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NGS-DRIVEN MUTATION PROFILING IN BREAST CANCER: BRIDGING THE GAP BETWEEN REAL-WORLD DATA AND PERSONALIZED THERAPY

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Abstract *Next-generation sequencing (NGS) has emerged as a revolutionary weapon in oncology, particularly in breast cancer, enabling precise mutant profiles and the evolution of individualized treatment systems. NGS-based mutant profiling in breast cancer, contributing to the development of a better understanding of familial variations and their results in clinical practice. The NGS makes it possible to call multiple genetic variations, including the well-known BRCA1/2 gene, as well as a fresh variation that may influence the curative response. Despite its constancy, there are still several impediments to NGS integration into routine clinical practice, including data interpretation, cost, ease of use, and insufficient standard protocols. It is necessary to validate NGS results and translate them into capable, personalized treatment, hands-on statistics, and clinical trials. Reverence must also be accorded to the fair results of family testing, in particular about incidental consequences. To ensure that all patients benefit from the personalized therapy, the future of NGS in breast cancer lies in exultant these problems and improving productivity. NGS is capable of redefining breast cancer medicines, providing a powerful, target therapy based on human characteristics.*

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Introduction

The prevalence of breast cancer as a cancer-related cause of death is high across the globe. Patients outcomes have been significantly improved by conventional treatment modalities, including surgery, chemotherapy, radiation, and targeted therapy. Still, breast cancer molecular complexity demands a more sophisticated method of selecting treatment. Next-generation sequencing (NGS) provides a complete family profile, the detection of a body mutant, the variation in transcript size, and gene fusion that initiates tumor progression (Moorcraft *et al*., 2015; Pereira *et al*., 2020). By integrating objective data (RWD) with NGS data, a personalized treatment plan for breast cancer can be optimized. Next-generation sequencing (NGS), allows high-throughput surveys of inheritable mutants, supplies perceptions of tumor heterogeneity, and directs personalized treatment for breast cancer (D'Argenio *et al*., 2015). As cancer genomics progresses, NGS's role in determining major ancestral variations in breast cancer is becoming more and more necessary for a personalized treatment strategy (Karlovich & Williams, 2019). Together with advances in NGS, clinicians are quick to identify the mutants of the estrogen receptor, HER2, and other major genes that contribute to the progression of breast cancer and curative resistance (Morash *et al*., 2018). The real-world data (RWD) deduced from the clinical environment is important for understanding how means such as familial transformation therapy affect and tolerant prognosis (Rajkumar *et al*., 2015). Despite the increasing utility of genomic information, the integration of related findings into clinical decision-making remains a challenge (Horgan *et al*., 2024). The progress of personalized therapy, as well as of the target ESR1 mutant, also known as the HER2 mutant, has shown the capacity of the NGS-driven mutant profile to inform treatment options (Kaur *et al*., 2013). There is a gap between the introduction of NGS in the laboratory and its use in the real world, together with several obstacles blocking proficient translation (Mardis, 2019). As NGS has become a mandatory

grouping of personalized medicine, understanding the complexities of breast cancer genomics and the use of put-into-practice intelligence in clinical practice are of paramount importance (Morganti *et al*., 2019). The following evaluation will be devoted to the latest development in terms of the mutant profiling based on NGS in breast cancer, with emphasis on the incorporation of the existing information into clinical practice and personalized therapy (Figure 1).

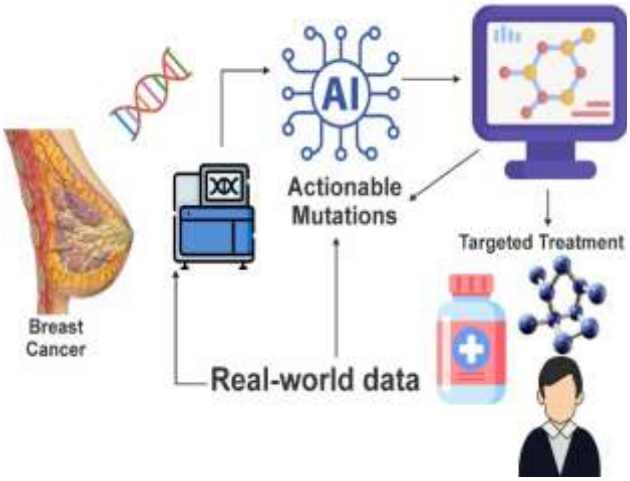

Figure 1: NGS-based mutation profiling in breast cancer, linking real-world genomic data to personalized therapy. The workflow emphasizes mutation detection, clinical interpretation, and targeted treatment selection

