Therapies of Breast Cancer

Berline Silva*

Editorial office, Clinical Oncology, Belgium

Corresponding Author*

Berline Silva

Editorial office, Clinical Oncology,

Belgium

E-mail: oncology@scholarlymed.com

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Abstract

Breast cancer is the most frequent cancer in women and the second leading cause of death from cancer in women in the United States. Breast cancer is a type of cancer that develops in the breast tissue, most usually in the inner lining of milk ducts or the lobules that supply milk to the ducts. Breast cancer is the second most frequent type of non-skin cancer (after lung cancer) and the fifth most common cause of cancer mortality in women worldwide, accounting for 10.4% of all cancer cases in women. Breast cancer claimed the lives of 519,000 people globally in 2004. Breast cancer is 100 times more common in women than in men, yet males have a worse prognosis due to detection delays. Cancer cells have DNA and RNA that are very similar (but not identical) to cells from the organism from whence they came. This is why they aren't always identified by the immune system, especially if it's already compromised.

Keywords: Immune system ● Lymphatic tissue ● DNA and RNA mutations

Introduction

A change/mutation of DNA and/or RNA causes cancer cells to originate from normal cells. These modifications/ mutations can occur naturally (ill Law of Thermodynamics-increase in entropy) or be induced by other factors such as nuclear radiation, electromagnetic radiation (microwaves, X-rays, Gamma-rays, Ultraviolet-rays, etc), viruses, bacteria and fungi, parasites (due to tissue inflammation/ irritation, heat, chemicals in the air, water, and food, mechanical cell-level injury, free radical [1]. Cancer arises when the immune system malfunctions and/or the number of cells created exceeds the immune system's ability to eradicate them. Under some conditions, such as an unfavorable environment (due to radiation, pollutants, etc.), a bad diet (unhealthy cell environment), people with genetic mutation predispositions and people of advanced age, the rate of DNA and RNA mutations might be excessive (above 80). Breast cancer refers to the uncontrolled growth and multiplication of cells that begin in the breast tissue, and is usually termed after the body part in which it first appeared. There are two types of tissues in the breast: glandular tissues and stromal (supporting) tissues. The milk-producing glands (lobules) and ducts (milk passageways) are housed in glandular tissues, while the fatty and fibrous connective tissues of the breast are found in stromal tissues. Lymphatic tissue immune system tissue that drains cellular fluids and waste is also found in the breast [2]. Breast cancer is the uncontrolled growth and proliferation of cells that starts in the breast tissue and is usually named after the body region where it initially appears. Breast tissues are divided into two categories: glandular tissues and stromal (supporting) tissues.

The milk-producing glands (lobules) and ducts (milk passageways) are found in glandular tissues, whereas stromal tissues contain the fatty and fibrous connective tissues of the breast. Lymphatic tissue, which is part of the immune system and drains cellular fluids and waste, can also be found in the breast. According to research, lobular carcinomas are more likely to be hormone receptor positive than ductal carcinomas. This distinction may help to explain why combined oestrogen and progestin postmenopausal hormone use is more significantly linked to lobular carcinoma risk than ductal carcinoma risk in seven studies. While several studies have looked into the clinical, pathologic, and epidemiologic differences between ductal and lobular carcinomas, little is known about the less common histologic types of breast cancer, such as mucinous, tubular, comedo, inflammatory, medullary, and papillary carcinomas, which account for about 10% of all cases. Using data from 11 population-based tumour registries that participate in the Surveillance, Epidemiology, and End Results (SEER) Program, the goal of this study is to characterize how rare histologic categories of breast cancer differ in stage, size, lymph node status, and oestrogen receptor. These distinctions must be evaluated in order to have a better knowledge of the nature of these tumours and to gain insight into the aetiologies and clinical characteristics of different forms of breast cancer [3]. Though several studies have looked into the clinical, pathologic, and epidemiologic differences between ductal and lobular carcinomas, little is known about the histologic types of breast cancer that account for about 10% of all cases, such as mucinous, tubular, comedo, inflammatory, medullary, and papillary carcinomas. The purpose of this study is to characterize how rare histologic groups of breast cancer differ in stage, size, lymph node status, and oestrogen receptor using data from 11 population-based tumour registries that participate in the Surveillance, Epidemiology, and End Results (SEER) Program. These distinctions must be investigated in order to acquire a better understanding of the nature of these tumours as well as the aetiologies and clinical characteristics of different types of breast cancer. Because there are a high number of inputs (genes) from which to forecast classes and a small number of samples, microarray classification is difficult, and it's critical to figure out which genes contribute the most to categorization. Several easy-to-use, minimally invasive cancer detection procedures based on peripheral blood or urine samples have recently been developed to lessen the physical stress on patients as well as the expenses and time required. Rapid progress has been achieved in cancer diagnostic and prognosis methods based on metabolome analysis, which commonly employs multivariate analysis techniques such computer-aided, machine-learning systems for data mining [4]. Although metabolome analysis is a promising method for detecting diseases such as cancer, it does have certain practical limitations. The need to quantify a large number of metabolites, data-redundancy issues such as the false-discovery rate (FDR) and overfitting, and cost limits are among them. "Focused metabolomics," which limits the objects of analysis to those that play roles in general metabolism and share physical similarities, is one approach to overcoming these issues.

