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# Instability of GATA3 or BRCA1 Gene is Associated to Breast Cancer: Case Study in Benin

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**Abstract** Breast cancer is the number 1 silent killer of women in Benin. For preventive screening some women relies on lump palpation and often disregard molecular biomarker profiling that could prevent them from developing this disease if performed early. Our objective is to investigate the biomarkers involved in breast cell differentiation (GATA3), growth regulation and genomic stability (BRCA1) to delineate them as biomarker to screen for breast cancer risk ahead of clinical symptoms. Key exons involved in each biomarker function are investigated Materials and methods: Upon ethical approval and signed informed consent, microbiopsy tissues was collected from 54 women diagnosed with breast cancer. Exon 4 of GATA3, Exon 1 and Exon 2 of BRCA1 were amplified by polymerase chain reaction (PCR) to investigate their integrity. The presence of amplification with one band is classified as no abnormality, the absence of amplification is classified as deletion while the presence of multiple bands is classified as polymorphism (mutation). Protein expression of GATA3 and BRCA1 were determined by western blot with anti-GATA3 and anti-BRCA1 IgG. Results: The PCR analyses revealed that in 13% cases, all 3 biomarkers targeted sequence were mutated and not amplified. Regarding GATA3-exon 4 amplification, 31% of samples have only 1 band while 54% have more than 2 bands. Regarding BRCA1-exon 1, one band is present in 63% while for BRCA1-exon 2 one band is present in 48% of samples. The Chi square test showed that GATA3-exon 4 and BRCA1-exon 2 have significant inverse variation ($p < 0.05$). Western blot analyses showed an existence of heterogeneity in GATA3 protein profile with many mutant bands while BRCA1 protein is absent in the majority of samples. Conclusion: It is worthy to emphasis a molecular screening for breast cancer patients before commencing therapy to prevent drug resistance due to matchless between cancer initiation mechanism and targeted therapy.

***Keywords:*** *Breast, cancer, GATA3-exon 4, BRCA1-Exon 2, genes, proteins*

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## 1. Introduction

The deadliest cancer women face in low-income countries is breast cancer. In Benin, breast cancer is a fast killer of women diagnosed with this affliction. The analysis of the molecular biomarkers linked to individual cancer is imperative to achieve successful targeted therapy. We have investigated two biomarkers involved in cell differentiation, cell growth regulation and DNA repair. One of investigated biomarkers is the GATA3 transcription factor present in luminal breast epithelial cells [1,2]. GATA3 is a highly conserved transcription factor with a role in gene promotor activation through binding to 5'-A/T-GATA-A/G-3' site within a targeted gene promotor or first exon [1]. GATA-3 gene is localized on chromosome 10 band p15; high frequency of GATA3 mutations were reported in luminal breast tumors while the loss of GATA3 was reported in some other breast cancer types [2,3,4]. The exon 4 of GATA3 was reported to be prone to missense mutation M294K within exon 4 and frameshift mutation on the splicing edge of exon 4 - exon 5 [2]. Breast cancer among men is rare and is not included in our study. The function of GATA3 as tumor suppressor or oncogene is not clear [2,4]. However, the presence of GATA3 in breast cancer could be a biomarker for good prognosis as it is able to reverse the epithelial mesenchymal transition hallmark of cancer cell [5,6,7]. Indeed, the expression of GATA3 is required for the normal development of mammary gland and for T4 lymphocyte cell type lineage determination in the immune system during hematopoietic development [2,3,4]. In breast luminal cells, the absence of estradiol maintains estrogen receptor alpha (ERα) in the cytoplasm but exposure to estradiol delocalizes ERα into the nucleus where it binds to DNA near wild type GATA3 (w-GATA3) and form a complex DNA-wGATA3-Erα, to regulate luminal epithelial cell growth [2]. In normal condition the complex DNA-wGATA3-ERα) is further degraded by

