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Original research

Genetic screening of FFPE breast cancer biopsies for the *BRCA1*-185delAG mutation in Trinidad and Tobago

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ABSTRACT

Objective. To investigate whether the quality and quantity of genomic DNA harnessed from existing formalin-fixed paraffin-embedded (FFPE) breast cancer biopsy tissue samples in the public health system of Trinidad and Tobago (T&T) were sufficient for downstream genetic testing and to investigate the occurrence of the common breast cancer susceptibility gene 1 (*BRCA1*) mutation, *BRCA1*-185delAG, in these samples.
Methods. Genomic DNA was extracted from 67 FFPE samples using a standard protocol (Qiagen). Samples were genotyped using polymerase chain reaction (PCR) and Sanger sequencing.
Results. The genomic DNA was highly fragmented in the 250–500 bp range. The quality and quantity only allowed testing of one variant. This study successfully genotyped 34 of 67 FFPE breast cancer tissue biopsy samples for the *BRCA1*-185delAG mutation. This mutation was not detected in the 34 samples.
Conclusion. Existing FFPE cancer tissue biopsies in the public health system in T&T are of limited utility for genetic testing. The absence of the *BRCA1*-185delAG mutation in the limited number of breast cancer samples tested does not preclude its existence in this population. Further investigations are needed to determine the extent of clinically relevant breast cancer–associated mutations in this population.

Keywords: Breast neoplasms; genes, BRCA1; Trinidad and Tobago; genetic testing.

Genetic testing is now routine for pathological investigations in settings where genomic medicine is pervasive. This is especially true in cancer diagnostics and therapeutics, where genetic testing informs patient-specific clinical action (1). However, this is not yet routine in the developing world, including in the Caribbean region and the nation of Trinidad and Tobago (T&T). Yet, the developing world contains diverse and understudied populations who may stand to benefit from advances in genomic medicine and who may reveal novel molecular mechanisms of disease. Furthermore, some developing regions such as the Caribbean are undergoing an epidemiological transition, whereby noncommunicable diseases such as cancer, diabetes, and heart disease are surpassing infectious disease as the leading causes of mortality (2). Investigating the prevalence of clinically relevant genetic factors in developing countries is crucial to ensuring equitable access to the benefits of genomic advances for human health.

Breast cancer is the most prevalent form of cancer globally, and it is the primary cause of cancer mortality in women worldwide (3). There are many different factors that can contribute to

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these mortality rates, such as access to a timely diagnosis, treatment options, and palliative care (4). Genetic testing has become integral in making an accurate diagnosis and selecting appropriate treatment methods for breast cancer patients to improve their survival rates (1). While other factors may have a role to play in the development of breast cancer, researchers suggest that 5% to 10% of cases result from inheriting a faulty gene (5). *BRCA1* and *BRCA2* are the most implicated genes, as more than 60% of women with mutations in one of these will develop the disease (6). Mutations in *PALB2*, *ATM*, *PTEN*, *TP53*, *CDH1*, and *STK11* have also been heavily implicated in the development of breast cancer (7). These are considered to be high penetrance predisposing genes; however, moderate penetrance genes exist as well, posing potential risks (7). These genes, in turn, form the basis of commercial cancer gene panels, which allow further genetic testing in clinical settings.

Breast cancer susceptibility gene 1 (*BRCA1*) is one of the most commonly linked tumor-suppressing genes to breast cancer, and mutations in this particular gene convey a risk of 50%–60% for the development of breast cancer (8). There is a 50% chance of inheriting a germline *BRCA1* mutation from a parent, and loss-of-function *BRCA1* mutations are inherited in an autosomal dominant fashion (5). *BRCA1* is also strongly associated with the development of other types of cancers, such as cervical, ovarian, uterine, pancreatic, and prostate (7). *BRCA1* encodes type 1 breast cancer susceptibility protein, which plays a role in repairing damaged DNA (9). There are approximately 6 000 documented variants of this gene in various databases, with around 1 800 classified as pathogenic and associated with cancer risk (9). A well-studied common pathogenic variant, *BRCA1*-185delAG, located in exon 2 of the *BRCA1* gene, causes a frameshift mutation through the deletion of two AG bases, resulting in a premature stop codon (9). This mutation produces a truncated, nonfunctional protein that disrupts the gene's tumor-suppressing function and increases the risk of developing breast cancer (9).