Breast Cancer Mutation Profiling with NGS

The NGS has emerged as a central device to recognize central ancestral mutations in breast cancer, including mutations in TP53, PIK3CA, BRCA1/2, ESR1, ERBB2, and AKT1 (Centers for Medicare assistance, 2018). These mutants are linked with various forms of breast cancer and their remedial effects on them. For instance, PIK3CA mutants are frequently detected in hormone receptor-positive (HR+) breast cancer and predict response to PI3K inhibitor alpelisib. In addition to it, the BRCA1/2 mutant predetermines the patient before the PARP inhibitor olaparib helps the patient. The comparison of unique genes over the same time and the de-mystification of oncology would become easy with the help of NGS. Next-generation sequencing (NGS) has significantly changed the environment for molecular studies in breast cancer and provides a unique capability for determining the familial mutations underlying tumorigenesis and treatment resistance. As NGS is used more and more in clinical practice, it has evolved into a key tool for mutant profiling facilitating personalized treatment plans for breast cancer patients (Massard *et al*., 2017; Bidard *et al*., 2022).

Genomics and important mutations in Breast cancer

Breast cancer is possible to be genetically heterogeneous, and different molecular subtypes might have varying profiles of the mutants. The BRCA1 and BRCA2 genes, which are related to family breast cancer susceptibility, are among the most well-known genetic variations in breast cancer (Kim *et al*., 2015). A non-hereditary mutant of an alternative gene, such as PIK3CA, TP53, ESR1, and HER2, has been implicated in tumor progression and curative responses (Suh *et al*., 2022). The appellation of the aforementioned mutant employing NGS confers the ability to classify breast cancer within molecular subtypes such as luminal A, luminal B, HER2-positive, and triple-negative individuals of the patients involved in a specific curative technique (Kwon *et al*., 2019). For instance, a HER2-positive breast tumor has a body mutant that directs its overexpression of the HER2 protein, which initiates tumorigenesis and makes the tumor more prone to HER2-targeted therapy such as trastuzumab and trastuzumab deruxtecan (Mosele *et al*., 2020). Similarly, resistance to endocrine therapy, including an aromatase inhibitor, and the value of resolving the current mutant for projecting curative responses (Sung *et al*., 2021).

Breast Cancer Mutation Profiling Technological Advancements

Among NGS breakthroughs, genome and exome sequencing, target gene panel, and full mutant profiling are observed in breast cancer. Such structures facilitate the detection of a broad range of familial changes, including individual nucleotide variation, insertion and omission, transcript overall variation, and administrative changes, in equally coded and non-coded regions of the genome (Park *et al*., 2019). The use of NGS in clinical oncology has been rapid, alongside the introduction of targeted panels targeting genes that are particularly relevant to breast cancer, such as BRCA1, BRCA2, PIK3CA, TP53, and ESR1 (Krzyszczyk *et al*., 2018). The panels mentioned above, although high-throughput statistics are important for the designation of clinically connected mutants (Gagan & Van Allen, 2015). The development of bioinformatics devices has significantly improved the sensitivity and correctness of mutant detection, e.g. for the detection of rare divergences that cannot be detected by standard sequencers (Shin, Bode, & Dong, 2017; Marabelle *et al*., 2020).

