may be used as prognostic factors or targets for gene therapy. However, in individualized applications, the diagnostic or therapeutic value of a single gene remains uncertain. Due to the lack of timely detection, dynamic monitoring and effective control of the occurrence of MLNM, the poor survival rate of MM LC still cannot be effectively controlled. Therefore, novel signaling pathways and molecular targets should be investigated and screened to develop novel diagnostic and therapeutic methods.

Microarray technology allows simultaneous analysis of alterations in the expression levels of multiple genes to obtain gene sets that can predict MLNM in LC with high accuracy. Clinical application of these gene sets is expected to maximize the survival period and narrow the surgical range (whether lymph node resection is required) for the benefit of patients. Previously, a number of studies (12-17) have performed bioinformatic analyses to investigate differentially expressed genes (DEGs) in various types of cancer, as well as their roles in different pathways, molecular functions and biological processes. Kikuchi et al (12) used microarray technology to obtain a set of genes which could predict MLNM and drug sensitivity. Li et al (13) applied the same method to identify the significant genes in the carcinogenesis and progression of hepatocellular carcinoma. Furthermore, multiple previous studies have also used microarray technology to obtain gene expression profiles to predict lymph node metastasis of other malignant tumors, including esophageal cancer (14), oral squamous cell carcinoma (15,16) and cervical cancer (17).

Therefore, the purpose of the present study was to download and analyze two expression profiling datasets of human samples from the Gene Expression Omnibus (GEO) database, and to identify DEGs between LC samples without MLNM (non-MM LC) and MM LC samples. Subsequently, Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway and Gene Ontology (GO) analysis were carried out. Protein-protein interaction (PPI) network analysis and co-expression network analyses were used to demonstrate the molecular pathogenesis underlying carcinogenesis and development of MM LC. Overall, 11 hub genes and 308 DEGs, which may be potential molecular targets or biomarkers for MM LC, were identified.

Materials and methods

Access to public data. The GEO (http://www.ncbi.nlm.nih.gov/geo) is an open platform for storing genetic data (18). In total, two expression profiling datasets [GSE23822 (19) (GPL6947 platform) and GSE13213 (20) (GPL6480 platform)] were obtained from GEO. The GSE23822 dataset contained four non-MM LC samples and four MM LC samples. Similarly, GSE13213 consisted of 22 non-MM LC samples and 22 MM LC samples.

Identification of DEGs using GEO2R. GEO2R (https://www.ncbi.nlm.nih.gov/geo/geo2r/) is an interactive online tool for the identification of DEGs from GEO series (21). GEO2R was used to identify DEGs between MM LC and non-MM LC tissue samples. If one probe set did not have the homologous gene, or if one gene had numerous probe sets, the data were removed. The rules of statistical significance were that P≤0.01 and fold change ≥1.5.

Functional annotation of DEGs by KEGG and GO analysis. Database for Annotation, Visualization and Integrated Discovery (DAVID; version 6.8, https://david.ncifcrf.gov/home.jsp), is an online analysis tool suite with the functions of integrated discovery and annotation (22). GO (http://geneontology.org) is widely used in bioinformatics, and covers three aspects of biology: biological process (BP), cellular component (CC) and molecular function (MF) (23). KEGG (https://www.kegg.jp) is one of the most commonly used biological information databases in the world (24). OmicShare (http://www.omicshare.com/tools), an open data analysis platform, was used to perform GO analysis (25). To analyze the biological pathway information of DEGs, the DAVID online tool was implemented. P<0.05 was considered to indicate a statistically significant difference.

