Introduction

Osteosarcoma (OS), which is the primary malignant bone tumor that arises within a bone, mostly originates in the metaphyses of long bones of adolescents and young adults (Bielack et al., 2002). OS included two types: metastatic and non-metastatic OS. All patients who was diagnosed metastatic OS, only 15-20% were treated using conventional chemotherapy regimens and surgical excision of each tumor site (Kaste et al., 1999). Meanwhile, most clinical trials in OS excluded patients with metastatic disease at presentation (Mialou et al., 2005), and the survival rate for patients diagnosed with OS in the last five years remains at 60%-70% (Pezzi et al., 1990). The cure of OS is rare after surgical treatment alone due to a high rate of systemic spread (Link et al., 1986). Therefore, exploring molecular mechanisms of OS progression will facilitate to develop effective therapeutic strategies for it.

In previous studies, the clinical manifestation of cancers such as OS is based on six essential alterations in cell physiology, including self-sufficiency in growth signals, insensitivity to growth inhibitory signals, apoptosis evasion, limitless replicative potential, sustained angiogenesis and tissue invasion (Fuchs and Pritchard, 2002; Charity et al., 2006; Kansara and Thomas, 2007; Luo et al., 2013). And there was a correlation between E-cadherin-regulated cell adhesion and anoikis evasion among human OS cells (MG-63) (Lin et al., 2014). At the same time, chromosomal abnormalities, such as amplifications of chromosomes 6p21, 8q24, and 12q14, as well as loss of heterozygosity of 10q21.1, 10 and 13, were identified as being among the most common genomic alterations in OS (Ta et al., 2009; Smida et al., 2010). Further more, the dysfunction of a variety of tumour associated genes, such as livin, had been proved to inhibit tumor cell apoptosis through multiple ways and be involved in OS pathogenesis (Li et al., 2014). Besides, transcription factor, activator protein 1 complex (AP-1) and myc, growth factors such as transforming growth factor (TGF) and insulin-like growth factor (IGF) played significant roles in OS, and cell adhesion and migration were identified in the pathogenesis of metastatic OS (Broadhead et al., 2011). Therefore, these
evidences suggested that the occurrence and development of metastatic OS are a complex process. Progresses have achieved in understanding the pathogenesis of metastatic OS, however, the molecular mechanism underlying its progression are still unclear.

Microarray analysis has been widely used in screening the possible targets for the treatment of metastatic OS (Diao et al., 2013). With the utilization of cDNA microarrays, the transcriptome profile of two OS cell lines has been detected, and 1098 DEGs were identified including 796 functionally characterized genes (Trougakos et al., 2010). Microarray analysis was also performed to determine histological subtype specific DEGs (Kubista et al., 2011). And the regulatory network, several signal pathways and pivotal genes were obtained in OS (Luo Deng et al., 2013). Therefore, microarray analysis is a good approach to identify key molecular events and pathways involved in metastatic OS.

In our study, microarrays were utilized for identifying the DEGs between metastatic OS samples and non-metastatic OS samples by the Multtest package. The functional enrichment analysis of DEGs was investigated by WebGestalt. Additionally, the protein-protein interaction (PPI) networks of the most significantly expressed genes were constructed by Hitpredict and the pathway enrichment analysis was performed by Kyoto Encyclopaedia of Genes and Genomes (KEGG) automatic annotation server (KAAS). We anticipate that our work could improve the understanding to the underlying molecular mechanisms of metastatic OS and could provide new insights for the diagnosis and treatment of metastatic OS.

Materials and Methods

Derivation of genetic data

The gene expression profile GSE37552 (Flores et al., 2012) was downloaded from the public functional genomics database Gene Expression Omnibus (GEO, http://www.ncbi.nlm.nih.gov/geo/). Total 4 specimens, including two human metastatic OS cell line models and two non-metastatic OS cell line models were available based on the GPL570 [HG-U133_Plus_2] Platform (Affymetrix Human Genome U133 Plus 2.0 Array).

