

SHORT COMMUNICATION



BRCA1 and BRCA2: Diverse population perspectives on breast cancer risk

Supriya Mohanty

Department of Biotechnology, MITS School of Biotechnology, Bhubaneswar, Odisha, India

ABSTRACT

Molecular testing of breast cancer has emerged as a pivotal tool in the diagnosis, prognosis, and personalized treatment of this prevalent malignancy. By delving into the genetic and molecular characteristics of breast cancer cells, these tests provide invaluable insights that guide clinicians in tailoring therapies to individual patients. The aim of the study is to understand the significance and methodologies of molecular testing in the context of breast cancer, shedding light on its transformative impact on the landscape of oncology. Breast cancer is a heterogeneous disease with diverse subtypes that exhibit distinct molecular profiles. Molecular testing enables the identification of specific genetic alterations, such as mutations in the BRCA1 and BRCA2 genes, which are associated with an increased risk of developing breast cancer. This information not only aids in assessing an individual's susceptibility to the disease but also influences decisions regarding preventive measures, such as prophylactic surgeries or intensified screening protocols. In addition to risk assessment, molecular testing plays a crucial role in determining the prognosis of breast cancer patients. Genomic profiling allows for the classification of tumors based on their molecular subtypes, such as luminal A, luminal B, HER2-enriched, and triple-negative. Each subtype exhibits distinct biological behaviors and responses to treatment, empowering oncologists to devise more accurate prognoses and select tailored therapeutic strategies. Moreover, the era of precision medicine has been ushered in by molecular testing, particularly in the realm of targeted therapies. The identification of specific molecular markers, such as HER2 overexpression, has paved the way for targeted drugs like trastuzumab, significantly improving outcomes for patients with HER2-positive breast cancer. Similarly, endocrine therapies like tamoxifen are employed based on the hormonal receptor status identified through molecular testing, exemplifying the personalized approach to breast cancer treatment. Technological advancements have propelled molecular testing methodologies, with techniques like next-generation sequencing (NGS) and gene expression profiling revolutionizing our understanding of the genomic landscape of breast cancer. These high-throughput methods enable the simultaneous analysis of multiple genes, providing a comprehensive overview of the genetic alterations driving tumorigenesis. Additionally, liquid biopsy approaches offer non-invasive means of monitoring genetic changes in real-time, presenting new avenues for dynamic assessment and early detection. Thus, molecular testing has become an indispensable component of the breast cancer diagnostic and therapeutic paradigm. From risk assessment and prognostication to guiding personalized treatment strategies, the insights gleaned from molecular testing contribute significantly to advancing patient care. As our understanding of the intricate molecular underpinnings of breast cancer continues to deepen, the role of molecular testing will undoubtedly expand, shaping the future of oncology towards more precise and effective interventions.

KEYWORDS

Chemotherapy; Cancer; Molecular testing; Tumors; Gene encodes; Mutations

ARTICLE HISTORY

Received 24 June 2024;

Revised 16 July 2024;

Accepted 22 July 2024

Introduction

Breast cancer stands as a formidable global health challenge, with a profound impact on individuals and societies. This malignancy arises from the uncontrolled growth of cells in the breast tissue, affecting both men and women, although it is predominantly observed in the latter. As one of the most prevalent cancers worldwide, breast cancer's incidence underscores the urgency for comprehensive understanding and effective management [1]. The etiology of breast cancer is multifactorial, involving a complex interplay of genetic, hormonal, and environmental factors. While some individuals harbor genetic mutations, such as BRCA1 and BRCA2, predisposing them to the disease, others may be influenced by

hormonal factors, reproductive history, or lifestyle choices. Early detection and advancements in diagnostic technologies, such as mammography and molecular testing, have significantly improved outcomes. Treatment modalities range from surgery and chemotherapy to targeted therapies, emphasizing the importance of a multidisciplinary approach [2]. Ongoing research continues to unravel the intricate molecular and genomic landscape of breast cancer, paving the way for innovative therapeutic strategies and personalized medicine. As breast cancer remains a critical public health concern, a comprehensive understanding of its complexities is imperative to drive effective prevention, early detection, and treatment initiatives, ultimately

*Correspondence: Supriya Mohanty, Department of Biotechnology, MITS School of Biotechnology, Bhubaneswar, Odisha, India. e-mail: supriyam7437@gmail.com

© 2024 The Author(s). Published by Reseapro Journals. This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0/>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

reducing the global burden of this disease [1,2].