Clinical Decision-Making NGS

The implementation of NGS outcomes in clinical care has changed the pattern of breast cancer regulations, as now they specify the options and estimates of the affordable outcomes. For instance, the detection of the PIK3CA mutant that is common in luminal breast cancer is guided by the blessing of targeted therapy, such as alpelisib, in patients with advanced diseases (Di Resta *et al*., 2018). Similarly, the use of NGS to identify ESR1 mutants stimulates the growth of selective estrogen receptor degraders (SERDs), similar to elacestrant, which can overcome resistance to conventional hormone therapy in ER-positive breast cancer (Qin, 2019). That is particularly important for triple-negative breast cancer (TNBC),

which lacks estradiol, progesterone, and the HER2 receptor and is regularly associated with poor prognosis. Recently, a study has shown that the TNBC tumor, together with the high number of tumor mutations (TMB), may benefit from the immune checkpoint inhibitor pembrolizumab (Moscow *et al*., 2018). The clinician can decide to select a fitting immunotherapy treatment on the basis of NGS that will enhance the clinical outcome. Despite the potential of NGS as an option to identify breast cancer mutants, this approach has several challenges to its clinical use. The difficulty in interpreting the large summaries of NGS data produced, specifically at the time managing alongside a discrepancy of uncertain significance (Buermans & den Dunnen, 2014; Schmid *et al*., 2018). Although NGS can identify mutants within the entire genome, the clinical role of the patched mutant residues whose nay is not widely adopted in academic writings needs to be more discoveries to enhance their role in tumorigenesis and resistance to treatments. While clinical trials have demonstrated the effectiveness of NGS-based therapy, translation of the above-mentioned outcomes into normal clinical contexts requires solving problems related to cost, convenience, and physician expertise (Modi *et al*., 2020). As NGS devices are simple, that's why any patient could be diagnosed and treated with the help of those devices, and would obtain more personalized and accurate treatment.

Real World Data and its Role in Precision Medicine Driven by NGS

Objective statistics (RWD), defined as health-related statistics gathered from different sources outside traditional clinical tests, have emerged as a key element in driving accurate medicine. RWD provides essential details on how inherited mutants and their associated treatments work in different tolerant groups of oncology in individuals using next-generation sequencing (Hess *et al*., 2020). The integration of RWD into NGS-driven corrective medicines may continue to be a crucial element in the design of personalized cancer therapy, providing clinicians and scientists with admirable information that bridges the gap between controlled clinical trials and the commonly tolerated social mandate (Radovich *et al*., 2016; Sparano *et al*., 2018).

Oncology and the Value of Real-World Data

In oncology, real-world evidence (RWE) derived from RWD has become an increasingly important tool for knowledge on treatment efficacy beyond clinical trials. Clinical trials, although crucial, commonly have strict inclusion and rejection standards that do not necessarily reflect the diversity of the long cohorts encountered in routine clinical practice (Zheng *et al*., 2020). Professionals and clinicians can get a more accurate picture of how therapy works in practice by using RWD, including a long-term register, an electronic vitality file, and a claim (Amin *et al*., 2017). Currently, the issue is especially vital to oncological treatment, as the success of the treatment depends on the personal strategies.

NGS and Combination of Real-world Data

NGS ought to form one of the key points in restorative medication, which would enable widespread mutant malignancies. NGS also allows an individualized approach to treatment relying on the molecular properties of the subsequent human tumor. As clinical trials indicate the efficacy of NGS-based therapy inferior to the control state, RWD provides a unique situation, revealing how this treatment works in several, hands-on tolerant inhabitants alongside changing comorbidities and care histories (Pereira *et al*., 2016). In the recent past, it has been suggested that integrated RFID could speed up and confirm the findings of the clinical trials. For instance, the use of NGS in breast cancer has shown that the appellation of potential variants such as BRCA1, BRCA2, and PIK3CA significantly influences treatment decisions, including the use of targeted therapy (Wang *et al*., 2017). The RWD will probably penetrate the potency and safety of the treatment into the greater, more diverse group for long-term patients who cannot be depicted in clinical trials. RWD can provide crucial information on how patients with rare mutants or those with coincident fortune react to therapy which is effective in trials (Piccart *et al*., 2021).