proteasome 26S as reported [2]. When this interaction is formed with mutant isoform of GATA3 (mGATA3) the turnover DNA-mGATA3-ERα interaction is no longer possible and the permanent activation of cell growth genes may lead to tumor development [2]. The presence of GATA3 in breast cancer correlates with ERα expression and is observed in luminal A breast cancer, all of which are characteristics for good prognosis [2,3,4,5,6,7,8]. In contrast, low or loss of GATA3 expression is observed in the luminal B subtype of breast cancer with higher histological grade, positive lymph nodes, widespread tumor mass and triple negative receptor (ERα-; PR- and low or HER2-) as reported earlier [2,3]. In the literature, somatic mutations of GATA3 were reported in 5% of breast cancer (luminal A and luminal B subtype) and is also observed in MCF7 cell line [8]. Preliminary studies in Benin have shown that the overexpression of mGATA3 in MCF7 cell line and in breast cancer micro-tissue lysates, correlates with the overexpression of Erα [8]. In MCF7 GATA3 and ERα can both be downregulated with SAHA drug (suberoyl-bis-hydroxamic acid, SBHA) in presence of lamin A while inducing cancer cell death [8]. Another biomarker with mutation-initiated breast cancer is the breast cancer gene 1 (BRCA1) known to be involved in DNA damage repair, genomic stability and cell apoptosis [9]. Germline mutations in BRCA1 gene account for 10–25% of inherited breast cancers [9]. Mutations in this gene have been mostly reported in triple negative breast cancers and ovarian cancers [9,10]. Our previous work has reported the mutation or loss of BRCA1 protein in Benin breast cancer patients [12,13]. Many studies were done in African-American and African-Caribbean women but very few were done in black-African women from Africa, including women from Benin. A recent study has found out that polymorphisms of GATA3 protein coexist with the absence of BRCA1 in breast cancer [11]. The loss of BRCA1 protein was also found to be related to mutations in exon 1 and 2, or epigenetic modifications, all of which correlate with a reduced median survival time [13]. Unlike hormone receptors and other cancer biomarkers, BRCA1 alteration was not genuinely investigated in west African women breast cancer tissues until our preliminary study [8,12,13]. It was reported that GATA3 and BRCA1 interact and function in synergy to control FOXC1 gene expression in the pathway of cell growth regulation [14]. The loss of GATA3 or BRCA1 will disrupt cell growth regulation capacity via FOXC1 and may prone cell proliferation [14]. According to the literature, GATA3 mutation is observed in tumors not associated with BRCA1 or BRCA2 mutations [15]. It was formally reported that germline mutations in BRCA1 gene account for 10 – 25 % of inherited breast cancers, somatic mutation of GATA3 is linked to 5% of breast cancers while the downregulations of BRCA1 mRNA and protein were observed in 30% of sporadic breast cancer [15,16,17]. As such, the forfeiture of interaction GATA3/BRCA1 could be epigenetic modifications or due to gene mutations [15,16]. A study has reported that the presence of GATA3 is associated with better overall survival [17]. The main objective of our study is to investigate the integrity of GATA3 (exon 4) and BRCA1 (exon-1, exon-2) genes and protein in breast cancer microbiopsy tissue DNA extracts, in contributing to the accessibility of potent targeted therapy based on specific molecular disorders. The determination of the molecular mechanisms surrounding BRCA1 and GATA3 profiles in breast cancer may help to classify patients for better personalized targeted therapy as well as better prognosis in sub-Saharan Africa.

## 2. Materials and Methods

All reagents needed for DNA extraction and polymerase chain reaction (PCR) were purchased from Sigma-Aldrich (USA) and included DNA ladder, agarose powder, EDTA powder, Phenol, Chloroform, Tris HCl, Boric acid, Ethidium bromide, Gel Red under UV light [12,13].

Most reagents needed for western blot were purchased from Bio-Rad (USA) as previously specified [12,13]. Primary antibodies directed against BRCA1, GATA3 or ß-actine were purchased from Santa-Cruz biotechnology (USA). Secondary anti-rabbit and anti-mouse were purchased from Bio-Rad (USA).

### 2.1. Ethical consideration

Institutional Review board and ethical approvals were obtained for this study [8,13]. The study has followed the guideline of Helsinki declaration. This study has received an ethical approval from the local research of ethical committee of the university of Parakou (CLER-UP), and was referenced as 0295 /CLERB-UP.

### 2.2. Microbiopsy Tissues Collection and Cell Lysate

Microbiopsy fragments of breast cancerous tissues was collected by the oncologist surgeon after signed informed consent was obtained. For the present study 54 participant samples were collected. Henceforward, woman breast cancer microbiopsy tissues were collected for cancer diagnosis and molecular alteration screening.

