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MIR-26A AND MIR-181C PROFILE HIGHLIGHT AS POTENTIAL PROGNOSIS BIOMARKERS IN TRIPLE-NEGATIVE BREAST CANCER PATIENTS

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Objective: This retrospective cohort study aims to investigate the relative expression profiles of microRNAs (miR 26a, 125b, 181a, 181c, and 340-5p) in patients with triple-negative breast cancer (TNBC) and their relationship with clinical outcome. **Methods:** We included 10 patients with TNBC, treated at the Mário Penna Institute, Brazil, and 5 patients without TNBC evidence, considered as control. This study was approved by the research ethics committee (CAAE protocol: 39741820.4.0000.9507). The total RNA extraction was performed from the formalin-fixed, paraffin-embedded (FFPE) tissues using the All Prep FFPE (Qiagen™). The RNA concentration was evaluated by the GE NanoVue Plus Spectrophotometer and complementary DNA (cDNA) for each target was synthesized, as appropriate. To analyze the transcripts, the TaqMan real-time PCR technique was used. The small nucleolar RNA RNU6-6P was used as an endogenous control. Changes in miRNA expression were measured by method 2(-ΔΔCq). **Results:** The expression profile of microRNAs showed a great variability among the TNBC patients, who reinforces the intratumoral heterogeneity of TNBC patients. One of 10 patients showed overexpression of all miRNA evaluated, while 2/10 had underexpression from all of them. An underexpressed profile of miR 181c and 26a was seen in those samples that had a tumor histopathological grade II (3/4) and the overall survival at 1–3 years. In contrast, the overexpression for both miRNAs was seen in 2/10 patients, independent of tumor histopathological grade, with the overall survival at 5–6 years. According to the literature, miR-26a and miR-181c suppressed the expression of MTDH and MAP4K4 genes, respectively, inhibiting the tumor-promoting effects in tumors. **Conclusion:** Our data appear to highlight the clinical evidence to use miRNAs as new prognosis biomarkers, allowing better stratification of patients. Studies are in progress to evaluate more patients and identify a molecular signature able to predict TNBC prognosis.

Keywords: Breast cancer. Biomarkers. MicroRNA. Triple-negative breast cancer.