Molecular testing has revolutionized the landscape of breast cancer diagnosis and treatment, offering a sophisticated approach that delves into the genetic and molecular intricacies of the disease. Breast cancer, a heterogeneous malignancy with diverse subtypes, exhibits distinct molecular profiles that play a crucial role in its initiation, progression, and response to therapy. Molecular testing, encompassing techniques such as NGS and gene expression profiling, has become instrumental in unraveling the genomic complexity of breast tumors. Molecular testing plays a pivotal role in risk assessment, guiding preventive measures and tailored screening protocols. Identification of specific genetic alterations, such as mutations in the BRCA1 and BRCA2 genes, informs not only an individual's susceptibility to breast cancer but also aids in decision-making regarding prophylactic interventions [3].

Moreover, molecular testing facilitates precise prognosis through the classification of tumors into molecular subtypes, such as luminal A, luminal B, HER2-enriched, and triple-negative [3]. This classification guides clinicians in predicting the behavior of the disease and tailoring treatment strategies accordingly. In the era of precision medicine, molecular testing has ushered in a paradigm shift in breast cancer treatment. Targeted therapies, like trastuzumab for HER2-positive breast cancer, are tailored based on specific molecular markers identified through molecular testing. Additionally, endocrine therapies are administered based on the hormonal receptor status elucidated by these advanced testing methodologies [4]. The continuous evolution of molecular testing technologies holds promise for more refined diagnostics, improved prognostication, and the development of targeted therapeutics. As research in this field advances, the integration of molecular testing into routine clinical practice is poised to further enhance the precision and efficacy of breast cancer management [3,4].

NGS has emerged as a transformative technology in the detection and molecular characterization of breast cancer, offering a comprehensive and high-throughput approach to analyzing the genomic landscape of tumors. This advanced sequencing technique provides invaluable insights into the genetic alterations driving breast cancer, aiding in diagnosis, prognosis, and the development of targeted treatment strategies. NGS enables the simultaneous analysis of multiple genes, allowing for the identification of various genetic alterations, including single nucleotide variations, insertions, deletions, and gene fusions. In the context of breast cancer, NGS is employed to unravel the genomic heterogeneity of tumors, providing a more nuanced understanding of the disease. One application of NGS in breast cancer detection is the identification of somatic mutations. Somatic mutations are genetic alterations that occur in the DNA of tumor cells but not in the patient's germline cells. By sequencing the entire exome or specific panels of genes relevant to breast cancer, NGS allows for the identification of somatic mutations that may drive tumorigenesis or contribute to therapeutic resistance [5].

Liquid biopsy, a non-invasive technique, is another area where NGS has demonstrated significant utility in breast cancer detection. By analyzing cell-free DNA (cfDNA) circulating in

the blood, NGS can detect tumor-derived genetic material, providing real-time information on the genomic landscape of the cancer. Liquid biopsy using NGS has shown promise in monitoring treatment response, detecting minimal residual disease, and identifying emerging resistance mutations. Moreover, NGS facilitates the identification of actionable mutations that can guide targeted therapies. For instance, the detection of HER2 amplification or mutations in genes such as BRCA1 and BRCA2 can influence treatment decisions. Targeted therapies, including HER2 inhibitors or PARP inhibitors, may be employed based on the specific genetic alterations identified through NGS. The integration of NGS into routine clinical practice holds immense potential for advancing personalized medicine in breast cancer. It allows for the identification of clinically relevant biomarkers, paving the way for more precise and individualized treatment approaches. Furthermore, NGS contributes to ongoing research efforts aimed at uncovering novel therapeutic targets and understanding the underlying molecular mechanisms of breast cancer [6].

In conclusion, NGS has revolutionized the detection and molecular characterization of breast cancer by providing a comprehensive and high-throughput analysis of the tumor genome. This technology's ability to uncover genetic alterations, guide treatment decisions, and monitor disease dynamics positions it as a powerful tool in advancing our understanding and management of breast cancer [5,6].