Tissues collection was carried out at the National teaching hospital CNHU-HKM of Cotonou (Benin) in the department of Visceral Surgery and Oncology. Individual tissue sample was collected in sterile tube containing 5 ml of sterile ice-cold phosphate buffer saline (PBS) to preserve tissue fragments and cells. Samples were kept in ice-cooler and delivered within an hour to the research Unit of Molecular Biomarker in Cancer and Nutrition (BMCN) located in the Institute of applied biomedical Sciences (ISBA), University of Abomey Calavi (UAC), for PCR and western blot processing as previously reported [8,12,13].

### 2.3. DNA Extraction Method

DNA extraction on microbiopsy fragment was done as previously reported [13]. In summary, cell membrane was disrupted with 0.5 ml of lysis buffer containing proteinase K (20 mg/ml) and RNAse and incubation at 55"C overnight. Henceforward, phenol was added to the cell lysate (V / V) and centrifuged at 10,000 rpm at 4°C for 10 min. The upper aqueous phase (supernatant) was collected in a new Eppendorf tube, followed by the addition of chloroform (V / V) and another centrifugation (10,000

rpm at 4°C for 10 min). The supernatant was collected in a new Eppendorf tube and ice-cold ethanol (96%) was added at -20°C for 4 h to precipitate the DNA. The DNA pellet was recovered after centrifugation (12,000 rpm at 4°C for 10 min), washed with ice-cold ethanol (70%) and then collected after centrifugation at 12,000 rpm at 4°C for 5 min. The DNA pellet was air-dried at 55°C for 20 min and solubilized in tris-EDTA (TE) buffer. DNA concentration was measured with a spectrophotometer (260 nm). Soluble DNA extract was stored in the freezer until needed for quantification and Polymerase Chain Reaction (PCR).

### 2.4. Polymerase Chain Reaction (PCR) Method for GATA3-exon4 and BRCA1-exon1 BRCA1-exon2 Analysis

The analyses using PCR method were carried out as previously reported [13]. DNA purity was assessed by amplifying the GAPDH gene before setting up PCR with specific primers targeting the specifically GATA3-exon4 and BRCA1-exon1 BRCA1-exon2. For each PCR reaction, positive and negative controls were used. PCR products were migrated on 1% agarose gel to separate amplicons by size. Amplified bands were detected by staining with ethidium bromide or Gel Red under UV light. The BRCA1 gene is mapped to chromosome 17q21 with 22 exons [16]. For this study only exon 1 and exon 2 were screened as their presence determine the possibility of transcription and translation of BRCA1 [13,16].

The presence or absence of BRCA1 exon1 or exon2 was determined by the molecular size of the amplified exon sequence [16]. Primer sequences for BRCA1 were previously displayed [13,16].

**Table 1. Primer sequences**

| | Target | Primer sequences |
|---|---|---|
| | BRCA1 -exon1 | Forward, B1Ex1 f: 5' TAG CCC CTT GGT TTC CGT G 3'<br>Reverse, B1Ex1 r: 5' TCA CAA CGC CTT ACG CCT C 3' |
| | BRCA1-exon2 | Forward, B1Ex2 f : 5' GAA GTTG TCA TTT TAT AAA CCT TT<br>Reverse B1Ex2 r : 5' TGT CTT TTC TTC CCT AGT ATG T 3' |
| | GATA3-exon4 | Forward Gt3a f : 5′-TCT GCA ATG CCT GTG GGC TCT AC-3′<br>Reverse Gt3b r : 5′-CTA ACC CAT GGC GGT GAC CAT GC-3′ |

### 2.5. Protein Isolation and Western Blot Analysis

Individual microbiopsy cancerous tissue fragment was lysed with 100 µl of RIPA buffer for 30 minutes at 4"C followed by the addition of 100 µl of 2X protein-denaturizing buffer composed of Tris-SDS-ß-mercaptoethanol-glycerol before boiling at 95"C for 5 min to achieve proper protein denaturation. Samples were stored at -20"C until needed. Western blot analysis was carried out after heating samples at 95"C for 5 min before loading on Bis-acrylamide gel electrophoresis for protein separation according to their sizes. For our study, we used a 10% gel to analyze GATA3 (59-50 kDa) protein, and a 7.5% gel to analyze BRCA1 (220 kDa) protein. Electrophoresis was performed at 100 volts for 1h for GATA3 and 3h for BRCA1. Proteins were separated according to their molecular weight as previously reported [12]. Henceforward, proteins were transferred on nitrocellulose membrane at 100 volts for 90 min (GATA3) or for 2h (BRCA1) in the presence of a transfer buffer composed of Tris-glycine and 20% methanol. The final phase is immunoblotting with specified antibody (BRCA1, GATA3 or ß-actin) followed by chemiluminescence revelation on radiography film with a developer as reported previously [8,12].