The *BRCA1*-185delAG mutation was initially discovered as a founder mutation in Ashkenazi Jews (10). However, the *BRCA1*-185delAG mutation also exists in non-Jewish populations (11, 14), and sometimes on different haplotypes, suggesting independent origin (11, 12, 15). This mutation has been frequently observed across different regions in India (12, 14, 16–22). More recently, it was identified as a recurrent mutation accounting for 24.6% of the pathogenic *BRCA1/2* variants found among 921 South Indian patients with breast and ovarian cancer (23). It is also reported in 7 of 479 patients in the newly established Bharat Cancer Genome Atlas (24–27). *BRCA1*-185delAG has also been reported in African populations, albeit rarely. These low rates may be attributed to undertesting and the understudied population (28). However, it has been detected in Egyptian cohorts (28, 29), and it was found in 44 of 94 predominantly triple-negative breast cancer patients in Ghana (30). Notably, the Bahamas has the highest reported rate of BRCA mutations globally, including *BRCA1*-185delAG, which begs further investigation into the Caribbean genomic landscape (31, 32). The Breast Cancer Information Core (BIC) Database has documented 2 038 patients with this mutation of 6 133 entries as of July 2019, making it the most popular mutation in that database (33). This is clinically relevant because genetic testing for this specific mutation can improve patient outcomes by staging interventions that reduce the risk of disease development or selecting the most appropriate method of treatment. Women carrying these mutations can engage in risk-reduction measures such as enhanced screening or prophylactic mastectomies, which lowers the risk of breast cancer by >90%, along with adequate genetic counseling for families (8). However, global genetic repositories lack data from developing nations, and the outcomes of genetic testing may differ drastically in these settings.

Trinidad and Tobago is a twin island republic located in the Caribbean with a population of around 1.5 million (34). The population is divided into two main ethnic groups, Africans, mainly of West African ancestry, and Indians, which account for approximately 34.2% and 35.4% of the population, respectively (35). There is also a significant admixed population, including African, Indian, and European ancestry, and a small minority of other ethnic groups inhabiting the region due to its complex history (35). According to the World Health Organization (WHO), the mortality rate due to breast cancer in T&T is the second highest in the Caribbean (36). The Global Cancer Observatory (GLOBOCAN) 2020 report demonstrated approximately 1 551 060 new cancer cases and 749 242 deaths in Latin American and Caribbean countries (37). Past data extrapolated from 2004 indicated that the mortality was 25.5 per 100 000 women in Trinidad, which showed an upward trend compared to previous years (38). Data were analyzed from the National Cancer Registry of Trinidad and Tobago from 1995 to 2007, whereby notable differences in the incidence and mortality rates of breast cancer in various ethnic groups across Trinidad were discovered (39). Women of African ancestry were more severely affected with an incidence of 66.96 per 100 000 and mortality of 30.82 per 100 000 as compared to women of East Indian (incidence: 41.04 per 100 000; mortality: 14.19 per 100 000) or mixed ancestry (incidence: 36.72 per 100 000; mortality: 13.80 per 100 000) (39). A retrospective investigation of reports from 2010–2015 obtained from Sangre Grande hospital in Trinidad, demonstrated that 5-year breast cancer survival rates are 74.3%, while the recurrence-free survival rate is 56.4% (40). Comparatively, The American Cancer Society reports an overall 91% 5-year breast cancer survival rate for women diagnosed with breast cancer from 2013 to 2019 (41). Developed countries display higher survival rates, likely due to ongoing surveillance, timely adoption of new diagnostic methods, and efficient implementation of novel treatment options (3). Although breast cancer screening and treatment is widely available and free in T&T, it is often diagnosed at an advanced stage (42). In conjunction with this, access to genetic testing for breast cancer mutations is currently only possible through a limited ad hoc mixture of research studies and private laboratory testing, despite efforts for a more formalized approach (43). This can lead to the high aforementioned recurrence and mortality rates observed in women in Trinidad, especially those under 50 years of age.