Real-World Data in precision medicine driven by NGS

1-Validation of Tumor Mutational Burden (TMB)

Location of a person where RWD is gradually being used for validation of tumor mutational burden (TMB) as a biomarker for predicting response to immunotherapy. TMB has been shown in clinical trials to correlate with increased responses to immune checkpoint inhibitors such as pembrolizumab in various malignancies, including NSCLC and melanoma (Bidard *et al*., 2022). The use of TMB as an anticipatory biomarker has been tested in all aspects of analysis so far. A recent analysis based on RWD suggests that TMB can continue to be a reliable predictor of immunotherapy efficacy in a wide range of alternative and other diverse societies, facilitating its use in clinical practice (Marabelle *et al*., 2020).

2- Mutational Hotspot and Novel Mutation Evaluation

Besides, it is supposed that RWD will be utilized in the case of tracking mutational hot spots and in the case of identifying new mutants still being represented in clinical trials. For instance, PIK3CA mutants commonly found in breast cancer are capable of remaining in clinical trials and are associated with a target therapy analogous to alpelisib (Barroso-Sousa *et al*., 2020). RWD among various survivor cohorts can be replaced with new capacity biomarkers that are likely to choose drugs to be used in a society with overwhelming amounts. The given facts can still be instrumental in demonstrating the work of medicines in rare types of breast cancer or in patients, who have shown a lack of success in the standard treatment.

3-Real Life Efficacy to Targeted Agents

Where RWD plays a critical role, there ought to be another location where the target treatment is founded on NGS outcomes. Target therapy, also known as HER2-targeted therapy in HER2-positive breast cancer, has been shown to significantly improve the clinical outcome (Winer *et al*., 2020). But real-time performance of these treatments may not be the same because there are factors that may be similar to attention attachment, comorbidities, and other factors particular to the patient. By analyzing RWD in countless persevering societies, scientists can identify components that probably lead to the success or failure of targeted therapy and provide complete information on their clinical use (McNulty *et al*., 2019).

4-Remedial resistance and overview

Resistance to the treatment of cancer is one of the greatest problems in cancer treatment. The ESR1 mutant systemically drives resistance to hormonal therapy, such as estradiol and aromatase inhibitors, in the context of breast cancer. RWD has the potential to be significantly involved in the continuous observation of the progress of a mutant in the actual span and tracking the strength of the future therapeutic. For instance, Modi *et al.* (2020) found that the ESR1 mutant is associated with resistance to aromatase inhibitors in the used background, highlighting the importance of integrating NGS-based mutant profile into the usual clinical considerations for steerage options and proctor resistance structures.

Obstacles and Shortcomings of Real-world Data

Although considerable progress has been achieved in the integration of RWD in the NGS-based corrective medicines, there are a few obstacles. Among the key drawbacks of the RWD, one may note the fact of the capability and completeness of customization of the vehicle. Unlike information from controlled clinical trials, RWD may be heterogeneous, with incompatibilities in data collection procedures, tolerant demographics, and medication regimens (Sparano *et al*., 2018). In addition, the presence of confusing factors analogous to comorbidities which may influence the effects of the medicinal product may complicate the interpretation of RWD (Shin *et al*., 2020). One should take into consideration the ethical and workable barriers to the application of RWD in clinical diagnosis. It is essential to ensure patient confidentiality and to obtain well-informed consent to use EHR knowledge in investigations to support boldness in medical practice (Giaquinto *et al*., 2022).

The Presentations on Translating NGS into Clinical Practice

Next-generation sequencing (NGS), which enables a thorough examination of organic heterogeneity in cancer, including breast cancer, has resurrected the correct medicine plot. The NGS's promise lies in its competence to identify sensitive mutants and draw up human curative verdicts. The actual translation of NGS results into routine practice, has multiple challenges. These obstacles range from technical limitations to moral and logistical obstacles which make it difficult to integrate NGS into common oncological techniques (Centers for Medicare & Medicaid Services [CMS], 2018).