Construction of the PPI network and identification of the significant module. Search Tool for the Retrieval of Interacting Genes (http://string.embl.de/), an online open tool, was applied to construct the PPI network of DEGs, and Cytoscape was used to present the network (26). Cytoscape (version 3.6.1) is a free visualization software (27). A confidence score >0.4 was considered as the criterion of judgment. Subsequently, the Molecular Complex Detection (28) (MCODE; version 1.5.1; a plug-in of Cytoscape), was used to identify the most important module of the network map. The criteria for MCODE analysis were as follows: i) Degree cut-off=2; ii) MCODE scores ≥5; iii) max depth=100; iv) node score cut-off=0.2; and v) k-score=2 (29). Subsequently, following the KEGG and GO analysis using the DAVID database and OmicShare website, functional annotation of genes for these modules was performed.

Analysis and identification of hub genes. The degrees were set (degrees ≥10), and the hub genes were excavated. A co-expression network of these hub genes was obtained from cBioPortal (http://www.cbioportal.org) (30). Furthermore, the Biological Networks Gene Oncology tool (BiNGO; version 3.0.3) was used to analyze and visualize the CCs, BPs and MFs of the hub genes (31). The clustering analysis of hub genes was performed using OmicShare (https://www.omicshare.com/tools/Home/Soft/getsoft/type/index) (25). The mean value of amount of gene expression was defined as the cut-off value for the high or low expression level. Additionally, Kaplan-Meier Plotter (http://kmplot.com/analysis/index.php?p=background), an online analysis tool, was utilized to perform survival analysis for the hub genes. The Kaplan Meier plotter (32) is capable of assessing the effect of 54,000 genes on survival in 21 different types of cancer. The largest datasets include breast (n=6,234), ovarian (n=2,190), lung (n=3,452) and gastric (n=1,440) cancer. The miRNA subsystems include 11k samples from 20 different cancer types. Primary purpose of the tool is a meta-analysis based discovery and validation of survival biomarkers. The P-value was achieved by using a log-rank test. University of California Santa Cruz (UCSC) Xena (https://xena.ucsc.edu/welcome-to-ucsc-xena/) was used to securely analyze and visualize the hub genes in the scope.
of public genomic datasets. The expression profiles of actin β (ACTB) and integrin subunit β1 (ITGB1) were analyzed and visualized using the online database Gene Expression Profiling Interactive Analysis (GEPIA; http://gepia.cancer-pku.cn/).

**Results**

**Screening of DEGs in MM LC samples.** Following analysis of the datasets (GSE23822 and GSE13213) with GEO2R, the difference between MM LC and non-MM LC tissues was presented in volcano plots (Fig. 1A and B). The analyses of GSE23822 and GSE13213 identified 1,297 and 4,552 DEGs, respectively (Fig. 1C). The Venn diagram demonstrated that the commonality between the two datasets included 308 DEGs, including the most upregulated genes [Erb-b2 receptor tyrosine kinase 2 (ERBB2) and ITGB1] and the most down-regulated genes [ACTB, RAB5B, member RAS oncogene family (RAB5B) and intersectin 2 (ITSN2)] (data not shown).

**Functional annotation of DEGs by KEGG and GO analyses.** The results of the GO analysis demonstrated that variations in the BP were primarily enriched in the GO terms ‘cellular process’, ‘metabolic process’, ‘response to stimulus’, ‘biological regulation’, ‘signaling’ and ‘localization’, ‘single-organism process’, ‘developmental process’, ‘cellular component organization or biogenesis’, and so on. Alterations in CC were mainly enriched in the GO terms ‘cell’, ‘membrane’, ‘extracellular region’ and ‘organelle part’. The variations in MF were enriched in the GO terms ‘binding’, ‘catalytic activity’, ‘molecular transducer activity’, ‘signal transducer activity’ and ‘molecular function regulator’ (Fig. 2). The enriched GO terms were ‘generation of precursor metabolites and energy’, ‘signal transduction’, ‘regulation of biological processes’, ‘regulation of cellular processes’, ‘cellular response to stimulus’, ‘cellular component organization or biogenesis’, ‘cellular component organization’, ‘anatomical structure morphogenesis’, and so on (Fig. 7A). The KEGG pathway analysis revealed that genes in the significant module were mainly enriched in ‘vasopressin-regulated water reabsorption’, ‘proteoglycans in cancer’, ‘thyroid hormone signaling pathway’, ‘phagosome’, ‘focal adhesion’, ‘microRNAs in cancer’, ‘bladder cancer’, ‘pathogenic *Escherichia coli* infection’, ‘endometrial cancer’ and ‘shigellosis’ (Fig. 7B).