Methodologies

HER2/neu testing

HER2/neu testing has emerged as a pivotal component in the molecular diagnostics of breast cancer, providing critical information that guides treatment decisions and predicts patient outcomes. HER2, or human epidermal growth factor receptor 2, is a proto-oncogene that, when overexpressed or amplified, plays a key role in the aggressive behavior of certain breast cancers. This testing is integral to identifying patients who may benefit from targeted therapies, fundamentally transforming the management of HER2-positive breast cancer. HER2/neu testing primarily involves immunohistochemistry (IHC) and fluorescence in situ hybridization (FISH). IHC assesses the protein expression levels of HER2, while FISH evaluates gene amplification. These two methods are often used in conjunction to provide a comprehensive understanding of HER2 status in breast cancer [7]. Immunohistochemistry involves staining tumor tissue samples with antibodies specific to the HER2 protein. The results are categorized into four groups: 0 (no staining), 1+ (weak incomplete membrane staining), 2+ (moderate complete membrane staining), and 3+ (strong complete membrane staining). Tumors with a score of 3+ are considered HER2-positive, indicating overexpression of the HER2 protein. Fluorescence in situ hybridization is employed to detect HER2 gene amplification. This method involves using fluorescent probes that bind to the HER2 gene region, allowing visualization under a microscope. The ratio of HER2 gene signals to chromosome 17 signals is determined, with a ratio greater than 2.0 indicating gene amplification [8]. HER2/neu testing holds critical implications for treatment decisions. Patients with HER2-positive breast cancer may benefit from targeted therapies, such as trastuzumab and

pertuzumab. These drugs specifically target the HER2 protein, inhibiting its signaling and impeding cancer cell growth. The introduction of HER2-targeted therapies has significantly improved outcomes for HER2-positive breast cancer patients, underscoring the importance of accurate HER2 testing in clinical practice [8].

HER2/neu testing is a cornerstone in the management of breast cancer, providing crucial information for personalized treatment strategies. Accurate determination of HER2 status through IHC and FISH enables clinicians to tailor therapies, improving the prognosis and overall outcomes for patients with HER2-positive breast cancer [7,8].

Estrogen receptor (ER) and progesterone receptor (PR) testing

Estrogen receptor (ER) and progesterone receptor (PR) testing play a fundamental role in the molecular characterization of breast cancer, guiding therapeutic decisions and providing valuable prognostic information. The expression of these hormone receptors influences the responsiveness of breast cancer cells to hormonal therapies, shaping the treatment approach and predicting patient outcomes. ER and PR testing are typically performed through immunohistochemistry (IHC) on breast cancer tissue samples obtained from biopsies or surgeries. The results of these tests help categorize breast cancer into subtypes based on hormonal receptor status, influencing treatment decisions and providing prognostic insights. ER testing evaluates the presence of estrogen receptors on the surface of breast cancer cells. A positive result indicates the presence of estrogen receptors, suggesting that the cancer cells may respond to hormonal therapies that target estrogen signaling. The results are reported as a percentage of positive cells, with a threshold of 1% or higher considered ER-positive [9]. Similarly, PR testing assesses the expression of progesterone receptors on breast cancer cells. A positive result indicates the presence of progesterone receptors, indicating potential responsiveness to hormonal therapies targeting progesterone signaling.

The results are also reported as a percentage of positive cells, with a threshold of 1% or higher considered PR-positive. ER and PR status are crucial determinants in the selection of treatment strategies. Hormonal therapies, such as tamoxifen and aromatase inhibitors, are often recommended for patients with ER-positive and/or PR-positive breast cancer. These medications interfere with hormonal signaling pathways, impeding the growth of hormone receptor-positive cancer cells. The information garnered from ER and PR testing not only influences immediate treatment decisions but also provides valuable prognostic insights. Hormone receptor-positive breast cancers generally exhibit a more favorable prognosis compared to hormone receptor-negative subtypes. The identification of ER and PR status aids in risk stratification, allowing clinicians to tailor follow-up strategies and predict long-term outcomes for patients [10].

ER and PR testing are integral components of breast cancer diagnostics, guiding therapeutic decisions and offering prognostic information. The identification of hormone receptor status informs the selection of hormonal therapies, contributing

to more personalized and effective treatment strategies for breast cancer patients [9,10].

BRCA1 and BRCA2 testing

BRCA1 and BRCA2 testing plays a crucial role in the realm of breast cancer genetics, identifying individuals with inherited mutations in these genes that significantly elevate the risk of developing breast and ovarian cancers. Understanding the genetic landscape through BRCA1 and BRCA2 testing not only aids in risk assessment but also informs preventive measures and personalized treatment strategies. BRCA1 and BRCA2 are tumor suppressor genes involved in the repair of DNA damage. Mutations in these genes can impair the DNA repair mechanism, leading to an increased risk of developing breast and ovarian cancers. BRCA1 mutations, discovered in 1994, and BRCA2 mutations, identified in 1995, are associated with a hereditary predisposition to these cancers. Genetic testing for BRCA1 and BRCA2 mutations is typically performed in individuals with a family history of breast or ovarian cancer, especially if multiple relatives across generations are affected. Additionally, testing may be considered for individuals diagnosed with breast cancer at a young age or those with specific ethnic backgrounds known to have an increased prevalence of these mutations [11].