Despite this upward trend in breast cancer incidence and mortality, the genetic landscape of breast cancer in the T&T population has not been sufficiently explored. One study explored the incidence of mutations in the *BRCA1*, *BRCA2*, and *PALB* genes in a cohort of 268 women with breast cancer in T&T (42). It showed that 28 patients (10.4%) possessed mutations in one of these genes, with 15 of those patients displaying *BRCA1* mutations (42). Another study of 118 breast cancer patients at the National Radiotherapy Centre in Trinidad analyzed 30 genes associated with hereditary cancer (44). They found that 25/118 patients (21.2%) harbored a pathogenic variant in one of these genes, with 13 of these occurring in *BRCA1* (44). A subset of this cohort

involving 90 patients revealed that 33.3% of patients were diagnosed with triple-negative breast cancer (TNBC) and 5/30 TNBC patients (16.7%) harbored a BRCA mutation (45). A third study of 298 women with breast (292) or ovarian (7) cancer from Trinidad investigated the frequency of mutations in 30 genes including *BRCA1* and *BRCA2*. It found that 62 (27.1%) patients had TNBC and 35 patients (11.7%) carried germline mutations, 19 of which were *BRCA1* mutations (31). Women of African descent, under 40 years of age, and possessing a *BRCA1* mutation tend to be the most at-risk population for the onset of TNBC, which has an unfavorable prognosis (6). The rates of TNBC reported in the Trinidadian population are higher than the rates reported in the United States of America, where TNBC accounts for 10%–20% of breast cancer patients and 10.6% of US TNBC cases harbor mutations in *BRCA1* or *BRCA2* (6). Though *BRCA1* mutations were detected in all of the aforementioned studies in T&T, no single mutation showed a significant recurrence in this population, and *BRCA1*-185delAG was not detected in any of the studies.

Collectively, the limited data from T&T do not preclude the possibility that the *BRCA1*-185delAG may exist in this population. On the contrary, the existence of *BRCA1*-185delAG in the Indian, West African, and Caribbean populations warrants its inclusion in genetic testing panels for these populations and their diasporas, including those in T&T. With significant subpopulations of West African, Indian, and mixed ancestry, it is crucial to investigate the frequency of *BRCA1*-185delAG, and other known clinically actionable breast cancer mutations, among breast cancer patients in T&T. Identified biologically relevant druggable aberrations can improve the treatment and survival of patients while contributing to the global cancer genetics landscape.

FFPE preservation of cancer biopsy tissue for pathological purposes is a routine practice globally, including in developing countries such as T&T. Moreover, FFPE biopsy tissue can be a viable source of genomic DNA for genetic testing, despite the well-established observation that FFPE samples generally produce a lower yield and quality of DNA compared to fresh tissue (46). By limiting the time between FFPE preservation and DNA extraction, and controlling the storage temperature of the blocks, the DNA quantity and quality obtained from the FFPE samples can be sufficient for successful downstream genetic testing applications (46). Banks of already existing FFPE biopsy samples are an attractive source for harnessing genomic DNA for genetic studies related to human disease, and in particular, for cancer genetics studies (47).

A natural starting point for clinically relevant breast cancer genetic testing is to test existing breast cancer tissue biopsy samples from patients in the public health system for known breast cancer associated mutations. This study used existing FFPE breast cancer biopsy samples (n = 67) from patients at the Eric Williams Medical Sciences Complex in T&T to test for the *BRCA1*-185delAG mutation.

METHODS

Ethics statement

Ethical approval was granted for this research by The University of the West Indies St. Augustine Campus Research Ethics Committee effective from May 23, 2014 (CEC-23/05/2014-01: A pilot study to help determine the prevalence of BRCA1 & 2 mutations in cancer patients, Trinidad, WI).

Sample collection and DNA extraction

Sixty-seven FFPE breast cancer biopsy samples were obtained from breast cancer patients at the Eric Williams Medical Sciences Complex via the Pathology department at the Faculty of Medical Sciences, The University of the West Indies, Trinidad and Tobago. No patient identifiers, demographic data, or clinical data, including details pertaining to breast cancer subtype or the ethnicity of the patients, accompanied the samples.

Genomic DNA was extracted using the QIAamp DNA FFPE Tissue Kit (Qiagen) with some minor modifications to the manufacturer's protocol. The initial centrifuge step was altered to 5 minutes and the AL buffer, along with the ethanol, was premixed to streamline the process. Xylene treatment was repeated twice when necessary to remove as much paraffin from the samples as possible before proceeding onto the subsequent steps.

