Identification of miR-660-5p targets involved in breast cancer progression

Villarreal-García V.[1,2], Estupiñan-Jiménez J. R. [1,2], Reséndez-Pérez D.[1,2], Vázquez-Guillén J. M.[1,2], Mar Aguilar F.[1,2], Vivas-Mejía P. E.[3,4] and González-Villasana V.[1,2]

[1]Departamento de Biología Celular y Genética, Facultad de Ciencias Biológicas, Universidad Autónoma de Nuevo León, 66455 Nuevo León, México

[2]Departamento de Inmunología y Virología, Facultad de Ciencias Biológicas, Universidad Autónoma de Nuevo León, 66455 Nuevo León, México

[3]Department of Biochemistry, [4]Comprehensive Cancer Center University of Puerto Rico, Medical Sciences Campus, San Juan 00936, Puerto Rico

Background: Breast cancer (BC) is the most diagnosed cancer in women globally. MicroRNAs (miRNAs) participate in different processes of BC; their deregulation can make them act as oncogenes or tumor suppressors, participating in cancer progression. Using the TCGA (The Cancer Genome Atlas) database, we found miR-660-5p significantly overexpressed and associated with poor survival in patients with this pathology. It is reported that miR-660-5p induces proliferation, migration, and invasion in BC. However, the specific targets of this miRNA that induce each of these processes are unknown. In this project we propose to identify the targets of miR-660-5p involved in proliferation, migration, invasion, and angiogenesis in BC cells.

Methods: The basal levels of miR-660-5p were determined by RT-qPCR. The effect of miR-660-5p was evaluated on proliferation, invasion, and migration processes in MDA-MB-231 and MCF-7 cells, and angiogenesis in HUVEC cells transfected with the miR-660-5p inhibitor. We identified targets of miR-660-5p using different databases, and we evaluated their expression by RT-qPCR in plate.

Results: In this study, we found that miR-660-5p is significantly upregulated in BC cells MDA-MB-231 and MCF-7, compared to normal breast cells MCF-10A. In addition, we observed a significantly decrease in the processes of proliferation, migration, and invasion in BC cells, compared to untreated cells and negative control group. Similarly, we observed a significantly decrease in the angiogenesis process in HUVEC cells, compared to untreated cells and negative control group. Likewise, by analyzing the different databases and the literature, we found a total of 28 miR-660-5p targets involved in oncological processes.

Conclusions: miR-660-5p is overexpressed in BC cells compared to healthy breast cells. Furthermore, miR-660-5p induces the processes of proliferation, migration and invasion in BC cells, and angiogenesis in HUVEC cells.