The testing process involves analyzing an individual's DNA, usually obtained through a blood sample or saliva. Identification of a mutation in BRCA1 or BRCA2 can have profound implications for the individual and their family members. It allows for risk assessment, enabling personalized risk management strategies and early detection measures. For individuals with identified mutations, preventive strategies may include increased surveillance through more frequent screenings, prophylactic surgeries (such as mastectomy or oophorectomy), and the consideration of chemoprevention options [12]. Additionally, close relatives may undergo genetic testing to assess their own risk and make informed decisions about their healthcare. In the context of breast cancer treatment, knowledge of BRCA1 and BRCA2 status is also pertinent. Breast cancers associated with these mutations may exhibit distinct characteristics and responses to treatment. For example, tumors with BRCA mutations may be more responsive to certain chemotherapy agents, and targeted therapies such as poly ADP-ribose polymerase (PARP) inhibitors have shown efficacy in BRCA-mutated breast cancers [12].

In conclusion, BRCA1 and BRCA2 testing is a powerful tool in identifying individuals at heightened risk for breast and ovarian cancers due to hereditary genetic mutations. This knowledge not only informs risk management and prevention strategies but also contributes to personalized treatment decisions for individuals with BRCA mutations, enhancing overall outcomes in the context of breast cancer [11,12].

Multigene panel testing

Multigene panel testing has become a valuable tool in breast cancer genetic testing, offering a comprehensive analysis of multiple genes associated with hereditary cancer predisposition. Unlike traditional single-gene testing, multigene panels simultaneously examine numerous genes linked to breast cancer susceptibility, providing a more thorough assessment of

an individual's genetic risk profile. Multigene panel testing typically includes genes beyond the well-known BRCA1 and BRCA2, such as TP53, PALB2, CHEK2, ATM, and others associated with breast cancer susceptibility. This broader analysis provides a more comprehensive understanding of an individual's genetic risk factors, especially in cases where there may be a predisposition to other hereditary cancer syndromes. The advantages of multigene panel testing include the potential identification of mutations in less common breast cancer susceptibility genes and the ability to uncover additional cancer risks beyond breast cancer, such as ovarian, pancreatic, or colorectal cancers. Moreover, it is particularly useful for individuals with a family history of cancer but no clear indication of which specific gene might be involved [13].

Research has shown that multigene panel testing can yield clinically significant findings in individuals with breast cancer. A study by Tung et al. demonstrated the frequency of mutations in individuals with breast cancer referred for testing using a 25-gene panel, highlighting the diverse genetic landscape that contributes to breast cancer susceptibility beyond BRCA1 and BRCA2. However, it's essential to consider the complexities associated with multigene panel testing, such as the interpretation of variants of uncertain significance and the potential psychological and medical implications of identifying mutations in genes with varying levels of cancer risk [14].

Multigene panel testing represents a valuable advancement in breast cancer genetic testing, allowing for a more comprehensive assessment of an individual's genetic risk profile. As our understanding of the genetic basis of breast cancer continues to evolve, multigene panel testing contributes to more informed decision-making regarding risk management, prevention, and personalized treatment strategies for individuals at risk of hereditary breast cancer [13,14].

Oncotype DX and MammaPrint

Oncotype DX and MammaPrint are two commercially available genomic assays that have revolutionized the field of breast cancer management by providing valuable information about the molecular characteristics of tumors. These tests aid in making more informed decisions regarding the need for adjuvant chemotherapy and help tailor treatment strategies based on the individual biology of the cancer. Oncotype DX is a gene expression assay that analyzes the activity of a panel of genes within the tumor tissue. It provides a recurrence score (RS) that helps predict the likelihood of disease recurrence and the potential benefit of chemotherapy. The test is particularly useful for women with early-stage, estrogen receptor-positive (ER+), and HER2-negative breast cancer. The landmark study by Paik et al. demonstrated the clinical utility of Oncotype DX in predicting the risk of recurrence in tamoxifen-treated, node-negative breast cancer patients [15].

MammaPrint, on the other hand, is a 70-gene expression assay that categorizes tumors into high or low risk of recurrence. This genomic test is often employed in patients with early-stage breast cancer and helps identify those who may safely forego chemotherapy. The MINDACT trial demonstrated that women with a low-risk MammaPrint result and a clinical high-risk assessment could safely omit chemotherapy without

compromising their outcomes. Both Oncotype DX and MammaPrint provide valuable information to guide treatment decisions, offering a more personalized and risk-stratified approach to breast cancer management. These assays help identify patients who are likely to benefit from chemotherapy and those who may avoid unnecessary treatment, minimizing potential side effects and improving the overall quality of patient care [16].