**Construction of the PPI network and identification of the significant module.** Construction of the PPI network and identification of the significant module were performed, and there were 315 edges and 167 nodes in the PPI network (Fig. 4). Furthermore, there were 26 edges and 11 nodes in the significant module (Fig. 5). Using DAVID, KEGG and GO analyses of DEGs involved in the significant module were performed. The results demonstrated that genes in the significant module were enriched in the following categories: ‘Cellular process’, ‘localization’, ‘signaling’, ‘cell’, ‘organelle’, ‘extracellular region’, ‘membrane’, ‘binding’, ‘molecular function regulator’ and ‘molecular transducer activity’ (Fig. 6). The enriched GO terms were ‘generation of precursor metabolites and energy’, ‘signal transduction’, ‘regulation of biological processes’, ‘regulation of cellular processes’, ‘cellular response to stimulus’, ‘cellular component organization or biogenesis’, ‘cellular component organization’, ‘anatomical structure morphogenesis’, and so on (Fig. 7A). The KEGG pathway analysis revealed that genes in the significant module were mainly enriched in ‘vasopressin-regulated water reabsorption’, ‘proteoglycans in cancer’, ‘thyroid hormone signaling pathway’, ‘phagosome’, ‘focal adhesion’, ‘microRNAs in cancer’, ‘bladder cancer’, ‘pathogenic *Escherichia coli* infection’, ‘endometrial cancer’ and ‘shigellosis’ (Fig. 7B).

**Hub gene selection and analysis.** Degrees ≥10 was considered as the criterion of judgment. A total of 11 genes were identified as hub genes using Cytoscape: ITGB1, MYC, ERBB2, NOTCH1, ACTB, RAB5B, arginine vasopressin (AVP), synaptotagmin 2 (SYN2), ITSN2, SH3 domain containing GRB2 like 2 endophilin A1 and vesicle associated membrane...

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Figure 1. Identification of differently expressed genes between non-MM lung cancer and MM lung cancer tissues. (A) Volcano plot of the difference between non-MM lung cancer and MM lung cancer tissues following analysis of the GSE23822 dataset with GEO2R. (B) Volcano plot presenting the difference between non-MM lung cancer and MM lung cancer tissues following analysis of the GSE13213 dataset with GEO2R. (C) Venn diagram demonstrating that 308 genes were contained in the GSE23822 and GSE13213 datasets simultaneously. MM lung cancer, lung cancer with mediastinal lymph node metastasis; non-MM lung cancer, lung cancer without mediastinal lymph node metastasis.
Figure 2. GO enrichment analysis of differentially expressed genes in the form of a secondary frequency diagram. GO, Gene Ontology.

Figure 3. GO and KEGG enrichment analysis of differently expressed genes. (A) GO enrichment analysis of DEGs in the form of an enrichment factor diagram. (B) Kyoto Encyclopedia of Genes and Genomes pathway analysis of DEGs. DEGs, differentially expressed genes; ErbB, Erb-b2 receptor tyrosine kinase; GO, Gene Ontology; Jak, Janus kinase.
protein 2 (VAMP2; Table I). A co-expression network of these significant genes was obtained using cBioPortal (Fig. 8). The BP, CC and MF analyses by BiNGO for these genes supported the results of the GO analysis (Figs. S1-S3). The results of the BiNGO analysis demonstrated that variations in the BP were also mainly enriched for the ‘cellular process’ term (Fig. S1). Changes in CC were also enriched in cell, membrane (‘plasma membrane’ and ‘plasma membrane part’) and organelle terms (Fig. S2). Additionally, the variations in MF were enriched in binding (‘kinesin binding’, ‘nitric-oxide synthase binding’ and ‘Hsp90 protein binding’), ‘molecular transducer activity’ (Fig. S3).