### 2.6. Statistical Analysis

Chi square test was used for statistical analysis. The significancy was considered for a P value < 0.05.

## 3. Results

### 3.1. GATA3 Gene Integrity in Breast Cancer Microbiopsy Tissue DNA Extracts

We observed the heterozygosity of GATA3 gene throughout the amplification of GATA3-exon4 Figure 1). Overall GATA3-exon4 has multiple isoforms in breast cancer DNA extract unlike BRCA1 or BRCA2. The loss of GATA3 was observed in 15% of samples while 23% of them had intact GATA3-exon4 and 54% of samples had polymorphism of GATA3-Exon4. Example of polymorphism with multiple bands is shown on the agarose gel (Figure 1). GAPDH is used as loading control (Figure 1).

### 3.2. BRCA1 Gene Integrity in Breast Cancer Microbiopsy Tissue DNA Extracts

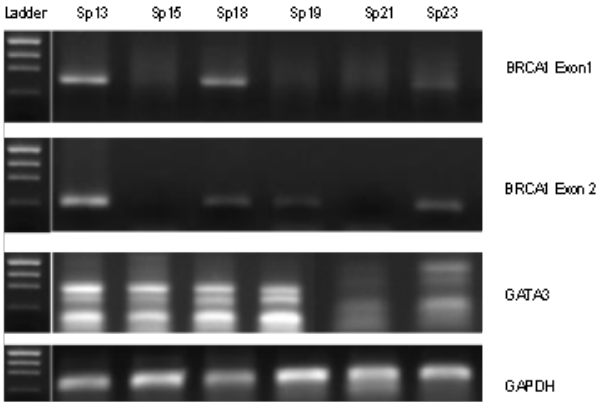


**Figure 1.** Gel showing PCR product of GATA3 and BRCA1. BRCA1-exon 1 or exon2 are either present or absent. GATA3-exon4 has several isoforms (100 - 200 pb) indicating the presence of polymorphisms

Exon1 and Exon2 mostly involved in gene transcription starting point were investigated for BRCA1. The analysis of Exon 1 and Exon2 integrities on BRCA1 gene demonstrated that exon 1 is absent in 37% of samples while exon2 was absent in 52% of samples no polymorphism was observed for these exons 1 and 2

(Figure 1). The analysis of combined deletion of Exon 1 and Exon2 on BRCA1 gene demonstrated that 37% of samples had deletion of both exons 1 and 2 as shown on the agarose gel (Figure 1).

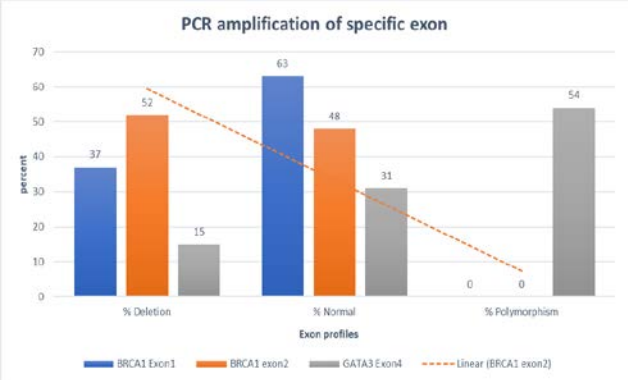


**Figure 2.** Histogram showing the Summary of PCR results for BRCA1-exon1, Exon 2 and GATA3-exon 4. Deletion of BRCA1 Exon1 and BRCA1-Exon2 are inversely associated to the polymorphism of GATA3-exon4