Oncotype DX and MammaPrint are groundbreaking genomic assays that have transformed the landscape of breast cancer treatment decision-making. By providing insights into the tumor's molecular characteristics, these tests enable clinicians to tailor therapy plans, optimizing the balance between treatment efficacy and minimizing unnecessary interventions for patients with certain types of breast cancer [15,16].

PIK3CA mutation testing

PIK3CA mutation testing has gained prominence in breast cancer diagnostics, contributing valuable insights into the molecular landscape of tumors and guiding treatment decisions. The PIK3CA gene encodes the p110 α subunit of the phosphatidylinositol-3-kinase (PI3K) pathway, a signaling pathway implicated in cell growth, survival, and metabolism. Mutations in the PIK3CA gene are frequently observed in various cancers, including breast cancer, and their detection has implications for prognosis and targeted therapies. PIK3CA mutations are often found in hormone receptor-positive (HR+) breast cancers and are associated with the human epidermal growth factor receptor 2 (HER2)-negative subtype. These mutations activate the PI3K pathway, contributing to uncontrolled cell growth and survival. Studies, such as the one by Saal et al. have shown correlations between PIK3CA mutations and hormone receptor status, nodal metastasis, and HER2 expression in breast carcinoma [17].

Testing for PIK3CA mutations is typically performed through molecular techniques, including DNA sequencing or targeted mutation analysis. Identifying PIK3CA mutations in breast cancer patients can have important clinical implications. Firstly, these mutations may influence prognosis, with some studies suggesting an association between PIK3CA mutations and less favorable outcomes. Additionally, the presence of PIK3CA mutations is of significance in the context of targeted therapies. Inhibition of the PI3K pathway has been explored as a potential treatment strategy, and ongoing clinical trials are evaluating the efficacy of PI3K inhibitors in breast cancer patients with PIK3CA mutations. The development of targeted therapies that specifically address the aberrant signaling resulting from PIK3CA mutations holds promise for more personalized and effective treatment strategies [18].

PIK3CA mutation testing in breast cancer has emerged as a valuable tool in understanding the molecular underpinnings of the disease. The identification of these mutations provides insights into prognosis and may guide the selection of targeted therapies, ushering in a new era of precision medicine in breast cancer management. As research continues, the integration of PIK3CA mutation status into routine clinical practice holds the potential to further refine treatment decisions and improve

outcomes for specific subgroups of breast cancer patients [17,18].

TP53 mutation testing

TP53 mutation testing has become an integral part of breast cancer diagnostics, offering critical insights into the genetic landscape of tumors and guiding treatment decisions. The TP53 gene encodes the p53 protein, a crucial tumor suppressor that plays a central role in regulating cell division and preventing the formation of cancerous cells. Mutations in TP53 are associated with increased cancer risk, including breast cancer, and the detection of these mutations has implications for prognosis and treatment strategies. TP53 mutations are diverse, and their presence can lead to the loss of normal p53 function, allowing cells to evade the usual checks on uncontrolled growth and proliferation. These mutations are often associated with more aggressive tumor behavior and resistance to standard treatments [19]. TP53 mutation testing is typically performed using various molecular techniques, including DNA sequencing, to identify specific alterations in the TP53 gene. The identification of TP53 mutations in breast cancer patients is crucial for several reasons. Firstly, TP53 mutations are associated with poorer prognosis, higher tumor grade, and increased resistance to conventional therapies. Studies, such as those conducted by Olivier et al. have emphasized the significance of TP53 mutations in influencing the clinical behavior of various cancers, including breast cancer.

Additionally, TP53 mutations are linked to distinct molecular subtypes of breast cancer. The Cancer Genome Atlas (TCGA) Network's comprehensive molecular portraits of breast tumors revealed that TP53 mutations are more prevalent in basal-like and HER2-enriched subtypes, which are often associated with a more aggressive clinical course [20]. Furthermore, the presence of TP53 mutations may influence treatment decisions. While tumors with TP53 mutations may exhibit resistance to certain chemotherapy regimens, ongoing research is exploring targeted therapeutic approaches for cancers harboring TP53 mutations. Understanding the TP53 mutational status allows for a more personalized and tailored approach to treatment, taking into consideration the unique genetic characteristics of the tumor [20].

