Specificity of the Fusion Genes in Adipocytic Tumors

Introduction

The highest prevalence of lipoma among human tumors makes adipocytic tumors the largest single group of mesenchymal tumors, in which liposarcoma represents the most common single type of soft tissue sarcoma. In a subset of lipoma, a specific t(12;16)(q13:p11), which liposarcoma consists of one well-differentiated (8% of the subtype), nineteen myloid (46% of the subtype), one de-differentiated (25% of the subtype) and one unclassified (6% of the subtype). In this report, the specificity of these fusion genes in adipocytic tumors was not determined. Recently, Ida et al. (2008) described that HMGA2-LPP transcripts were not detectable in twenty cases of well-differentiated liposarcoma. Here, for the first time to the best of our knowledge, we reported that neither HMGA2-LPP nor LPP-HMGA2 fusion transcript was detectable in liposarcoma and lipoma.

Materials and Methods

Tissue samples. Tissues from 98 lipomas and 74 liposarcomas were obtained at the time of surgery with written informed consent and stored at −80 °C.

Reverse transcription-polymerase chain reaction (RT-PCR) and DNA sequencing analysis. Total RNA was extracted with RNeasy Lipid Tissue Mini Kit (QIAGEN, Hilden, Germany), according to the manufacturer’s instructions. After DNase (Invitrogen, Carlsbad, CA, USA) treatment, cDNA was synthesized using the total RNA as template, random hexamers, and Superscript II Reverse Transcriptase (Invitrogen) and 10 pmol of each primer. Denaturation for 2 minutes at 95 °C was followed by 35 cycles of 30 seconds at 95 °C and 60 seconds at 72 °C. For the nested PCR, detecting HMGA2-LPP fusion transcript, while three (4%) with EWS-CHOP fusion transcript, each including ten with both HMGA2-LPP and LPP-HMGA2 transcripts. On the other hand, neither TLS-CHOP nor EWS-CHOP fusion transcript was detectable in lipoma.

Discussion

HMGA2-LPP or LPP-HMGA2 fusion transcripts were linked to benign mesenchymal tumors, such as lipoma, pulmonary chondroid hamartoma, and soft tissue chondroma. However, the specificity of these fusion genes in adipocytic tumors was not revealed. The present study provided the first evidence, as much as we know, showing that neither TLS-CHOP nor EWS-CHOP fusion transcript was detectable in lipoma. The consequent significance should be that the specificity of TLS-CHOP and EWS-CHOP to liposarcoma among adipocytic tumors helps distinguishing liposarcoma from candidate lipoma, once TLS-CHOP or EWS-CHOP transcript was detectable.

Results

Expression of fusion genes in lipoma. Out of 98 lipomas, nineteen (19%) were associated with HMGA2-LPP fusion transcript, while thirteen (13%) with LPP-HMGA2 fusion transcript, each including ten with both HMGA2-LPP and LPP-HMGA2 transcripts. On the other hand, neither TLS-CHOP nor EWS-CHOP fusion transcript was detectable in lipoma.

Expression of fusion genes in liposarcoma. Neither HMGA2-LPP nor LPP-HMGA2 fusion transcript was detectable in liposarcoma. Conversely, out of 74 liposarcomas, twenty-two (30%) were associated with TLS-CHOP fusion transcript, while three (4%) with EWS-CHOP fusion transcript. Histological subtypes of TLS-CHOP detection in liposarcoma consisted of one well-differentiated (8% of the subtype), nineteen myloid (46% of the subtype), one de-differentiated (25% of the subtype) and one unclassified (6% of the subtype). In this study, the specificity of TLS-CHOP and EWS-CHOP fusion transcripts was detectable in one case of well-differentiated liposarcoma, one case of de-differentiated liposarcoma, and one case of unclassified liposarcoma, while one case of de-differentiated liposarcoma revealed EWS-CHOP expression. At this moment, it is unclear whether these four cases should be re-diagnosed as myxoid liposarcoma, or TLS-CHOP or EWS-CHOP fusion transcripts could be detectable in other histological subtypes.

In summary, this report ascertained the specificity of the representative fusion genes in a variety of adipocytic tumors. Taking the advantage of the fusion genes as molecular markers, the distinction between lipoma and liposarcoma could be facilitated in some condition. Further studies on the correlation between fusion genes and clinicopathological features of adipocytic tumors are encouraged to establish the individuality of each tumor.

Acknowledgements