Technical and analytical Problems

One of the challenges of converting NGS decisions into clinical practice is the challenge of studying facts. The NGS produces an enormous quantity of genomics information that must be methodized and interpreted using high-tech bioinformatics equipment. Categorized in a very large number of mutants not all of which are clinically significant. In breast cancer, for instance, the NGS analysis shows that PIK3CA and AKT1 genes probably have definite clinical protocols for their curative use (Martinez-Martin & Magnus, 2019). Lack of a comprehensive database linking mutants with clinical implications could also make interpretation of the beyond decision worse. The issue of adequately extrapolating the practical effect of the new mutant poses more impediments. There are probably several NGS mutants with unknown pathogenicity in this region and their role in the progression of the disease otherwise in response to thoughtlessness leftovers is not effectively specified (Pereira, Oliveira, & Sousa, 2020). The presence of rare mutants in certain breast cancer subtypes is frequently missing the supporting details needed to develop an effective medicine protocol (Modi *et al*., 2020). The uncertainty that drives the current state asserts doubt on the trustworthiness of NGS information to be applied to clinical practice and requires an upgraded and more exhaustive mutant database and improved methods of forecasting the effects of a mutant.

Expense and Availability Problems

Another helpful aspect in hindering the clinical prevailing penetration of NGS tools is its expensive innovations. Although the monetary value of sequence ownership has decreased significantly over the past decade, NGS residues are expensive, particularly during an era when it is necessary to employ specialized equipment, reagents, and skilled staff for fact confirmation (Tsimberidou *et al*., 2012). The financial acquisition of NGS in the clinical setting might limit its functionality, especially within a low-resource environment. Consequently, there is frequently a disparity between the use of NGS-based trials in the setting of study centers and community hospitals. Such an imbalance in admission can create conflicting stands of focus as only some forbearing localities would get the advantage of NGS-based corrective administration. The downstream costs related to ancestral support, continuous monitoring, and the use of possibly a mutant may also increase the overall cost of care (Schmid *et al*., 2018) as the costs of the sequence themselves are reduced. Such a tax burden is likely to deter those involved in healthcare aid provision from incorporating NGS in their clinical

practice although they can compensate those who remain consistent in their endeavors.

Regulatory and Ethical Values

The capacity of administration and ethical property, and increment in the presence of NGS in clinical practice. One of the greatest issues is the absence of definite information of the clinical application of some of the familial findings. Some mutants, such as the BRCA gene, exhibit curative effects (e.g., PARP inhibitors for breast cancer with a BRCA mutation), and several option mutants need more clarity (Goodwin *et al*., 2016). This brings about confusion to the clinicians at the point when they make decisions on the top of an otherwise informed choice of medicine purely due to inheritable test results. On the same note, the ancestral test morality is valuable. Since NGS discloses the whole range of changes in the family, some of which bear unknown clinical importance, there is apprehension regarding the degree of information that is available to patients. NGS may reveal a random decision related to cancer diagnosis, similar to a mutant linked together with a different inheritable state (Drilon *et al*., 2017). The patient might not always be prepared to be receiving such details and this would raise questions about possible psychological impacts of such news that would probably change lives of the patient in that it does not have any noticeable pathway. When ancestors' data are collected and shared, a privacy panic develops. To ensure the safety of the patients and make it possible to use of physiologic specimens in the process of finding facts, it is a sensitive issue that necessitates the creation of strong permissible and administrative provisions. The use of genital information in clinical determination has also been subject to increasing questions about the duration of treatment and the possibility of familial intolerance (Consortium, 2017).

Clinical Standardization and Implementation

Another barrier to implementing NGS decisions in clinical practice is the necessity to have a unified process of both familial testing and statistical interpretation. Currently, there is a need for a fundamental change in the procedures used by individual laboratories to sequence and analyze inherited statistics (Levy & Myers, 2016). This standardization requirement makes it hard to compare results across institutions and predict the incompatibilities along with reasonable recommendation that can be done in a family discovering way. Increasingly stricitious clinical protocols on use of NGS-based therapy are on the rise. Although the exact mutants, such as HER2 and BRCA, have been successfully repaired, the assorted mutants found through NGS do not have a universally accepted curative approach (Calistri & Palù, 2015). This misconception is undermining the ability of NGS to be utilized in routine clinical thinking since the doctors are likely to be vague in their quest to obtain credible results.