Amino acids are one of the best options for targeted metabolomics since they are either eaten or generated endogenously, and they serve important physiological functions as both basic metabolites and metabolic regulators. Because their profiles have been recognised to be impacted by metabolic abnormalities in specific organ systems generated by specific disorders, plasma free amino acids (PFAAs), which circulate abundantly as a medium linking all organ systems, would be the most appropriate target for measuring amino acids. Furthermore, plasma samples from patients are simple to obtain. PFAA profiles in cancer patients have also been described by several researchers. Despite evidence of a link between PFAA profiles and certain types of cancer, few studies have looked into using PFAA profiles for diagnosis because, while PFAA profiles differ significantly between patients, individual amino acid differences do not always provide sufficient discrimination abilities. The introduction of DNA microarray technology changed the scale of genomics research, allowing researchers to study thousands of genes in a single experiment.

The relative amount of mRNA in isolated cells or biopsied tissues from patients is measured using a DNA microarray. Gene expression patterns can be used to classify different types of tumours since transcriptional alterations correctly represent the status of disease, including cancer. Cancer diagnosis is currently based on a number of histological findings, including immunohistochemistry techniques that detect cancer biomarker molecules. However, due to physical similarity and a dearth of accessible cancer biomarkers, these techniques have limitations. Accurate diagnosis boosts the effectiveness of cancer treatment. Systematic techniques to categorise tumour types using gene expression data have been researched based on the concept of gene expression patterns as fingerprints at the molecular level [5]. Exosomes, shedding vesicles, prostasomes, and apoptotic bodies are membrane vesicles with a diameter of 40 nm-1,000 nm that are released by a variety of cell types, including red blood cells, platelets, lymphocytes, dendritic cells, endothelial cells, and cancer cells. According to their secretory mechanisms, these vesicles were divided into two groups. Exosomes are produced in multivesicular endosomes, whereas microvesicles and shedding vesicles are produced by direct budding from the plasma membrane. Although the components of EVs vary by cell, a common collection of molecules is believed to be present in all EVs, regardless of origin. Proteins like tumour susceptibility gene 101 (TGS101), CD9, and CD63 are among these molecules, and several of these proteins are regarded to be key components of EVs. In order to establish the presence of EVs, researchers used immunoblotting to detect these so-called EV flag proteins. To our knowledge, no studies have used numerous cell lines to undertake a comparison analysis. Furthermore, new EV proteomic studies have revealed that these EV flag proteins are not found in all EVs. These data highlight the importance of having dependable EV marker proteins. Using four prostate cell lines and five breast cell lines, we conducted a systematic analysis of 11 well-known EV marker proteins. In the EVs produced from each cell line, we discovered that CD9 and CD81 were present in similar amounts [6]. The quantity of the other studied EV proteins, on the other hand, varied amongst starting cell types. As a result, we believe that CD9 and CD81 could be useful EV markers. These findings emphasise the significance of having reliable EV marker proteins. We conducted a systematic investigation of 11 well-known EV marker proteins using four prostate cell lines and five breast cell lines. We discovered that CD9 and CD81 were present in similar amounts in the EVs produced by each cell line. The amount of the other EV proteins investigated, on the other hand, differed according on the beginning cell type. As a result, CD9 and CD81 may be useful EV indicators, according to our findings. There are also IF-associated proteins that arrange IFs into bundles and networks, including as plectin, ankyrin, desmoplakin, filaggrin, and others [4].

The interactions between IFs and other cytoskeletal components and organelles are known to be coordinated by IFassociated proteins. IFs and IF-associated proteins work together to stabilise and strengthen various organs by organising cytoplasmic space within cells and cells that make up tissue architecture. Vimentin, a 57-kDa protein, is one of the type III IF protein family's most frequently expressed and highly conserved proteins. Vimentin expression begins on embryonic day 8.5 (E8.5) and becomes dominant in the primitive streak stage in mice, however vitamin expression was shown to be limited to connective tissue mesenchymal cells in the central nervous system and muscle in adult mice. Pancreatic precursor cells, Sertoli cells, neural precursor cells, trophoblast giant cells, fibroblasts, endothelial cells lining blood arteries, renal tubular cells, macrophages, neutrophils, mesangial cells, leukocytes, and renal stromal cells have all been found to contain vimentin [7].

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