DNA quality (260/280 and 260/230 ratios) and quantity (concentration) was determined using a Nanodrop 2000 Spectrometer (Thermo Scientific). The size profile of the extracted genomic DNA was determined using agarose gel electrophoresis on a 1.5% agarose gel.

Genotyping for the *BRCA1*-185delAG mutation

Polymerase chain reaction (PCR) with previously published primers designed specifically for the *BRCA1*-185delAG mutation was conducted on samples with sufficient DNA (10). The forward and reverse primer sequences were 5′GAAGTTGTCATTTTATAAACCTTT3′ and 5′GTATGTAAGGTCAATTCTGTTC3′. The PCR reaction mix consisted of a 25-µL reaction with 2x Taq PCR Premix (Bioland, USA), 0.2 µM forward and reverse primer, nuclease-free water, and 100–200 ng genomic DNA. The PCR cycling conditions included initial denaturation for 5 minutes at 94°C followed by 30 cycles of denaturation for 10 seconds at 94°C, annealing for 30 seconds at 46°C, extension for 30 seconds at 72°C, and a final extension for 5 minutes at 72°C before holding at 4°C. The results of the amplification were visualized using agarose gel electrophoresis on a 1% agarose gel stained with ethidium bromide run for 30 minutes at 100 V. A 242-bp amplicon indicated a positive PCR product. Reactions that resulted in no visible PCR amplicon were subjected to a second round of PCR as described above using 2 µL of the previous PCR reaction as the template. PCR amplicons underwent Sanger sequencing at McLab (California, USA). The genotype of the *BRCA1*-185delAG mutation was determined by visual analysis of the Sanger sequencing chromatograms obtained.

Genotyping for additional *BRCA1* mutations

The authors then attempted to genotype samples with any remaining DNA for the *BRCA1*-5443T>G and *BRCA1*-5296del4 mutations using the PCR protocol described with primers designed using the UCSC Genome Browser, Primer 3, and UCSC In-Silico PCR tool. The forward and reverse primer sequences for *BRCA1*-5294del4 were 5′CTGTCATTCTTCCTGTGCTC3′ and 5′CATTGTTAAGGAAAGTGGTGC3′. The forward and reverse primer sequences for *BRCA1*-5443T>G were 5′AAGCTCTTCCTTTTTGAAAGTCTG3′ and 5′GTAGA GAAATAGAATAGCCTCT3′.

RESULTS

Genomic DNA extracted from FFPE samples is highly fragmented with low yield and quality

Genomic DNA was successfully extracted from 38 of 67 samples. The concentrations ranged from 1.7 to 215.8 ng/µL, with an average of 37 ng/µL, and 27 of the 38 samples achieved a concentration of >10 ng/µL (Figure 1). The 260/280 values depicting contamination of the DNA with proteins and RNA ranged between 1.66–2.77 with an average of 2.02 (Figure 1). The 260/230 values depicting contamination of the DNA with organic compounds ranged between 0.22 and 3.39 with an average of 1.6 (Figure 1). High molecular weight genomic DNA was not obtained from any of the FFPE samples. The genomic DNA was fragmented in the 250–500 bp range (Figure 2).

FIGURE 1. Extracted DNA concentration versus 260/280 and 260/230 ratios; DNA concentrations, 260/280 and 260/230 values for genomic DNA extracted from breast cancer FFPE samples obtained from the Mt. Hope General Hospital, Trinidad