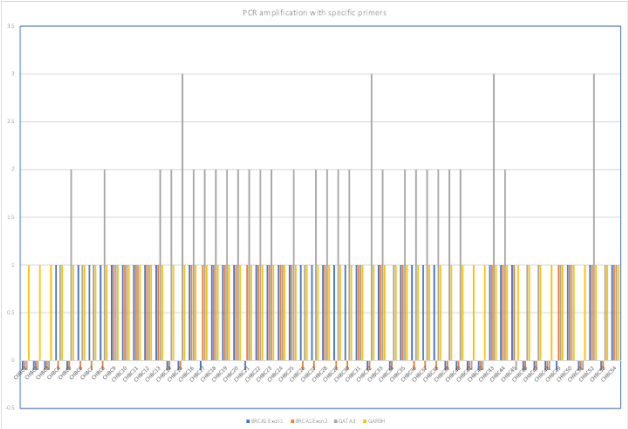

**Figure 3.** Individual histogram showing that individual amplification for BRCA1 Exon1, BRCA1 Exon 2 and GATA3 Exon 4. GAPDH is a control for the PCR amplification. Most of the participants barring the deficiency of BRCA1-exon1 or BRCA1-exon2 have a polymorphic amplification of GATA3-exon4

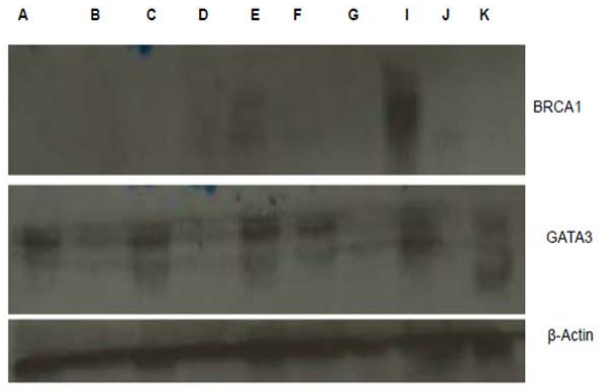


**Figure 4.** Western blot showing protein expression profile for GATA3, BRCA1 and ß-actine. The majority of samples has lost BRCA1 protein while mutated GATA3 isoforms are prominent in most samples with band sizes higher (lines A, C, E, F, K) or lower than the normal GATA3 size around 49 - 50 kDa as in line I. Samples in lines B, D, G, J show low or no GATA3 expression.

Most of the participants barring the deficiency of BRCA1-exon1 or BRCA1-exon2 have a various amplification band sizes for GATA3-exon 4 (Figure 1). The histogram in Figure 2 was designed to represent individual distribution of band amplification or absence of amplification for BRCA1-exon1, BRCA1-exon2 and GATA3-exon4.

To facilitate graphic designs and statistical analyses, numbers were assigned to the targeted exon PCR data equivalent to the number of amplified bands observed on the agarose gel. Thus, a normal amplification with one band was given 1, abnormal amplification with more than 1 band was given 2-4 accordingly to the number of isoforms recorded; the absence of amplification was given -0.01. Chi square test was used for statistical analysis. Overall, the loss of biomarkers BRCA1-exon1, BRCA1-exon2 and GATA3-exon4, was observed in 7/54 (13%) of samples. The statistical analysis with Chi square test has shown that the inverse variation between the amplification of BRCA1-exon2 and GATA3-exon4 is significant ($P = 0.0307$). The variation between BRCA1-exon1 and GATA3-exon 4 is not significantly appealing ($p = 0.11$). The histogram (Figure 3) shows that most samples with negative BRCA-exon2 are associated with polymorphic isoforms of GATA3-exon4 (p,0.05). The negative association of BRCA1-exon1 deficiency and GATA3-exon4 polymorphism is not significant (p>0.05). Histogram of GAPDH gene is the loading and PCR control (Figure 3).

Individual histogram showing that individual amplification for BRCA1-exon1, BRCA1-exon-2 and GATA3-exon 4. GAPDH is a control for the PCR amplification. Most of the participants barring the deficiency of BRCA1 Exon1 or Exon2 have a polymorphic amplification of GATA3-exon4.

## 3.4. Profile of GATA3 and BRCA1 Proteins in Microbiopsy Cell Lysates

The protein expression profiles of GATA3 and BRCA1 proteins subsequently to a western blot are displayed in Figure 4. We observed that GATA3 protein is expressed in 64% of biopsy samples and absent in 36% of them. Conversely, BRCA1 protein expression is observed in 20% of biopsy samples and absent in 80% of them.

