Differential expression of microRNAs in uterine leiomyosarcoma

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BACKGROUND: microRNA (or miRNA) is a small non-coding RNA molecule (around 20-22 nucleotides), resulting from cleavage of a larger non-coding RNA (pri-miRNA, miRNA primitive), which functions in RNA silencing and in post-transcriptional regulation of gene expression. It has been reported in many tumors as responsible for alteration of their target genes stability and they have been associated with cellular transformation and tumorigenesis.

HYPOTHESIS: microRNAs are potential biomarkers and have been widely studied to assist in the prediction and prognosis of the diseases. The aim of this study is to identify microRNAs expression profile related to tumor development in uterine leiomyosarcoma samples.

METHODS: Formalin-fixed, paraffin-embedded samples from 37 patients bearing uterine leiomyosarcoma (2 myometrium as the reference group) were selected from the files of the Anatomic Pathology Department in A C Camargo Cancer Center, Sao Paulo, Brazil and Obstetrics and Gynecology Department from Hospital das Clinicas da Faculdade de Medicina da Universidade de Sao Paulo (Sao Paulo, Brazil). Total RNA was obtained using ReliaPrep™ FFPE Total RNA Miniprep System (Promega). The miScript II RT Kit (Qiagen) was used in order to perform the cDNA synthesis. Real-Time PCR reaction was performed using the miScript miRNA PCR Array (Qiagen) and the miScript SYBR Green PCR Kit (Qiagen) for analysis of 84 miRNA sequences described as human cancer-related genes.

RESULTS: Among 84 miRNA sequences, three upregulated miRNAs, hsa-miR-124-3p (fold change=37,8574), hsa-miR-372-3p (fc=22,3015) and hsa-miR-206 (fc=19,9742) and three downregulated, hsa-miR-193a-5p (fc=0,4718), hsa-miR-1-3p (fc=0,4686) and hsa-miR-10a-5p (fc=0,4084) were selected for analysis in our samples comparing to myometrium. Aside from mir-206, these microRNAs have not been described in uterine leiomyosarcoma yet. Moreover, literature shows miR-206 downregulated in breast cancer with BRCA1 mutation, hepatocellular carcinoma and lung squamous cell carcinoma, which diverges from our results. Validations and further evaluations are necessary to verify miRNA functions and to investigate their differential expression in uterine leiomyosarcoma and associate it to clinical pathological information of the patient.