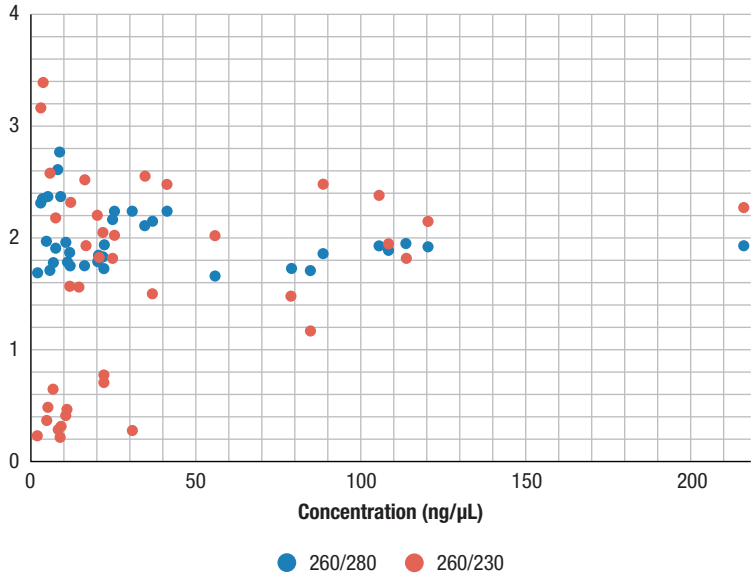
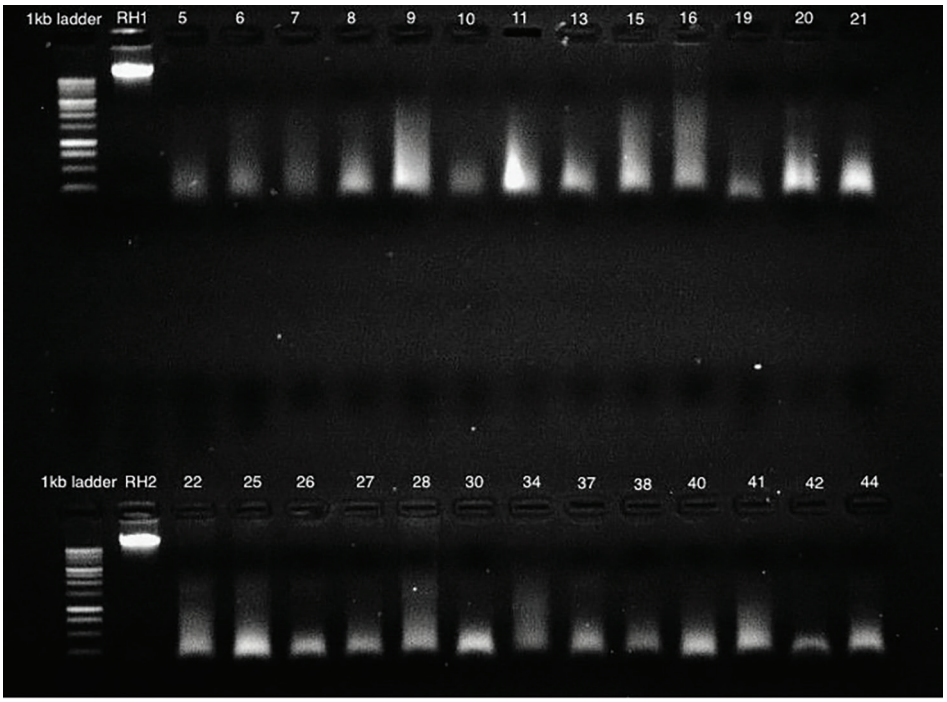


FIGURE 2. A 1.5% agarose quality control gel showing size profiles of gDNA extracted from the FFPE tissue samples (samples 5–44); RH1 and RH2 are positive controls of gDNA extracted from blood samples from a 35-year-old female without breast cancer



BRCA1-185delAG mutation not detected in 34 FFPE breast cancer biopsy samples

Thirty-four samples were successfully genotyped by PCR and Sanger sequencing for the *BRCA1*-185delAG mutation. PCR amplicons were visibly apparent in 18 samples only by agarose gel electrophoresis (Figure 3). Fifteen samples produced no visible PCR amplicons by agarose gel electrophoresis (Figure 3) but were nevertheless successfully sequenced. None of the 34 samples that were successfully genotyped possessed the *BRCA1*-185delAG mutation. The Sanger sequencing data are available upon request.

BRCA1-5443T>G and *BRCA1*-5296del4 genotyping unsuccessful

Subsequent attempts to genotype samples with remaining DNA for two additional BRCA mutations resulted in no visible PCR amplicons by agarose gel electrophoresis.

DISCUSSION

This study successfully genotyped 34 breast cancer patients from T&T using FFPE biopsy tissue for the common *BRCA1*-185delAG mutation. This mutation was not detected in the cohort. Attempts to genotype for the additional well-studied *BRCA1*-5443T>G and *BRCA1*-5296del4 mutations were unsuccessful. This was possibly due to the limited quantity and severely degraded nature of the DNA obtained from the FFPE samples. This study did not obtain enough genomic DNA from the FFPE samples to do further tests for other known mutations associated with breast cancer.