The heterozygosity of wild type GATA3 protein (wGATA3) which binds to “A/T-GATA3-A/G” and mutated GATA3 protein (mGATA3) is also observed (Figure 4). Overall, 64% of ductal carcinoma expressed GATA3 while only 20 % of ductal carcinoma expressed BRCA1 (Figure 4). This molecular heterogeneity should be taken into consideration prior to prescribing anti-cancer drugs to breast cancer patient.

The observation of multiple bands of GATA3 protein by western blot method, suggests the presence of mutations giving different sizes of GATA3 (mGATA3) protein compared to the wild type (w GATA3). Hence, wGATA3 and mGATA3 have different sizes suggesting the presence of polymorphisms.

## 3.5. Discussion

Cell differentiation and genomic stability biomarker analyses done on women breast cancer microbiopsy tissue

lysates, showed that 20% of breast cancers have lost BRCA1 expression due to gene mutations and were linked to shorter median survival time, while 80% of them have lost BRCA1 protein due to epigenetic modifications in Benin Republic [8,13]. It was already reported that GATA3 and estrogen receptor alpha (ERα) function in synergy to regulate cell growth with progesterone receptor (PR) [8]. Erα, PR and HER2/Neu are primordially assessed by immunohistochemistry (IHC) in Benin and used as biological parameters for targeted therapy for receptor positive breast cancer (RPBC) vs triple negative breast cancer (TNBC) as published [8,12,13].

No study has reported the link between GATA3 and BRCA1 in breast cancer patients seeking for potent treatments in Benin Republic. Assessing GATA3 by western blotting could contribute to the prognosis and better classification of luminal breast cancer in black women in Benin and worldwide. Beside epigenetic events, mutation, or deletion could also be involved in expression failure. The absence of GATA 3 protein activity linked to mutation in zing finger sequence of the gene, could be explained for 15% of samples. The frequency of BRCA1 protein absence linked to the mutation on exon 1 could be explained for 37% of samples. The frequency of BRCA1 protein absence linked to the mutation in exon 2 could be explained for 52% of sample. The impairment of both Exon1 and Exon 2 of BRCA1 was noticed for 31% of samples. In 7/54 (13%) cases none of the 3 biomarkers GATA3 exon 4, BRCA1 Exon1 and BRCA1Exon2 were amplified. Most of the participants barring the deficiency of BRCA1-exon1 or exon2 have a polymorphic amplification of GATA3 exon4. The abnormal amplification of GATA3 exon-4 might affect the biding to the promoter of targeted gene thus impacting its transcription factor and cell growth regulatory activities. This preliminary data suggested that the failure of gene amplification in-vitro may reflect an in-vivo failure to the transcription of BRCA1 gene in these samples, all of which may result in failure of protein translation in-vivo. The multiple bands linked to the amplification of GATA3-zinc finger domain sequence, suggested the presence of some GATA3 antagonist isoforms (mGATA3) which may fail to interact properly with target DNA sequence to activate the synthesis of downstream target proteins involved in cell differentiation and gene regulation activities.

In this study, we have assessed gene profile of sensitive sequences for BRCA1 and GATA3 by PCR amplification while protein expression profile was assessed by western blot, to determine the specific molecular alteration initiating breast cancer for each patient. In most breast cancer tissue lysates, several isoforms for GATA3 were observed for gene and protein, but there is no data on GATA3 mutation in familial breast cancer in Benin Republic. Taken together, whether breast cancer is initiated by the absence or mutation of GATA3 protein, the end point seems to be their inability (mGATA3 and BRCA1) to form a repressor complex to inhibit cell growth proteins FOXC1 all of which may favor the initiation of breast cancer [14]. Further analysis will clarify the later suggestion. Our data is strengthening the introduction of molecular biomarker data to oncologists in Benin. The latest consideration prior to personalized targeted therapy in the future will improve cancer survival rate in low-income countries including Benin. Majority of cancer linked to epigenetic modifications are overlooked because molecular biomarker analyses are not well known by physicians involved in African onco-therapy. Cancer due to epigenetic modification should not be treated the same way as cancer due to gene mutation. Gene silenced subsequently to epigenetic modifications can be restored with drugs inhibiting DNA methylation (DNMTI) and histone deacetylase (HDACI) as previously reported [8]. However, cancer associated to tumor suppressor gene mutations should be treated with drug that inhibit cancer cell DNA replication and promote apoptosis (Taxol and derivatives) as reported for breast cancer treatment with adverse effects [18,19]. Also, cancer linked to deficiency of GATA3 subsequently to deficiency of retinoic acid (RA) should be treated with RA supplementation [20,21]. It was reported that 80% of breast cancers among young women are linked to epigenetic modifications worldwide. Surely, some chemical changes initiate cell transformation and sustain drug resistance during treatments of these cancer [18,19,20,21]. The presence of normal GATA3 in breast cancer is a biomarker for good prognosis as we were able to reverse cancer cell to epithelial type [8]. The 20% of breast cancer samples with no BRCA1 expression due to gene mutations was linked to shorter median survival time, while 80% of them with the lost BRCA1 protein due to epigenetic modifications can be treated with specific drugs to prolong their lifespan [13].

