Extracellular vesicle miRNAs profile as predictors of pathological complete response in breast cancer undergoing neoadjuvant therapy

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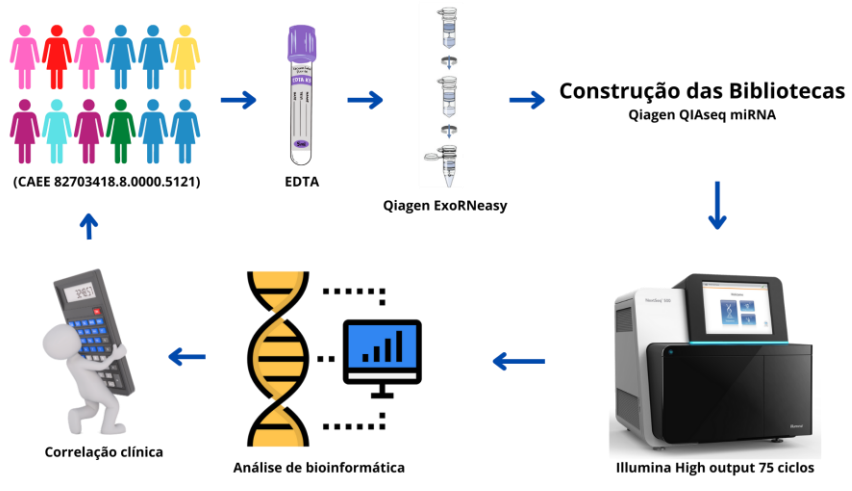
INTRODUCTION

Neoadjuvant therapy in breast cancer allows for the assessment of the degree of pathological response in the surgical specimen, providing prognostic and predictive information to guide subsequent treatments. Pathological complete response (pCR) is a prognostic factor widely associated with overall survival and is commonly used as a surrogate endpoint in neoadjuvant studies. Small non-coding RNAs, such as miRNAs, play crucial roles in various carcinogenic pathways and show promise as predictors of pCR. Developing a molecular signature of miRNAs extracted from tumor-derived extracellular vesicles (EVs) in peripheral blood holds potential for use as a biomarker. This approach could optimize neoadjuvant protocols to increase pCR rates and reduce toxicity. Therefore, this study seeks to initiate the development of less invasive and personalized methodologies to improve therapeutic outcomes in breast cancer.

OBJECTIVE

To investigate the association between miRNAs derived from EVs and pathological complete response in patients with breast cancer undergoing neoadjuvant therapy.

METHODOLOGY



RESULTS AND DISCUSSION

Among the 48 patients analyzed, a differential expression profile was noted in 12 patients with triple-negative breast cancer. Bioinformatics analysis revealed that overexpression of hsa-mir-489-5p was present in patients who achieved pCR, while overexpression of hsa-mir-1237-3p was observed in those without a complete pathological response (Figs. 1 and 2).

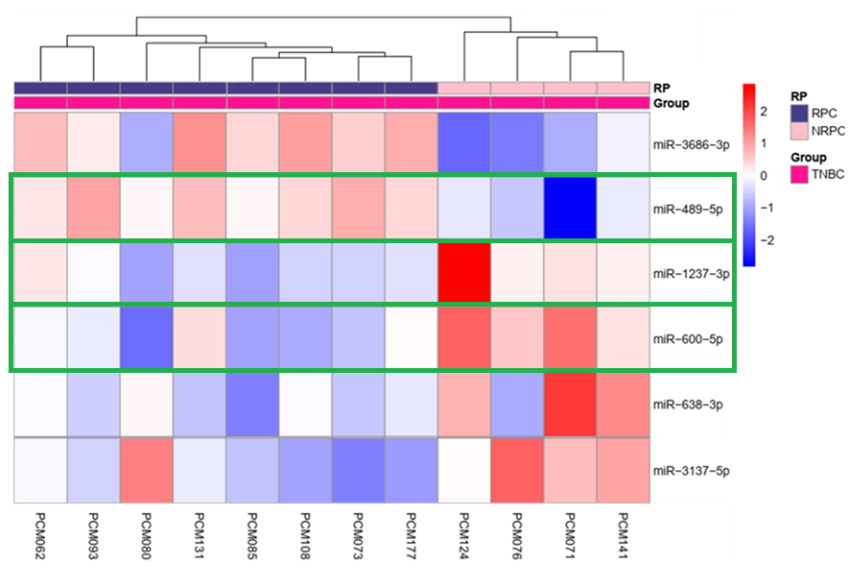


Figure 1: Profile of miRNAs related to Pathological Complete Response. miR-489-5p stands out as a tumor suppressor, and miR-1237-3p and miR-600-5p as oncomirs.

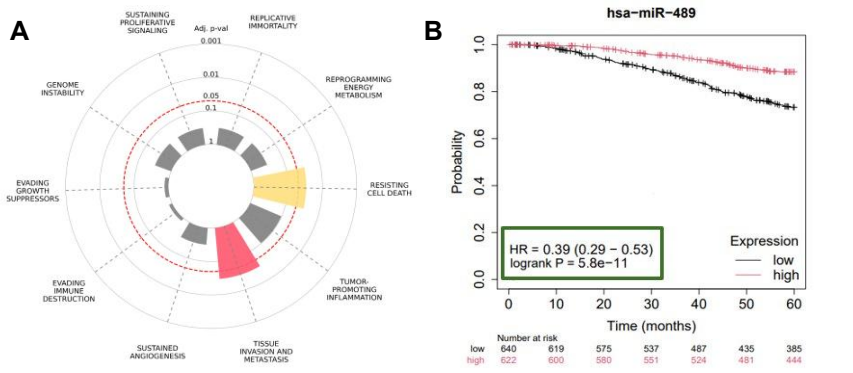


Figure 2: Impact of miRNA signature on survival pattern. A – This miRNA signature, along with its potential target genes, directly impacts pathways related to cell death and metastasis. **B –** The overexpression of miR-489-5p stands out as a tumor suppressor, positively impacting overall survival.

CONCLUSION

These findings suggest that hsa-mir-489-5p acts as a tumor suppressor, while hsa-mir-1237-3p functions as an oncomiR, showing predictive potential for pCR. These miRNAs may represent a potential new tool for predicting response to neoadjuvant treatment, contributing to a more personalized and less invasive approach to breast cancer management.

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