This study attempted to utilize existing FFPE samples for extracting DNA for genetic testing as FFPE preservation of cancer biopsy tissue is routine in the public health system in T&T. However, the FFPE samples were originally intended for histological applications only and not for DNA extraction. As such, no special measures were taken to preserve DNA quality and quantity or record associated clinical and demographic data for

FIGURE 3A. PCR products of breast cancer samples 5 to 22; RH1 is the PCR product using gDNA extracted from a blood sample from a 35-year-old female without breast cancer

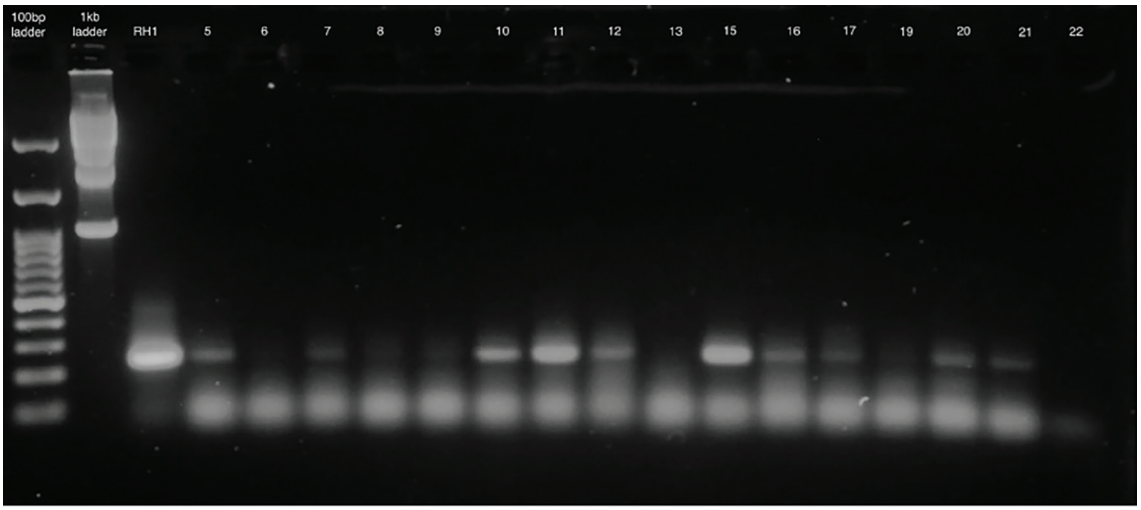
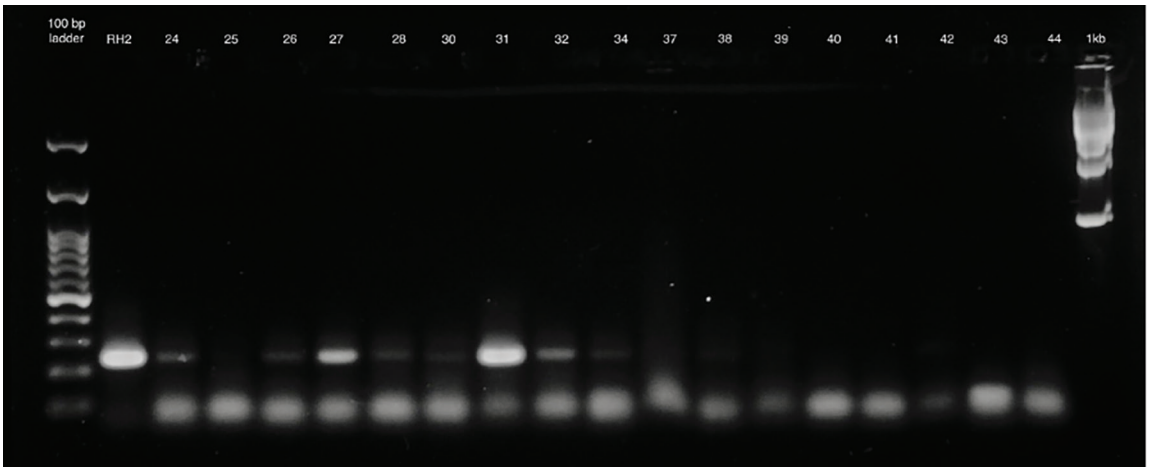