Integration and Generation of Evidence through clinical Trials

Since NGS has recently been involved in enhancing personalized therapy strategies, its actualization into clinical practice is further impeded by a limited number of clinical trial evidence of the curative efficacy of target-specific mutants in routine care. Even though a few of the mutants detected by NGS themselves have not been thoroughly tested in large, randomized clinical trials (West, 2016). Through this, there has emerged a need of good signals being linked with the comprehensive mutant equation towards getting improved clinical outcomes after a targeted counteraction. To address the current space, there is a need to conduct more clinical experiments along with the priority granted to the personalized medical treatments offered by NGS. These trials should include many tolerant communities as well as stratification based on family characteristics to initiate a principally effective treatment for a specific type of cancer (Finn *et al*., 2015). Doctors can be hesitant to employ NGS-guided therapy until the next motif is available as it has no guarantees in regard to the advantages of the treatment.

Table 1: Summary of key studies on next-generation sequencing (NGS) in breast cancer

Study	Research Question (RQ)	Participants (Sample Size & Type)	Breast Cancer Type (Familial or Not)	Findings (History & Investigations)	Limitations	MMAT Score (out of 5)
Morash *et al*., (2018)	Integration of NGS into oncology	Secondary review	Not specified	Application of NGS in clinical workflows	Lacks empirical data	4
Martinez-Martin & Magnus, (2019)	Ethical issues in clinical genomics	Bioethical analysis	Not applicable	Privacy, incidental findings, consent	No primary data	3
Suh *et al*., (2022)	NGS applications in real-world breast cancer	143 patients	Both familial and sporadic	Mutation profiling using NGS	Single-center; selection bias	5

Morganti *et al.*, (2019)	NGS in clinical implementation	Review across studies	Mixed	Clinical and logistical challenges	Non-empirical	3
Horgan *et al.*, (2024)	Implementation gap of NGS	Stakeholder analysis	Not defined	Barriers in policy/system	Lacks patient-level data	3
Modi *et al.*, (2020)	Efficacy of HER2-targeted therapy	184 HER2+ patients	Likely sporadic	Clinical response to trastuzumab deruxtecan	Phase 2; limited follow-up	5
Gagan & Van Allen, (2015)	Can NGS guide treatment?	Literature synthesis	Not specified	Impact of NGS in oncology	Review article	4
Rajkumar *et al.*, (2015)	Utility of gene panels in Indian women	South Indian breast/ovarian patients	Familial	Improved mutation detection	Population-specific	5
Barroso-Sousa *et al.*, (2020)	High TMB in breast cancer	Data from TMB cohorts	Mixed	Prediction of immunotherapy response	Cohort-based; focused	4
Shin *et al.*, (2020)	Hereditary mutations in breast cancer	Panel-tested patients	Familial	Germline mutations characterized	Panel-limited scope	4
McNulty *et al.*, (2019)	Polymorphism filtering in tumor sequencing	Bioinformatics analysis	Not specific	Technical optimization	Lacks clinical correlation	3
Bacher *et al.*, (2018)	NGS in myeloid malignancy	Patients with hematologic disorders	Not applicable	Diagnostic limitations of NGS	Not focused on breast cancer	3
Calistri & PalÃi, (2015)	Bias in NGS discovery	Review article	Not specified	Unbiased sequencing commentary	Opinion-based	3
Kanzi *et al.*, (2020)	Inheritance pattern via NGS	Genomic inheritance analysis	Familial	Inheritance and mutation calls	No clinical data	4
Tsimberidou *et al.*, (2012)	Early personalized medicine trials	Patients in phase I trials	Sporadic	NGS integrated into trial protocols	Early phase design	4
Mosele *et al.*, (2020)	ESMO NGS recommendations	Guidelines from panel	Mixed	NGS utility standards	Consensus-based	4
Park *et al.*, (2019)	ER+ tumors in young women	Young breast cancer patients	Not defined	NGS profiles of molecular clusters	Age-specific group	4
Winer *et al.*, (2020)	TMB and pembrolizumab in TNBC	TNBC patients in trial	Triple-negative	TMB as a predictive biomarker	Limited subgroup analysis	4
Toy *et al.*, (2013)	ESR1 mutations in resistant cancer	Patients with hormone resistance	Sporadic	ESR1 LBD mutations	No intervention outcomes	4
Piccart *et al.*, (2021)	Use of 70-gene signature	MINDACT cohort	Mixed	Improved decision making	Resource-heavy method	5

Future Prospects

The potential of reshaping the treatment of breast cancer is immense as the NGS-based mutant profile has started to increase. Some major areas will require the enhancement in the use and combination of NGS in matters of breast cancer.