DEGs analysis

The probe-level data were converted into expression measures, and the expression values of all probes in each sample were reduced to a single value by taking the average expression value. Then the missing parts of data were imputed (Troyanskaya et al., 2001), and the complete data were standardized (Fujita et al., 2006). Under the condition of the normal tissue as the control, we applied the multtest package in R language (v.2.13.0) (Smyth, 2005) to identify the DEGs between metastatic OS samples and non-metastatic OS samples. Only the genes, with \( P\)-value<0.05 and \(|\log\text{ fold change (FC)}|>1\), were screened out as DEGs.

Functional enrichment analysis

WebGestalt (Zhang et al., 2005; Duncan et al., 2010), which is a Web-Based Gene Set Analysis Toolkit, was utilized for enriching the functions of the DEGs based on the hypergeometric distribution, with the false discovery rate (FDR) less than 0.05.

Construction and analysis of interaction network

The down- and up-regulated DEGs with maximum expression degree were screened out, and in order to depict the relationship of two genes and their possible interactional objectives, Hitpredict (Patiland Nakamura, 2005; Patil et al., 2011) database was used to obtain the PPI networks, in which the two genes involved (retained the predicted objects with the highest likelihood ratio).

Pathway enrichment analysis

According to the constructed the PPI networks, the pathway enrichment analysis of genes in the PPI networks, Table 1.

Table 1. The top 10 Regulated DEGs in metastatic OS with P-value<0.05

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<th>Gene</th>
<th>Symbol</th>
<th>ID</th>
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<th>P-value</th>
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Figure 1. The PPI Networks of A2M and BCAN. A) The PPI network of A2M and its interactive proteins; B) The PPI network of BCAN and its interactive proteins.
Results

Screening DEGs in metastatic OS

Basing on the microarray analysis, a total of 237 genes were detected to be differentially expressed in metastatic OS samples, including 94 up-regulated genes and 143 down-regulated genes. In the DEGs, A2M (Alpha-2-Macroglobulin) was most significantly expressed in up-regulated genes, and BCAN (brevican) was the most significant down-regulated genes. The top 10 up-regulated DEGs and top 10 down-regulated DEGs were listed in Table 1.

Functional enrichment analysis of the DEGs

To analyze the function of the DEGs in metastatic OS, the DEGs were mapped to the WebGestalt. Table 2 displayed 18 functions of the DEGs, and the most significant function is response to hormone stimulus.

Network constructing

A2M and BCAN were screened out as the most significant genes in the DEGs, and Hitpredict was used to construct the PPI networks of A2M and BCAN. The network of A2M included 15 genes, such as IL1B (Interleukin), LRP1 (low-density lipoprotein receptor-related protein 1) and PDGF (platelet-derived growth factor), while there were 11 proteins in the network of BCAN (brevican), such as matrix metalloproteinases (MMP2) and Fibulin2 (FBLN2).

Pathway enrichment analysis

In order to gain further insights into the changes of biological pathways in metastatic OS, the proteins of the network were analyzed by KAAS software. Consequently, only 12 significant pathways of the proteins involved in the network of A2M were obtained (Table 3), and MAPK (Mitogen-activated protein kinase) signal pathway was the most significant pathway.

Discussion

Due to the low cure rates and lacking of the specific drugs with no toxicity for metastatic OS, exploring the mechanism and the effective prevention strategy of OS is urgent for us. In this study, we analyzed the DEGs between metastatic OS samples and non-metastatic OS samples. Finally, 237 genes were screened out as the DEGs. Based on the DEGs we obtained, the function analysis showed
that DEGs were significantly related to the function of the response to hormone stimulus.

