Short Communication Journal of Molecular and Cellular Biochemistry 2020
Vol.4 No.2

Glycobiology 2020: Hyaluronan Metabolism is Associated with DNA Repair Genes in Breast and Colorectal Cancer. Screening of Potential Progression Markers Using qPCR- Ina Sevic, Center for Basic and Applied Research (CIBA), CIT NOBA

Ina Sevic [1], Fiorella Mercedes Spinelli [1], Daiana Lujan Vitale [1], Antonella Icardi [1], Lucia Romano [2], Alejandra Brandone [3], Paula Giannoni [4], Carolina Cristina [2], Marcela Fabiana Bolontrade [5] and Laura Alaniz [1]

[1]Laboratorio de Microambiente Tumoral, Centro de Investigaciones Básicas y Aplicadas (CIBA), CIT NOBA, Universidad Nacional del Noroeste de la Pcia. de Bs. As. Consejo Nacional de Investigaciones Científicas y Técnicas (UNNOBA-CONICET), Junín B6000, Argentina.
[2]Laboratorio de Fisiopatología de la Hipófisis, Centro de Investigaciones Básicas y Aplicadas (CIBA), CIT NOBA, Universidad Nacional del Noroeste de la Pcia. de Bs. As. Consejo Nacional de Investigaciones Científicas y Técnicas (UNNOBA-CONICET), Junín B6000, Argentina.
[3]Hospital Interzonal General de Agudos Dr. Abraham F. Piñeyro, Junín B6000, Argentina.
[4]Clínica Centro, Junín B6000, Argentina.
[5]Instituto de Medicina Traslacional e Ingeniería Biomédica (IMTIB)-CONICET-Instituto Universitario del Hospital Italiano-Hospital Italiano Buenos Aires (HIBA), Buenos Aires C1199ACL, Argentina.

Introduction:
In this work, we compared mRNA levels of Hyaluronan (HA) metabolism members and BRCA genes, known to be involved in the tumoral process, between tumor and non-tumor adjacent tissue and its correlation with previously proposed biomarkers (ER, PR, HER2 and KI67) in order to assess their value as a progression biomarkers. We show alteration in HA metabolism in colorectal but not breast cancer. However, we found a decrease in Hyaluronidase 1 HYAL1 levels in the breast but not colorectal cancer. We also show lower HA levels in tumor compared with normal tissue that could indicate a possible influence of tumor on its surrounding “normal” tissue. In both breast and colorectal cancer, CD44 and BRCA2 showed a strong positive correlation. Besides, our results show first indicators that qPCR of the analyzed genes could be used as an easy and low-cost procedure for the evaluation of molecular markers we propose here.

Objectives: Nine patients with colorectal and eight with bosom malignant growth were chosen for the examination. The investigation included people more than 18 years old from the Surgery Department of Hospital Interzonal General de Agudos "Abraham Piñeyro" (HIGA) and Clinica Centro. The patients had recently marked an educated assent, affirmed (30.08.2018) by the morals board of the Hospital Austral, Province of Buenos Aires (17-006). Seven sound contributors (without malignancies, immune system or ceaseless infections) were chosen as control of plasma tests. This work was been done after The Code of Ethics of the World Medical Association. The examinations were completed adhering to the standards of the Declaration of Helsinki of 1975, modified in 2013.
Three kinds of tests were gathered: tumor tissue (TT) disposed of at the hour of the medical procedure, non-tumor tissue nearby the tumor (NAT) and fringe blood. Tissue examples were gathered in the activity room and were assessed by a pathologist.

The focal point of this investigation were patients with bosom and colorectal malignant growth since these two tumours are viewed as the most incessant diseases in our district. Chosen patients did not already get treatment for the momentum ailment. Patients with a propelled phase of disease or metastasis were barred from this examination. The colorectal malignant growth study included nine patients (6 females and 3 guys) with mean age 67.4 ± 10.3 years. For the bosom malignant growth study, the patients were all female (8 patients) with mean age 61.3 ± 12.4 years. None of the colorectal malignant growth patients got radiotherapy or chemotherapy while two of the bosom disease patients got the treatment, 8 and 25 years back, for another infection, and were restaged for this new tumor. Histopathologic finding for all the bosom disease patients was intrusive carcinoma of no uncommon sort (NST), while for the colorectal patients was for the most part adenocarcinoma of the colon. TNM stages were controlled by a pathologist.

Results and Discussion: In order to establish the correlation between HA metabolism genes with previously recommended biomarkers, we first analyzed ER, PR, HER2 and KI67 in TT of the breast cancer patients and KI67 in TT of the colorectal cancer patients by immunohistochemistry (IHC). For the calculation of KI67 nucloes constructive cells, values less than 15% were considered low, 15-35% were intermediate and more than 35% were considered high. We found a high amount of KI67 positive cells in all (42%–63%) but two (7% and 9%) colorectal cancer patients, while in breast cancer we found three low (10%, 10% and 15%), two middle (30% and 35%) and three high (40%, 40% and 70%). All breast cancer patients were RE (+), all but one was RP (+) and only one was HER2(+). We had no triple negative patient subgroups.

This work is partly presented at 10th Glycobiology World Congress Webinar July on 17-18, 2020