FIGURE 3B: PCR products of breast cancer samples 24 to 44; RH2 is the PCR product using gDNA extracted from a blood sample from a 35-year-old female without breast cancer



future research. In this case, only 67 FFPE blocks of sufficient volume and definitively sourced from breast cancer patients could be obtained from the Pathology department. Besides a diagnosis of breast cancer, additional clinical and demographic data, including age, ethnicity, and tumor subtypes, related to the samples were irretrievable. The age and storage conditions of the FFPE blocks used in this study were also not available. This may explain the overall low quantity and quality of DNA obtained from the samples. Furthermore, the majority of the samples produced no visible PCR amplicon (Appendix, Figures 2 and 3). This is potentially due to the genomic DNA obtained from FFPE preservation being fragmented to sizes smaller than the expected amplicon length of 242 bp, thereby limiting the amount of viable template for the PCR reaction. In the majority of PCR reactions, excess unused primers that appeared as bands near the bottom of the agarose gel were observed, indicating unsuccessful binding to the target sequence.

Due to the limited sample size, and the limited cumulative breast cancer genetic data from T&T, including the detection of other *BRCA1/2* mutations at modest frequencies in other investigations in this population, one cannot ignore the possibility that *BRCA1*-185delAG or other *BRCA1/2* mutations may still be present and clinically actionable in this population. In fact, collectively, these data underscore the possibility of the existence of other known or novel genetic contributors to breast cancer in this underexplored population. Small Island Developing States such as T&T present the additional opportunity for discovery of novel disease-causing founder mutations. Further efforts are ongoing to more comprehensively investigate the underlying genetic contribution to breast cancer risk and development in Caribbean populations using gene panel testing and whole exome sequencing with high-quality DNA. These include the Eastern Caribbean Health Outcomes Research Network project, the Africa Caribbean Cancer Consortium, and the Human Heredity, Environment and Health in the Caribbean initiative to prospectively biobank and sequence breast cancer samples across the Caribbean, and investigate gene-environment interactions contributing to disease incidence. As of 2023, there exists local capacity in the private sector for next-generation sequencing-based cancer gene panel testing. Previously, there was an accumulation of as-yet-unpublished data from next-generation sequencing-based cancer genetic testing accessed abroad, through both private and public health efforts. These data are expected to further our understanding of the contributions of known and novel mutations to breast cancer in this population. This in turn will subsequently inform the development of relevant gene panels and genetic testing protocols for the public health system.

The benefits for building genomic medicine capacity in the health care system of T&T have been clearly laid out previously (48). Yet, adoption of these practices has been slow and is not yet a priority in the current health care agenda. The routine use of FFPE for preserving cancer biopsy tissue in the public health system of T&T presents an unprecedented opportunity to drive future research and advance cancer prevention, treatment, and overall quality of life. However, to fully harness this potential, it is essential to standardize FFPE protocols to ensure optimal DNA quality and quantity. In particular, a biobanking initiative that mandates parallel expeditious DNA extraction using standard protocols from fresh tissue before FFPE preservation is critical. Additionally, with patient consent, deidentified DNA should be banked with associated demographic and clinical data in secure electronic formats to facilitate meaningful population-level genetic studies while maintaining individual patient privacy. Establishing such consistent methodologies must be regarded as both a necessary technical advancement and a matter of justice for patient care and health equity. Given that following the COVID-19 pandemic, public health laboratories in T&T and the wider Caribbean are now well equipped with molecular biology capacity for implementing DNA extraction and PCR-based genetic testing, this is an opportune time for such an intervention.

Conclusion

Variants in *BRCA1* are the most common genetic contributors to breast cancer and the well-studied *BRCA1*-185delAG mutation has been observed in both Indian and Ghanian populations, which are historically related to the Indian and African subpopulations of T&T. Yet, the authors were unable to identify the *BRCA1*-185delAG mutation in the cohort of 67 breast cancer patients from T&T. The variant was not detected in 34 successfully genotyped patients, and sufficient DNA was not obtained from the remaining 33 patient samples. Despite the limited sample size, these findings highlight the need to revisit FFPE sample preservation protocols to extend the use of FFPE as a viable and inexpensive option for exploring the genetic landscape of breast cancer in the low-resourced settings in T&T.