1. The ability to interpret large amounts of data analyzed by the NGS will be one of the most promising spheres of the future ages identity, and the development of bioinformatics is a specific tool and methodology. To fulfill a crucial responsibility in advancing the interpretation of mutants, and plausible, progress in machine intelligence (machine

acumen) and ML (machine learning), it will be necessary to assist clinicians in resolving clinically linked mutant excess precisely. The accuracy of clinical advice will be enhanced by the development of a complete database on all mutants that combine ancestral changes with clinical outcomes (Finn *et al*., 2015). Since the excess mutant is confirmed by clinical trials, we can expect clear clinical recommendations for a wider range of ancestral variations; nay is not used in academic writing for only a well-known discrepancy similar to BRCA1/2 (Kwon *et al*., 2019).

2. With the further advances of sequence techniques, the financial space of dimension is likely to acquire NGS additional low-value medical assistive support and patients. Efforts to simplify the administration structure and develop cost-effective test procedures will facilitate the widespread use of NGS therapy, particularly in resource-limited environments (Park *et al*., 2019). This would make it easier to introduce clear medicines and the patient would be benefited even further by being offered personalized treatment for cancer.

3. The processes of standardizing the NGS trial process and aligning intelligence interpretation recommendations across borders will continue to be necessary to progress. The introduction of regulations that will be similar to the FDA and the EMA will prove necessary in order to have a more pronounced model to help create a health-certain and safe practice in the implementation of NGS in clinical practice (Kanzi *et al*., 2020).

4. Molecular profiling will offer a very sound indication of as how effective the targeted therapy of a specific familial mutant identified by NGS will be as part of a clinical trial. To confirm the clinical utility of NGS-guided therapy and to investigate the promise of a novel curative compound target, Large-scale, multicenter studies will be necessary (Levy & Myers, 2016; Hess *et al*., 2020). Since NGS is gradually gaining its position as a routine element of clinical oncology, the aspect of the clinical trials involvement in the availability of being granted validated personalized treatment will be effective in the evolvement of the choice of treatment to patients with breast cancer, and other afflictions along with other afflictions.

5. As a promise, there is the need to come to terms with the positive side and the psychological side of familial testing as NGS is increasingly realized in oncology. Health care professionals and their patients will be required to learn how to deal with the complexities of family facts, especially those are disclosed accidentally or in other forms besides the unclear importance. To ensure that patients fully perceive the results of ancestral testing and to alleviate the distress caused by familial sensitivity to different environments (Bacher *et al*., 2018). To overcome them, it is still necessary to implement default procedures of sanctions and healthy life-testing.

Conclusion

The implication of NGS-based mutant profiles in clinical practice in breast cancer gives a necessary assurance to the transformation of the model of treatment. The future of precision medicine in oncology may be bright since it is considered that there are some barriers to its development in terms of interpreting data, costs, efficacy, and standardization. NGS could play an important role in revolutionizing personalized cancer treatment along with the other innovativeness, better clinical guidelines, and enhanced collaboration between scholars, physicians, and policymakers. In case of providing the assistance of recent high-tech equipment convenient to the whole living population, disregarding of their geographic locations. We are in a position to go on to a close destination where breast cancer shall be considered according to the family features of the survivors who will have improved outcomes and more effective drugs.

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SM and AM: Conceptualization, Manuscript Writing. Supervision, Methodology Design, Manuscript Review & Editing. JI, AF, AZ, JI and MM: Literature Review and Reference Management, Editing Support. QA: Funding Acquisition, Institutional Coordination, Final Manuscript Approval. All authors have read and approved the final manuscript.

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