TP53 mutation testing is a critical component of breast cancer diagnostics, providing essential information about the genetic makeup of tumors and influencing prognostic assessments and treatment decisions. As our understanding of the role of TP53 mutations in breast cancer continues to evolve, the integration of TP53 testing into routine clinical practice holds promise for refining risk stratification and optimizing therapeutic strategies for patients with breast cancer [19,20].

Result and Discussion

Breast cancer is a complex and heterogeneous disease, necessitating advanced molecular testing for accurate diagnosis, prognosis, and treatment decisions. In recent years, various molecular tests have been developed to analyze the genomic landscape of breast tumors. This discussion focuses on key molecular tests, including Oncotype DX, MammaPrint, PIK3CA mutation testing, and TP53 mutation testing, highlighting their significance in breast cancer management.

Oncotype DX

Oncotype DX, a gene expression assay, provides a recurrence score (RS) that aids in predicting the risk of disease recurrence and guiding chemotherapy decisions for hormone receptor-positive, HER2-negative breast cancer. The landmark study by Paik et al. demonstrated the clinical utility of Oncotype DX, influencing treatment decisions and reducing unnecessary chemotherapy use in low-risk patients [20].

MammaPrint

MammaPrint, a 70-gene expression assay, categorizes tumors into high or low risk of recurrence. The MINDACT trial by Cardoso et al. showed that MammaPrint results can help identify patients who may safely forego chemotherapy, contributing to a more personalized approach to breast cancer treatment [20].

PIK3CA mutation testing

PIK3CA mutations, common in hormone receptor-positive breast cancers, activate the PI3K pathway, influencing prognosis and treatment response. Saal et al. found correlations between PIK3CA mutations and hormone receptors, nodal metastasis, and HER2 expression. PIK3CA mutation testing has become crucial for identifying patients who may benefit from targeted therapies inhibiting the PI3K pathway [21].

TP53 mutation testing

TP53 mutations, associated with aggressive tumor behavior and resistance to treatment, play a significant role in breast cancer prognosis. Studies, including Olivier et al. highlight the diverse consequences of TP53 mutations in various cancers, influencing clinical outcomes. TP53 mutation testing guides treatment decisions, allowing for more personalized approaches and consideration of targeted therapies [21].

Recent statistics underscore the impact of molecular testing on breast cancer management. According to a study by Tung et al. multigene panel testing, including genes like BRCA1, BRCA2, and others, identified clinically significant mutations in breast cancer patients. The integration of multigene panel testing into clinical practice has increased the identification of hereditary cancer predisposition, informing risk management and prevention strategies [21].

In a study by Kurian et al. germline multiple-gene sequencing results influenced breast and ovarian cancer penetrance estimates in women. This emphasizes the role of comprehensive genetic testing in understanding hereditary risk and making informed decisions about preventive measures [21].

Furthermore, the comprehensive molecular portraits of breast tumors from the Cancer Genome Atlas (TCGA) Network (2012) revealed the prevalence of specific mutations in various molecular subtypes. This genomic characterization forms the basis for targeted therapies, improving treatment efficacy and outcomes [22].

Molecular testing has significantly advanced our understanding of breast cancer, enabling a more precise and personalized approach to diagnosis and treatment. Oncotype DX and MammaPrint aid in risk stratification and guide chemotherapy decisions, reducing unnecessary treatments.

PIK3CA and TP53 mutation testing provide insights into tumor biology, influencing prognosis and treatment strategies.

Statistics from studies highlight the real-world impact of molecular testing, identifying hereditary mutations and guiding risk management decisions. As molecular testing technologies evolve, their integration into routine clinical practice holds promise for further improving breast cancer outcomes, minimizing overtreatment, and optimizing targeted therapeutic approaches. The molecular insights garnered from these tests contribute to the ongoing progress in the era of precision medicine for breast cancer.

Future roadmap

The future roadmap of molecular testing for breast cancer is poised to witness significant advancements, driven by ongoing research, technological innovations, and a growing understanding of the complex molecular landscape of breast tumors. Several key trends are anticipated to shape the future of molecular testing in breast cancer.

Integration of multi-omics approaches

Future molecular testing is expected to move beyond individual gene assessments, incorporating multi-omics approaches such as genomics, transcriptomics, proteomics, and metabolomics. Comprehensive analyses of the entire molecular profile of tumors will provide a more holistic understanding of the disease, enabling more accurate diagnosis, prognosis, and targeted treatment strategies [22].

Liquid biopsies and circulating biomarkers

The utilization of liquid biopsies, particularly the analysis of circulating tumor DNA (ctDNA) and other circulating biomarkers, is a promising avenue. Liquid biopsies offer a non-invasive means to monitor disease progression, detect minimal residual disease, and identify emerging genetic alterations, providing real-time information about the dynamic nature of breast cancer [23].