In previous studies, the regulation of hormone was supposed to be a vital function in the progression of cancers, such as prostate cancer (Linja et al., 2001). The etiology of breast cancer is becoming clearer by investigating the molecular alterations in germ line and somatic cell genes, and the interaction of these genes with steroid hormones (MacMahon et al., 1973; Hulkaand Moorman, 2008). Moreover, bisphenol A (BPA) is an environmental estrogen and its exposure may interact with the -22 G/C polymorphism of the LOX gene, thereby increasing the risk of OS (Jia et al., 2013). Therefore, these evidences suggest that the response to hormone stimulus may play a vital role in metastatic OS, but the mechanism needs to further study.

Furthermore, we found that A2M was the most significantly expressed in up-regulated genes, and it was also identified in the previous research of OS (LuoDeng et al., 2013). In general, A2M is a high-molecular weight homotetrameric glycoprotein and functions as a physiological guardian (Rehman et al., 2013). Many researches focus on its function in the Alzheimer’s disease and depression (Blennow et al., 2000; Fujita et al., 2003), and few are in cancer even OS. Consequently, in order to articulate the roles of A2M in metastatic OS, we performed PPI network and identified its interactive proteins, for instance, IL1B, LRP1 and PDGF. IL1B encodes the proinflammatory cytokine IL-1β with multiple biological effects (Lee et al., 2003), and represents the potential effects in the gastric cancer (Kulnambetova et al., 2014). Very recent study also confirms that the genetic polymorphisms of IL1B are strongly associated with OS risk (He et al., 2014). LRP1 is a ubiquitously expressed endocytic receptor belonging to the LDL-receptor family (Herzand Strickland, 2001). LRP-1 can promote cancer cell invasion via supporting ERK and inhibiting JNK signaling pathways (Langlois et al., 2010), and has been identified as a molecular signaling partner for platelet-derived growth factor receptor (PDGFR) (Boucherand Gotthard, 2004). Moreover, PDGFR is considered as a therapeutic target and a prognostic marker for imatinib mesylate therapy in OS (Kubo et al., 2008). PDGF released from platelets plays an important role in promoting OS cell growth by activating the PDGFR-Akt signaling axis (Takagi et al., 2014). Hence, these genes may process important functions in metastatic OS.

In addition to the interactive regulation of the genes, several significantly pathways correlated with OS were also found. MAPK signal pathway, the most significant one, plays a crucial role in cancer progression including angiogenesis, proliferation, apoptosis and metastasis (Tingting et al., 2010). It also may be involved in OS by activating cyclin D1 (Hu et al., 2001), and its activation was closed related to the therapeutic strategy in OS (Yang et al., 2008). Additionally, the pharmacological inhibition of the MAPK pathway could enhance the antitumoral effect of mammalian target of rapamycin (mTORC1) inhibition by rapamycin in cancer cells (Carracedo et al., 2008). Inhibition of mTORC1 and mTORC2 by the combination of sorafenib and everolimus contribute to anti-tumor activity in OS preclinical models (Pignochino et al., 2013). Meanwhile, focal adhesion and pathways in cancer were included in these pathways. Taking focal adhesion as example, focal adhesion kinase signaling plays a pivotal role in anti-tumor effects of Yangzheng Xiaoji in human OS (Jiang et al., 2013), and inhibition of focal adhesion kinase induces apoptosis in OS SAOS-2 cells (Wang et al., 2014). Therefore, these evidences suggest that MAPK signal pathway and focal adhesion are more likely to be the crucial mechanisms involved in metastatic OS.

In consequence, our studies analyze the DEGs in metastatic OS tissues compared to non-metastatic OS controls and identify the functions of the DEGs by a computational bioinformatics approach. Response to hormone stimulus may process an important function in metastatic OS. Meanwhile, A2M and its interactive proteins, such as IL1B, LRP1 and PDGF may play a vital role in metastatic OS and be considered as potential targets for the treatment of it. Besides, MAPK signal pathway, focal adhesion and other pathways enriched by proteins in the network may be crucial mechanisms involved in metastatic OS. Our research may provide a new strategy in the medical therapy of metastatic OS. However, no experimental validations and less sample size are limitations in the present study, and further experiments are still necessary for confirming our conclusion.

References


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