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Short Communication

Biomarkers for Osteosarcoma: Acquisition and Constraints from Genomics and Proteomics

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ABSTARCT

Osteosarcomas are among the most prevalent cancer bone tumors, and the characterization of useful cancer cell biomarkers and target proteins is needed to anticipate the diagnostic prognosis of treatment and response to therapy as well as to establish novel therapeutic approaches. Gene transnational and overexpression investigations, also known as Genomics and Proteomics, can provide crucial insights into tumor biology which can be obtained by other techniques. Imaging and biopsy are now used to diagnose bone tumors, necessitating the development of less intrusive methods for accurate diagnosis. Recent genomics and proteomics investigations have revealed a number of intriguing Deoxyribo Nucleic Acid (DNA) and protein biomarkers with strong prognostic, diagnostic, and/or predictive abilities for various forms of bone cancers. The possible biomarkers for the more prevalent type of Osteosarcomas bone cancers that were discovered in the investigations were reviewed in this short communication.

Keywords: Neurobiology; Pain; Clinical research; Immunology; Medicine; Bone research

INTRODUCTION

There are currently no diagnostic biomarkers for osteosarcoma. Osteosarcoma (formed from osteoblastic cells), Ewing sarcoma (produced from round bone marrow cells), and chondrosarcoma are the most commonly diagnosed malignant bone tumours, sometimes known as "sarcomas" (derived from cartilage tumor). Soft tissues, such as fat, muscle, nerves, and blood vessels, can also form tumours. Soft tissue sarcomas include rhabdomyosarcomas, neurofibrosarcomas, and angiosarcomas, but lipoblastoma and neurofibroma are benign soft tissue tumours. To reduce mortality and increase limb salvage procedures, biomarkers for early disease detection are desperately needed [1]. Diagnostic, prognostic, and predictive biomarkers are in high demand in oncology research work to the compelling need to improve patients' clinical outcomes [2]. Genomic and proteomic technologies are currently the two most extensively used biomarker finding techniques. Early discovery of recurrent r metastatic disease might also induce an initial treatment decision and action, thereby improving the patient's prognosis [3]. According to prior study, the higher amount of serum alkaline phosphatase generated by osteoplastic activity in the tumors could be employed as a marker. However, the enzyme has been found to be elevated in patients with liver disorders, making it inappropriate for use as a bone tumours marker [4]. Furthermore, this marker may be more useful for tracking the evolution of bone tumours than for diagnosing cancer.

The employing of High-throughput screening methods, such as array-based comparative genomic hybridization analysis and cDNA microarray technology, enable for the discovery of genes crucial for tumor diagnosis and clinical characteristics by analyzing millions of DNA and mRNA sequences. Sarcomas are mesenchyme tumours that are malignant. Mesenchyme tissue is a group of non-epithelial bodily structures that includes the reproductive, glial, hematopoietic, and lymphoid tissues. Lip sarcoma is one of the most frequent soft tissue sarcomas in adults, and it is one of the most difficult cancers to detect. The majority of reports on lip sarcoma miRNAs profiling have been limited to De Differentiated Lipo Sarcoma (DDLS).

The investigation found more than 40 miRNAs that were deregulated in DDLS but not in normal adipose tissue or Well Differentiated Lipo Sarcoma (WDLS) using deep sequencing of short RNA libraries and hybridization based microarrays. MiR-21 and -26 were found to be elevated, whereas miR-143 and -145 were found to be down regulated. Furthermore, down regulation of BCL2, topoisomerase 2A, Protein Regulator of Cytokinesis 1 (PRC1), and Polo-Like Kinase 1 (PLK1) by repression of miR-143 in DDLS cell lines decreased cell growth and promoted death [5]. A clinical relationship among miRNA deregulation and liposarcoma has recently been discovered in research articles. The frequent amplification of miR-26a-2c in 75 liposarcoma samples using a single SNP array. Not only in WDLS/DDLS, but also in MLS, this miRNA was elevated. Importantly, independent of histological subtype, elevated miR-26a-2 expression was associated with poor patient survival in both kinds of liposarcoma. The Regulator of Chromosomal condensation and BTB domain-containing protein 1 (RCBTB1) was discovered

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to be one of the targets of miR-26a-2, which affects cellular death [6].

DESCRIPTION

Proteomics is the study of proteins on a global level, focusing on their structures and activities. Electrophoresis, mass spectrometric methods, protein labeling, protein arrays, antibody based methodologies, imaging, and bioinformatics technology are all used in proteomics research. 2-DE and 2D-DIGE were the most commonly used proteomics systems in bone tumor biomarker research. Gel free platforms, such as SELDI-TOF MS and LC-MS, have recently gained popularity among proteomics researchers, owing to the low sample volume requirements and the ability to do quantification analysis. Gel-free platforms provide more automation choices and are believed to be less time-consuming than 2-DE platforms.

To discover differentially expressed proteins that could serve as serum biomarkers for OS prognosis, researchers used 2-D-DIGE on proteins generated from serum collected from patients with Osteo Sarcoma (OS) and controls. MALDI-TOF mass spectrometric analysis and database interrogation were used to identify proteins that were differentially expressed [7]. By using two-dimensional difference gel electrophoresis, the proteomic profiles of five pairs of cell lines (normal *vs.* tumoral) were obtained, and 56 distinct protein spots were discovered (t test, $p<0.05$). Following that, we used nano-LC-ESI-MS/MS to identify some of these proteins, 16 of which were chosen based on the difference in relative abundance between osteosarcomas and paired normal bones, as well as the genomic evidence supporting their involvement [8]. SELDI-TOF-MS found six differentially expressed protein peaks with high statistical significance. Two of the proteins were down regulated while four were up regulated. In three osteosarcoma cell lines, the expression of 653 genes was altered by more than twofold. The expression of 310 genes increased, whereas the expression of 343 genes dropped. The link test statistics were used to merge the two sets of biomarker candidates, revealing that 13 genes were possible biomarkers for osteosarcoma early diagnosis. Cytochrome C1 (CYC-1) was chosen for further experimental confirmation among these genes [9].

CONCLUSION

There are currently few reliable biomarkers for monitoring tumour progression, which is one of the major issues with soft tissue sarcomas. Several studies have revealed that miRNAs and proteins can be used as new biomarkers for sarcoma monitoring and differential diagnosis using patient derived serum or plasma. In comparison to other cancers, bone and soft tissue sarcomas are very uncommon. The key research priority right now is the development of diagnostic and prognostic modalities, the identification of novel treatment targets, and the understanding of sarcomagenesis mechanisms. As a result, multiple methodologies are now being used to use proteomics technologies to discover tumor specific proteins in sarcoma. There are currently no particular markers that may be utilized to diagnose bone cancers. To reduce mortality and increase limb salvage procedures, biomarkers for early disease detection are desperately needed. Early discovery of recurrent or metastatic disease might also induce an initial treatment decision and action, thereby improving the patient's prognosis.

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