Artificial intelligence (AI) and machine learning

Advancements in artificial intelligence and machine learning algorithms will play a pivotal role in data interpretation and pattern recognition. These technologies will enhance the accuracy and efficiency of molecular testing, aiding in the identification of subtle genetic variations and the prediction of treatment responses based on complex datasets [24].

Incorporation of functional genomics

Functional genomics, exploring the functional consequences of genetic alterations, will gain prominence. Understanding how specific mutations impact cellular processes and response to treatments will facilitate the development of more targeted and effective therapies [25].

Real-world evidence and population genomics

The integration of real-world evidence, including data from diverse populations, will be crucial for ensuring the broad applicability of molecular testing. Population genomics initiatives will contribute to a more comprehensive understanding of genetic variations across different ethnicities, enabling more equitable and personalized healthcare strategies [25].

Conclusion

Molecular testing has greatly helped the knowledge, diagnosis, and management of breast cancer. By identifying important genetic mutations, including those in BRCA1 and BRCA2, and estimating hormone receptor and HER2 status, these tests allow healthcare providers to adapt treatment plans for each patient. Innovations such as NGS and liquid biopsies have increased the capacity to identify genetic changes and track disease advancement in real-time, leading to more tailored and efficient treatments. As advancements progress, molecular testing will keep influencing the future of breast cancer treatment, providing hope for more targeted, less invasive, and highly efficient options, ultimately enhancing patient outcomes.

Disclosure statement

No potential conflict of interest was reported by the authors.

References

1. Ferlay J, Colombet M, Soerjomataram I, Mathers C, Parkin DM, Piñeros M, et al. Estimating the global cancer incidence and mortality in 2018: GLOBOCAN sources and methods. *Int J Cancer*. 2019;144(8):1941-1953. <https://doi.org/10.1002/ijc.31937>
2. DeSantis CE, Ma J, Gaudet MM, Newman LA, Miller KD, Goding Sauer A, et al. Breast cancer statistics, 2019. *CA Cancer J Clin*. 2019 ;69(6):438-451. <https://doi.org/10.3322/caac.21583>
3. Murtaza M, Dawson SJ, Tsui DW, Gale D, Forshew T, Piskorz AM, et al. Non-invasive analysis of acquired resistance to cancer therapy by sequencing of plasma DNA. *Nat*. 2013;497(7447):108-112. <https://doi.org/10.1038/nature12065>
4. Lefebvre C, Bachelot T, Filleron T, Pedrero M, Campone M, Soria JC, et al. Mutational profile of metastatic breast cancers: a retrospective analysis. *PLoS Med*. 2016;13(12):e1002201. <https://doi.org/10.1371/journal.pmed.1002201>
5. Perou CM, Sørlie T, Eisen MB, Van De Rijn M, Jeffrey SS, et al. Molecular portraits of human breast tumours. *Nat*. 2000;406(6797):747-752. <https://doi.org/10.1038/35021093>
6. Slamon DJ, Leyland-Jones B, Shak S, Fuchs H, Paton V, Bajamonde A, et al. Use of chemotherapy plus a monoclonal antibody against HER2 for metastatic breast cancer that overexpresses HER2. *N Engl J Med*. 2001;344(11):783-792. <https://doi.org/10.1056/NEJM200103153441101>
7. Slamon DJ, Clark GM, Wong SG, Levin WJ, Ullrich A, McGuire WL. Human breast cancer: correlation of relapse and survival with amplification of the HER-2/neu oncogene. *science*. 1987;235(4785):177-182. <https://doi.org/10.1126/science.3798106>
8. Wolff AC, Hammond ME, Allison KH, Harvey BE, Mangu PB, Bartlett JM, et al. Human epidermal growth factor receptor 2 testing in breast cancer: American Society of Clinical Oncology/College of American Pathologists clinical practice guideline focused update. *Arch Pathol Lab*. 2018;142(11):1364-1382. <https://doi.org/10.5858/arpa.2018-0902-SA>
9. Allred DC, Brown P, Medina D. The origins of estrogen receptor alpha-positive and estrogen receptor alpha negative human breast cancer. *Breast Cancer Res*. 2004; 6:1-6. <https://doi.org/10.1186/bcr938>
10. Hammond ME, Hayes DF, Dowsett M, Allred DC, Hagerty KL, Badve S, et al. American Society of Clinical Oncology/College of American Pathologists guideline recommendations for immunohistochemical testing of estrogen and progesterone receptors in breast cancer. *J Clin Oncol*. 2010;28(16):2784-2795. <https://doi.org/10.1200/JCO.2009.25.6529>
11. Miki Y, Swensen J, Shattuck-Eidens D, Futreal PA, Harshman K, Tavtigian S, et al. A strong candidate for the breast and ovarian cancer susceptibility gene BRCA1. *Science*. 1994;266(5182):66-71. <https://doi.org/10.1126/science.7545954>
12. Wooster R, Bignell G, Lancaster J, Swift S, Seal S, Mangion J, et al. Identification of the breast cancer susceptibility gene BRCA2. *Nat*.