Hierarchical clustering revealed that the hub genes could differentiate the MM LC samples from the non-MM LC samples (Fig. 9). Subsequently, a Kaplan-Meier plotter was used to perform overall survival (OS) analysis (Figs. 10 and 11). The samples for OS analysis, derived from the Kaplan-Meier plotter, were different from those used in the analysis of DEGs. Patients with LC with genomic alterations in high expression of ITGB1 (Fig. 10A), high expression of MYC (Fig. 10B), low expression of NOTCH1 (Fig. 10D), high expression of ACTB (Fig. 10E), high expression of AVP (Fig. 11B), low expression of SYNJ2 (Fig. 11C), low expression of ITSN2 (Fig. 11D) and high expression of VAMP2, exhibited poorer OS. However, via the GEPIA, the expression of ACTB (Fig. 10F), ERBB2 (Fig. 10C) RAB5B (Fig. 11A) and SH3GL2 (Fig. 11E), were not associated with OS. In the UCSC Xena analysis, hierarchical clustering revealed that these hub genes could differentiate the patients with LC from the normal patients (Fig. 12A). Among the hub genes, ACTB and ITGB1 had the highest score of 6.415, suggesting that they may serve important roles in the occurrence or development of MM LC. Using the database of the Kaplan-Meier plotter, the present study identified that high expression of ACTB was associated with poor OS in patients with LE (P<0.001). Additionally, high expression of ITGB1 was associated with worse OS (P=0.024).
The expression profiles of ACTB and ITGB1 in human tissues were visualized using GEPIA. The present study revealed that ACTB and ITGB1 exhibited lower expression levels in lung squamous cell carcinoma compared with the matched normal samples, but no statistically significant difference was identified (P>0.05; Fig. 12B and C).

Discussion

LC causes the highest cancer-associated mortality rate in China and the majority of countries worldwide. The most common pathological type of LC is non-small-cell LC, which accounts for 80-85% of LC cases (33). Optimization...
of LC treatment strategies depends on accurate pathological staging and International Association for the Study of Lung Cancer pathological TNM staging (34). In clinical practice, patients with stages 0, I, II and IIIa may benefit from surgery. For patients with MLNM, neoadjuvant chemotherapy could prolong their postoperative survival (35). For patients without surgical indications, the definite diagnosis of mediastinal lymph node staging could effectively reduce the irradiation area of the radiation target area, which may reduce the incidence of radioactive lung injury. Therefore, if MLNM can clearly defined prior to treatment, it is of great significance to develop appropriate treatment schemes to improve the prognosis of patients.

Currently, there are numerous clinical diagnostic methods for MLNM of LC, including computed tomography (CT), positron emission tomography (PET) and PET-CT. CT is the most widely used diagnostic method for MLNM. A previous study demonstrated that imaging methods continue to have limitations in the evaluation of MLNM, and some patients cannot be clearly diagnosed or are misdiagnosed (36). Diagnosis of MLNM using CT is mainly based on the size of lymph nodes. The larger the

Figure 7. GO and KEGG enrichment analysis of hub genes. (A) GO enrichment analyses of hub genes in the form of an enrichment factor diagram. (B) Kyoto Encyclopedia of Genes and Genomes pathway analysis of hub genes. GO, Gene Ontology.