Author contributions. SCA performed experiments, analyzed the data, and drafted the paper. DB, RE, and RT collected the data and performed experiments. AR conceived the original idea, obtained ethics approval, and edited the manuscript. RR conceived the original idea and obtained ethics approval. WW edited the manuscript. CR and CU contributed data and edited the manuscript. RH conceived the original idea, planned the experiments, supervised the project, analyzed the data, and drafted the paper. All authors reviewed and approved the final version.

Conflicts of interest. The authors declare no conflict of interest and no financial disclosures.

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Tamizaje genético para la mutación *BRCA1*-185delAG en biopsias de cáncer de mama fijadas con formol e incluidas en parafina en Trinidad y Tobago

RESUMEN

Objetivo. Investigar si la calidad y cantidad del ADN genómico obtenido de muestras de tejido procedentes de biopsias de cáncer de mama fijadas con formol e incluidas en parafina existentes en el sistema de salud público de Trinidad y Tabago eran suficientes para las pruebas genéticas posteriores, así como investigar la presencia de la mutación 185delAG del gen de susceptibilidad al cáncer de mama de tipo 1 (*BRCA1*) en estas muestras.

Métodos. Se usó un protocolo estándar (Qiagen) para extraer ADN genómico de 67 muestras fijadas con formol e incluidas en parafina. Se llevó a cabo la determinación del genotipo de las muestras mediante reacción en cadena de la polimerasa (PCR) y secuenciación de Sanger.

Resultados. El ADN genómico mostró niveles altos de fragmentación, con un tamaño que oscilaba entre 250 y 500 pb. La calidad y cantidad del ADN obtenido solo permitieron analizar una variante. En el estudio se logró determinar correctamente el genotipo para la mutación *BRCA1*-185delAG en 34 de las 67 muestras de biopsia de tejido de cáncer de mama fijadas con formol e incluidas en parafina. No se detectó la mutación en ninguna ellas.

Conclusiones. Las biopsias de tejido canceroso fijadas con formol e incluidas en parafina existentes en el sistema de salud pública de Trinidad y Tabago tienen una utilidad limitada para las pruebas genéticas. La ausencia de la mutación *BRCA1*-185delAG en el número limitado de muestras de cáncer de mama analizadas no descarta su existencia en esta población. Será necesario realizar nuevas investigaciones para dilucidar el grado de presencia de mutaciones asociadas al cáncer de mama de trascendencia clínica en esta población.

Palabras clave: Neoplasias de la mama; genes BRCA1; Trinidad y Tobago; pruebas genéticas.

Rastreamento genético de biópsias de câncer de mama FFPE para detectar a mutação 185delAG no gene *BRCA1* em Trinidad e Tobago

RESUMO

Objetivo. Investigar se a qualidade e a quantidade de DNA genômico aproveitado de amostras de tecido de biópsia de câncer de mama fixadas em formalina e incluídas em parafina (FFPE, na sigla em inglês) existentes no sistema público de saúde de Trinidad e Tobago eram suficientes para testes genéticos posteriores e investigar a ocorrência da mutação comum 185delAG no gene 1 de suscetibilidade ao câncer de mama *(BRCA1*) nessas amostras.

Métodos. O DNA genômico foi extraído de 67 amostras FFPE usando um protocolo padrão (Qiagen). As amostras foram genotipadas usando a reação em cadeia da polimerase (PCR, na sigla em inglês) e o sequenciamento de Sanger.

Resultados. O DNA genômico estava altamente fragmentado na faixa de 250 a 500 pb. A qualidade e a quantidade permitiram o teste de apenas uma variante. Este estudo conseguiu genotipar 34 de 67 amostras de biópsia de tecido de câncer de mama FFPE para detectar a mutação 185delAG no gene *BRCA1*. Essa mutação não foi detectada nas 34 amostras.

Conclusão. As biópsias de tecido de câncer FFPE existentes no sistema público de saúde em Trinidad e Tobago têm pouca utilidade para testes genéticos. A ausência da mutação 185delAG do gene *BRCA1* no número limitado de amostras de câncer de mama testadas não exclui sua existência nessa população. São necessárias mais investigações para determinar a extensão das mutações clinicamente relevantes associadas ao câncer de mama nessa população.

Palavras-chave: Neoplasias da mama; genes BRCA1; Trinidad e Tobago; testes genéticos.