

BREAST CANCER, LOCALLY ADVANCED AND METASTATIC
Publication

Abstract: 385

CANCER STEM CELL-LIKE CELLS: A THERAPEUTIC MODEL IN BREAST CANCER PATIENTS, WHERE ANY OTHER RECOMMENDED THERAPY HAS FAILED

I. Papasotiriou¹, M. Chatziioannou², M. Toloudi², E. Ioannou², R. Hammon³, U. Jacob⁴, N. Hembry⁵, A. Kopic⁴

¹ *Research & Development-Clinical, Research Genetic Cancer Centre Ltd, Filotas, GREECE*

² *Research & Development, Research Genetic Cancer Centre Ltd, Filotas, GREECE*

³ *Clinical, ATMC, Texas, TX, UNITED STATES OF AMERICA*

⁴ *Clinical, Privatlinik AMC, Dornstetten-Hallawangen, GERMANY*

⁵ *Clinical, Litfield Medical House, Bristol, UNITED KINGDOM*

Introduction

Nowadays, the difficulty to treat metastatic breast cancers is high. Many clinical therapeutic lines have failed and there is no suggested therapeutic approach (in literature) concerning this type of tumors. The last decades, circulating tumor cells (CTCs) are the state - of - the -art in cancer therapy. In the present study, CTCs were isolated and identified. CSCs (cancer stem cells) were isolated from the above population of CTCs and their gene pattern was compared with those from the primary tumor as well as with those from the metastatic tumor. This study attempts to find a correlation between the CTCs and the metastatic regions in comparison with the primary tumor as well as to find out if all the CSCs have the same hallmarks in the selected breast cancer stem cell populations.

Materials and methods

In order the protocol to be performed, CTCs from patient's blood samples were isolated and then cultured in appropriate conditions. CSCs were identified and isolated from the population of CTCs. mRNA was extracted and was used for Microarray hybridization assays. The same procedure was repeated for primary tumor as well for metastatic tumor samples. The expression pattern of primary tumor cells was compared with those in the metastatic tumor. Finally, the therapeutic approach which was based on the above findings, was designed.

Results

The results showed that the gene expression pattern of metastatic sites is similar to that of metastatic sites and less to that of the primary site. Then, the patients followed a therapeutic approach based on the data of the clinical results which were evaluated within a six- month period showing that the patients showed an objective response rate.

Conclusion

The results showed that the entity that determines the clinical outcome in breast cancer, is the sub-population of CTCs, the circulating CSCs. Moreover, there are various types of CSCs in one patient, and not only one, as they have different growth mechanisms in primary and secondary tumors.

Disclosure

All authors have declared no conflicts of interest.