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Distinct expression of miRNAs and its association with survival in triple-negative breast cancer and non-triple-negative breast cancer breast tumor subtypes from a cohort of patients from south of Brazil

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Objective: The main objective of this study was to determine the expression levels of miR-26a-5p, miR-126-3p, and 182-5p and their association with clinical parameters in patients with the triple-negative breast cancer (TNBC) and non-TNBC subtypes in a cohort of patients from South of Brazil. **Methodology:** The miRNAs were selected based on their common regulatory interactions of gene targets involved in the cell adherence and junction and critical associated cancer signaling pathways. Primary tumors of TNBC (n=30) and non-TNBC (n=52) patients were obtained before treatment from Erasto Gaertner Hospital, Curitiba, PR. The clinical data included: age, tumor size and TNM stage, lymph node and distant metastasis, comorbidity (ies), and survival status. The tumor samples and adjacent non-tumor tissue samples were subjected to tissue microdissection, RNA isolation, and RT-qPCR. This was approved by CONEP (894,864). **Results:** The three miRNAs showed significantly different expressions between the TNBC and adjacent non-tumor tissues ($p<0.001$). In the non-TNBC group, only miR-126-3p showed a significant difference ($p<0.01$). Expression analysis revealed significantly lower expression of miR-26a-5p ($p<0.01$) and higher expression of miR-126-3p and miR-182-5p ($p<0.001$ and $p<0.01$, respectively) in TNBC compared with non-TNBC tissues. No significant differences were observed in clinicopathological data between the groups or in their association with miRNA expression. However, higher expressions of the miR-26a-5p and miR-126-3p were significantly associated with patient mortality in the TNBC group ($p<0.05$ and $p<0.01$, respectively). **Conclusion:** Our findings demonstrated a distinct pattern of expression of miR-26a-5p, miR-126-3p, and 182-5p between TNBC and non-TNBC breast cancer subtypes and revealed a significant association of these miRNAs on the survival of the TNBC patients. These observations underscore the potential of these miRNAs as valuable biomarkers for subtype classification and their impact on TNBC survival. By delineating specific molecular signatures associated with each subtype, our study contributes to the understanding of the underlying biological mechanisms driving TNBC and non-TNBC tumors.

Keywords: triple-negative breast cancer, TNBC; non-triple-negative breast cancer, non-TNBC; miRNAs; miR-26a-5p; miR-126-3p; miR-182-5p.