Mário Penna Journal - molecular and clinical cancer research, Belo Horizonte, v. 2, n.2, p. 81-84, jul./dez. 2024. DOI: 10.61229/mpj.v2i2.50

Anais: 3° Simpósio de Especialidades Oncológicas e Seminário de Iniciação Científica do Instituto Mário Penna

ANÁLISE DE miRNAs EM VESÍCULAS EXTRACELULARES DE PACIENTES COM CÂNCER DE OVÁRIO: identificação de potenciais biomarcadores para diagnóstico e prognóstico

ANALYSIS OF miRNAs IN EXTRACELLULAR VESICLES FROM OVARIAN CANCER PATIENTS: identification of potential biomarkers for diagnosis and prognosis

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RESUMO

Palavras-chave: miRNAs; câncer de ovário; vesículas extracelulares.

Data de submissão: 27/02/2025.
Data de aprovação: 14/03/2025.

1. INTRODUCTION

Ovarian cancer (OC) is the eighth most common malignancy among women worldwide[1]. In Brazil, an estimated 7,310 new cases of the disease are expected during the 2023-2025 triennium[2]. The lack of specific symptoms in the early stages and limitations in screening tests hinder early diagnosis, posing one of the greatest challenges in treating this disease. Thus, there is a pressing need to identify new biomarkers that can aid in the diagnosis and prognosis of OC patients. Currently, extracellular vesicles (EVs) are being extensively studied across various tumors due to their crucial role in cell communication, transporting proteins, DNA, and RNAs[3]. Among the transported RNAs, miRNAs

have demonstrated the ability to influence several tumorigenic processes, such as cell proliferation, invasion, migration, and chemoresistance[4].

2. OBJECTIVE

Based on these findings, the present study proposes identifying the miRNAs profile in circulating EVs to create biomarker panels in patients with OC.

3. METHODOLOGY

This study is a prospective observational study. Thirty-two patients diagnosed with OC, treated at Hospital Luxemburgo, who provided informed consent, were included in the research (CAAE - 82703418.8.0000.5121). Blood samples were collected, EVs were isolated, and total RNAs were extracted to construct small RNA libraries. The samples were then sequenced on the NEXTseq 550 (Illumina™), and the processing and identification of the sequences generated were assessed using UNITAS 1.8.0 software. Differential expression of miRNAs was then analyzed with the DESeq2 package.

4. RESULTS

Initial results indicated a distinct miRNA expression profile in OC patients compared to the control group. A total of 2,064 differentially expressed miRNAs (DEMs) were identified in OC patients. Among the DEMs, miR-486-5p and miR-16-5p stood out, showing negative regulation compared to the control group. Previous studies have demonstrated the tumor-suppressive activity of these miRNAs, which regulate cell proliferation, survival, and apoptosis[5,6].

5. CONCLUSION

With these initial findings, we reinforce the potential of miR-486-5p and miR-16-5p as biomarkers for ovarian cancer. However, additional validations are necessary to strengthen and confirm these results.

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NOTAS

CONFLITOS DE INTERESSE

Os autores declaram que não há nenhum conflito de interesse.

CONTRIBUIÇÃO

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ORIGEM DA PUBLICAÇÃO

A origem da publicação é de um trabalho de doutorado em andamento que foi apresentado no 3º Simpósio de Iniciação Científica e 1º Encontro de Pós-graduandos do Instituto Mário Penna.

FINANCIAMENTO

Programa Nacional de Apoio à Atenção Oncológica - Pronon e Fundação de Amparo à Pesquisa do Estado de Minas Gerais – FAPEMIG.

APROVAÇÃO ÉTICA

CAAE: 82703418.8.0000.5121 ASSOCIAÇÃO MÁRIO PENNA.

AGRADECIMENTOS

The authors thank Fundação de Amparo à Pesquisa do Estado de Minas Gerais (FAPEMIG APQ-02564-22), Rede Mineira de Pesquisa Translational em Oncologia (RED00059-23; FAPEMIG), and Programa Nacional de Oncologia, Brazilian Ministry of Health (Pronon grant NUP.25000.159953/2014-18 e NUP.25000.079266/2015-09).