Figure 8. Hub genes and their co-expressed genes were analyzed using cBioPortal. Nodes with a bold black outline represent hub genes. Nodes with a thin black outline represent co-expressed genes. The blue arrows represent ‘Controls state change of’. The green arrows represent ‘Controls expression of’. The grey arrows represent ‘In complex with’.
<table>
<thead>
<tr>
<th>No.</th>
<th>Gene symbol</th>
<th>Full name</th>
<th>Function</th>
<th>(Refs.)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>ITGB1</td>
<td>Integrin subunit β1</td>
<td>Diseases associated with ITGB1 include gallbladder cancer and breast cancer. Among its related pathways are ERK signaling and focal adhesion. Gene Ontology annotations related to this gene include protein heterodimerization activity and signaling receptor binding.</td>
<td>(49)</td>
</tr>
<tr>
<td>2</td>
<td>MYC</td>
<td>V‑myc avian myelocytomatosis viral oncogene homolog</td>
<td>Activates the transcription of growth-related genes. Binds to the VEGFA promoter, promoting VEGFA production and subsequent sprouting angiogenesis.</td>
<td>(52)</td>
</tr>
<tr>
<td>3</td>
<td>ERBB2</td>
<td>Erb-b2 receptor tyrosine kinase 2</td>
<td>Regulates outgrowth and stabilization of peripheral microtubules. Involved in the transcription of ribosomal RNA genes by RNA Pol I and enhances protein synthesis and cell growth.</td>
<td>(53)</td>
</tr>
<tr>
<td>4</td>
<td>NOTCH1</td>
<td>Notch 1</td>
<td>Affects the implementation of differentiation, proliferation and apoptotic programs. Involved in angiogenesis; negatively regulates endothelial cell proliferation and migration and angiogenic sprouting.</td>
<td>(54)</td>
</tr>
<tr>
<td>5</td>
<td>ACTB</td>
<td>Actin β</td>
<td>Among its related pathways are ERK signaling and cytoskeleton remodeling regulation of actin cytoskeleton by q GTPases.</td>
<td>(55)</td>
</tr>
<tr>
<td>6</td>
<td>RAB5B</td>
<td>RAB5B, member RAS oncogene family</td>
<td>Protein transport. Probably involved in vesicular traffic.</td>
<td>(56)</td>
</tr>
<tr>
<td>7</td>
<td>AVP</td>
<td>Arginine vasopressin</td>
<td>Vasopressin has a direct antidiuretic action on the kidney, it also causes vasoconstriction of the peripheral vessels.</td>
<td>(57)</td>
</tr>
<tr>
<td>8</td>
<td>SYNJ2</td>
<td>Synaptotagin 2</td>
<td>Inositol 5-phosphatase which may be involved in distinct membrane trafficking and signal transduction pathways.</td>
<td>(58)</td>
</tr>
<tr>
<td>9</td>
<td>ITSN2</td>
<td>Intersectin 2</td>
<td>May mediate the inhibitory effect of Rac1 on endocytosis.</td>
<td>(59)</td>
</tr>
<tr>
<td>10</td>
<td>SH3GL2</td>
<td>SH3 domain containing GRB2 like 2, endophilin A1</td>
<td>May regulate the formation of CCPs. Seems to be involved in CCPs maturation including invagination or budding.</td>
<td>(60)</td>
</tr>
<tr>
<td>11</td>
<td>VAMP2</td>
<td>Vesicle associated membrane protein 2</td>
<td>Involved in the targeting and/or fusion of transport vesicles to their target membrane. Modulates the gating characteristics of the delayed rectifier voltage-dependent potassium channel potassium voltage-gated channel subfamily B member 1.</td>
<td>(61)</td>
</tr>
</tbody>
</table>