- 1995 D;378(6559):789-792. <https://doi.org/10.1038/378789a0>
13. Tung N, Battelli C, Allen B, Kaldate R, Bhatnagar S, Bowles K, et al. Frequency of mutations in individuals with breast cancer referred for BRCA 1 and BRCA 2 testing using next-generation sequencing with a 25-gene panel. *Cancer*. 2015;121(1):25-33. <https://doi.org/10.1002/cncr.29010>
 14. Kurian AW, Hughes E, Handorf EA, Gutin A, Allen B, Hartman AR, et al. Breast and ovarian cancer penetrance estimates derived from germline multiple-gene sequencing results in women. *JCO Precis Oncol*. 2017; 1:1-2. <https://doi.org/10.1200/PO.16.00066>
 15. Paik S, Shak S, Tang G, Kim C, Baker J, Cronin M, et al. A multigene assay to predict recurrence of tamoxifen treated, node negative breast cancer. *N Engl J Med*. 2004;351(27):2817-2826. <https://doi.org/10.1056/NEJMoa041588>
 16. Cardoso F, van't Veer LJ, Bogaerts J, Slaets L, Viale G, Delaloge S, et al. 70-gene signature as an aid to treatment decisions in early stage breast cancer. *N Engl J Med*. 2016;375(8):717-729. <https://doi.org/10.1056/NEJMoa1602253>
 17. Saal LH, Holm K, Maurer M, Memeo L, Su T, Wang X, et al. PIK3CA mutations correlate with hormone receptors, node metastasis, and ERBB2, and are mutually exclusive with PTEN loss in human breast carcinoma. *Cancer Res*. 2005;65(7):2554-2559. [https://doi.org/10.1158/0008-5472-CAN-04-3913](https://doi.org/10.1158/0008-5472.CAN-04-3913)
 18. Cancer Genome Atlas Network. Comprehensive molecular portraits of human breast tumours. *Nat*. 2012;490(7418):61-70.
 19. Olivier M, Hollstein M, Hainaut P. TP53 mutations in human cancers: origins, consequences, and clinical use. *Cold Spring Harb Perspect Biol*. 2010;2(1):a001008. <https://doi.org/10.1056/NEJMoa041588>
 20. Paik S, Shak S, Tang G, Kim C, Baker J, Cronin M, et al. A multigene assay to predict recurrence of tamoxifen treated, node negative breast cancer. *N Engl J Med*. 2004;351(27):2817- 2826. <https://doi.org/10.1056/NEJMoa041588>
 21. Kurian AW, Li Y, Hamilton AS, Ward KC, Hawley ST, Morrow M, et al. Gaps in incorporating germline genetic testing into treatment decision-making for early-stage breast cancer. *J Clin Oncol*. 2017;35(20):2232-2239. <https://doi.org/10.1200/JCO.2016.71.6480>
 22. Chaudhary K, Poirion OB, Lu L, Garmire LX. Deep learning-based multi-omics integration robustly predicts survival in liver cancer. *Clin Cancer Res*. 2018;24(6):1248-1259. <https://doi.org/10.1158/1078-0432.CCR-17-0853>
 23. Siravegna G, Marsoni S, Siena S, Bardelli A. Integrating liquid biopsies into the management of cancer. *Nat Rev Clin Oncol*. 2017;14(9):531-548. <https://doi.org/10.1038/nrclinonc.2017.14>
 24. Litton JK, Rugo HS, Ettl J, Hurvitz SA, Gonçalves A, Lee KH, et al. Talazoparib in patients with advanced breast cancer and a germline BRCA mutation. *N Engl J Med*. 2018;379(8):753-763. <https://doi.org/10.1056/NEJMoa1802905>
 25. Hoadley KA, Yau C, Hinoue T, Wolf DM, Lazar AJ, Drill E, et al. Cell-of-origin patterns dominate the molecular classification of 10,000 tumors from 33 types of cancer. *Cell*. 2018;173(2):291-304.