CCPs, clathrin-coated vesicles; VEGFA, vascular endothelial growth factor A.
lymph nodes, the higher the metastasis rate. The average size of the short diameter of normal lymph nodes depends on the region in which they are located. McLoud et al (37) evaluated 443 lymph nodes in 143 patients using CT. The sensitivity to lymph nodes of various regions was 17-78%, and the specificity was 72-94%. The previous study demonstrated that there were some differences in the sensitivity and specificity of diagnosis using CT to evaluate mediastinal lymph nodes in different subgroups (31). In addition, PET is superior to CT in the diagnosis of MLNM, since PET considers not only lymph node size, but also lymph node metabolism information. A meta-analysis by Toloza et al (38) of PET examination of 1,045 patients in 18 studies manifested that PET was more accurate than CT, and the total sensitivity and specificity were 0.84 (95% CI, 0.78-0.89) and 0.89 (95% CI, 0.83-0.93), respectively. However, the diagnostic method of PET has relatively high rates of false negatives and false positives (39). Furthermore, PET-CT effectively combines the technical advantages of CT and PET, which could significantly improve the accuracy of preoperative diagnosis of MLNM in LC. However, several previous studies have reported that PET-CT has high specificity and low sensitivity (40,41). The sensitivity of PET-CT in preoperative assessment of MLNM of lung adenocarcinoma is too low, and further surgical staging is required for patients with LC without MLNM detected by PET-CT.

To overcome the limitations of imaging evaluation of MLNM, previous studies have attempted to identify molecular biomarkers of MM LC (7-10). During the past decades, bioinformatics technology has been generally used to screen
potential genetic targets of diseases, which assisted the authentication of DEGs and underlying pathways associated with the occurrence and recurrence of diseases.

Following analysis of the two microarray datasets in the present study, DEGs between non-MM LC and MM LC were identified. A total of 308 DEGs were contained in the two datasets simultaneously. From the KEGG and GO analyses, the interactions of the DEGs were explored. The DEGs were mainly enriched in the GO terms ‘cellular process’, ‘signaling’, ‘cell’, ‘organelle’, ‘binding’, ‘molecular transducer activity’

Figure 10. Overall survival analysis of five hub genes (A) Overall survival analysis of ITGB1, (B) MYC, (C) ERBB2, (D) NOTCH1, (E) ACTB, using a Kaplan-Meier plotter online platform. (F) Overall survival analysis of ACTB using GEPIA. P<0.05 was considered to indicate a statistically significant difference. ACTB, actinβ; ERBB2, Erb-b2 receptor tyrosine kinase 2; HR, hazard ratio; ITGB1, integrin subunit β1; TPM, transcripts per million.
and ‘molecular function regulator’. Among the hub genes, ACTB and ITGB1 exhibited the highest score of 6.415 via the MCODE analysis, suggesting that they may serve important roles in the occurrence or development of MM LC.

Figure 11. Overall survival analysis of the other six hub genes using a Kaplan-Meier plotter online platform. Overall survival analysis of (A) RAB5B, (B) AVP, (C) SYNJ2, (D) ITSN2, (E) SH3GL2 and (F) VAMP2. P<0.05 was considered to indicate a statistically significant difference. AVP, arginine vasopressin; HR, hazard ratio; ITSN2, intersectin 2; RAB5B, RAB5B, member RAS oncogene family; SH3GL2, SH3 domain containing GRB2 like 2, endophilin A1; SYNJ2, synaptojanin 2; VAMP2, vesicle associated membrane protein 2.

Actin β, encoded by the ACTB gene, is widely present in non-muscle cells in the form of a ball or fiber, and participates in the construction of the cytoskeleton and cell movement. As a downstream regulatory protein, actin β has the function
of maintaining normal cell migration, growth, differentiation and signal transduction (42). Therefore, it may also be involved in the occurrence mechanism of vascular remodeling. Numerous previous studies (43-45) have demonstrated a close association between ACTB and the occurrence of tumors. Lim et al (43) reported that the mutation of ACTB may cause pilocytic astrocytoma in their clinical experience. Furthermore, the fusions of ACTB and glioma-associated oncogene homolog 1 (GLI1) were regarded as a specific genetic abnormality, which could result in a distinctive type of actin-positive, perivascular myoid tumors, known as 'pericytoma with the t (7;12) translocation' (44). Furthermore, Castro et al (45) reported that the extremely unusual translocation t (7;12) may lead to the gene fusion of ACTB and GLI1, which may induce an infrequent gastric tumor derived from the pyloric wall of the stomach. The results of the present study revealed that the expression levels of ACTB in MM LC were downregulated; therefore, the production of actin β was reduced, which may lead to abnormal growth, differentiation and exfoliation of LC cells. The detached cancer cells first enter the mediastinal lymph nodes to form a cancer embolus. According to the Kaplan-Meier survival analysis, patients with low expression levels of ACTB had a good prognosis (P<0.05). However, the expression levels of ACTB had no significant effects on the prognosis based on the survival analysis of GEPIA (P>0.05). The influence of ACTB expression on the prognosis was undefined; therefore, more data are required to verify the suggested effect.

ITGB1 is a member of the integrin family of proteins. Integrin family proteins are involved in the regulation of cell adhesion and recognition processes, including hemostasis, embryogenesis, immune response, tissue repair and tumor cell metastasis (46). Yan et al (47) reported that the expression levels of ITGB1 were associated with OS and metastasis.

Figure 12. Expression analysis of hub genes. (A) Hierarchical clustering of hub genes using University of California Santa Cruz Xena. Samples next to the brown bar are normal samples and the samples next to the blue bar are lung cancer samples. Upregulation of genes is marked in red. Downregulation of genes is marked in blue. (B) Expression profile of actin β in human tumor and normal tissues as obtained using GEPIA. (C) Expression profile of integrin subunit β1 in human tissues as obtained using GEPIA. GEPIA, Gene Expression Profiling Interactive Analysis; LUSC, lung squamous cell carcinoma.
in patients with aggressive breast cancer. Wang et al (48) reported that linc-ITGB1 promoted the invasion and migration of gallbladder cancer cells by activating epithelial-mesenchymal transition, and knockout of ITGB1 significantly inhibited the metastasis and invasion of gallbladder cancer cells. Klahan et al (49) knocked out ITGB1 in breast cancer cells and revealed that calcium influx decreased, resulting in a significant decrease in the invasion and metastasis of triple-negative breast cancer cells. Wang et al (50) reported that ITGB1 serves important roles in the occurrence and metastasis of LC. The findings of Qin et al (51) suggested that microRNA-134 suppresses migration and invasion of non-small cell LC by targeting ITGB1. The present study demonstrated that the expression levels of ITGB1 were upregulated in MM LC. According to the OS analysis, patients with high expression levels of ITGB1 had a poor prognosis. The reason for this may be that high ITGB1 expression induces the occurrence of MLNM, which could invade the systemic organs along the lymphatic duct, causing systemic organ failure and a shorter lifespan. Based on the aforementioned results, the alterations in the expression levels of ITGB1 may be a molecular mechanism for stimulating the metastasis and invasion of LC cells to the mediastinal lymph node. However, currently, studies regarding ITGB1 are rare, so more efforts should be made in the future.

There are some limitations of the present study. First, the results of the present study are based on bioinformatics analysis only. Therefore, they require laboratory work to be verified using a large set of samples of patients with LC. Currently, it is difficult to obtain the ethical approval documents and informed consent. In the next stage of research, ethical approval and informed consent will be obtained to perform verification of the results of the present study in humans and animals.

In conclusion, the present study aimed to identify DEGs which may be involved in the occurrence or development of LC. Finally, 308 DEGs and 11 hub genes were identified by comparisons between MM LC and non-MM LC samples, which could be used as diagnostic and therapeutic biomarkers for MM LC. The present study provided novel insight for the diagnosis and treatment of MM LC. The results suggested that data mining and integration could be a promising tool to predict biomarkers of malignant tumors. However, the present study is only a preliminary report, and the number of samples in the present study was limited. Since cancer biomarkers only have meaning if they are integrated with clinical data, further experiments should be conducted to confirm the conclusions of the present study.

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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

NZ performed the experiment, and was a major contributor in writing and submitting the manuscript. SWZ made substantial contributions to the conception and design of the study, as well as the acquisition, analysis and interpretation of the data, and also designed the draft of the research process. NZ was involved in critically revising the manuscript for intellectual content. 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.

References


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