## 3.6. Conclusion

Cancer death rate is increasing in low-income countries due to the gap of acknowledge of epigenetic regulation of cancer cells. Hence the majority of cancers were linked to epigenetic modifications that regulate cell division. Cancer therapy should specifically be considered for the restauration of the molecular pathway to unlock tumor suppressor protein expression while bolting the expression of cell proliferation proteins. Epigenetic modification can be reversed with proper histone deacetylase inhibitor drugs (HDACI) like SAHA or curcumin derivatives. Meanwhile, patients with tumor suppressor gene mutations (BRCA1) can be treated with PARP inhibitors (Nirapaib, Velipaib, Olaparib, etc.). Breast cancer initiation by germline mutation of BRCA1 was well documented worldwide but not in Benin Republic. In our research unit, we have demonstrated for the first time in Benin that the deficiency in BRCA1 is more related to epigenetic modifications than gene mutations while GATA3 abnormality is more related to mutations in the exon4 and exon4-exon5 junction. According to the literature GATA3 and BRCA1 proteins work in synergy to regulate cell proliferation. The failure in either one can initiate cell transformation and cancers in the breast.

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Authors' contributions: CDC is the head of the unit of molecular biomarkers in cancer and nutrition (BMCN), she has designed, funded and wrote the article including graphic design and statistical analysis. SYH is a postdoctoral who has collected the cancer tissues and performed PCR and western blot benchworks. FHRG is the oncology surgeon who has diagnosed cancer patients and performed cancer tissue microbiopsies.

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Conflict of interest: No conflict of interests is reported. No AI was used to write this article.

# References

[1] Bates DL, Chen Y, Kim G, Guo L, Chen L. Crystal structures of multiple GATA zinc fingers bound to DNA reveal new insights into DNA recognition and self-association by GATA. J Mol Biol. 2; 381(5): 1292–1306, Jul 2008.

[2] Takaku M, Grimm SA, Wade PA. GATA3 in breast cancer: tumor suppressor or oncogene? Gene Expr.; 16(4): 163–168, Dec 2015.

[3] Asselin-Labat ML, Sutherland KD, Barker H, Thomas R, Shackleton M, Forrest NC, et al. Gata-3 is an essential regulator of mammary-gland morphogenesis and luminal-cell differentiation. Nat Cell Biol; 9(2): 201-9, Feb 2007.

[4] Tindemans I, Serafini N, Di Santo JP, Hendriks RW. GATA-3 function in innate and adaptive immunity. Immunity; 41(2): 191-206, Aug 2014.

[5] Eeckhoute J, Keeton EK, Lupien M, Krum SA, Carroll JS, Brown M. Positive cross-regulatory loop ties GATA-3 to estrogen receptor alpha expression in breast cancer. Cancer Res.; 67(13): 6477-83, Jul 2007.

[6] Chou J, Lin JH, Brenot A, Kim JW, Provot S, Werb Z. GATA3 suppresses metastasis and modulates the tumour microenvironment by regulating microRNA-29b expression. Nat Cell Biol.; 15(2): 201-13, Feb 2013.

[7] Yan W, Cao QJ, Arenas RB, Bentley B, Shao R. GATA3 inhibits breast cancer metastasis through the reversal of epithelial-mesenchymal transition. J Biol Chem.; 285(18): 14042–51, Apr 2010.

[8] Capo-chichi CD, Gnangnon F, Mekpossi C, Houngue S, Xu XX, Olory-Togbé JL. Presence of Lamin A is Required for GATA3 and ERα Downregulation by Histone Deacetylase Inhibitor in Breast Cancer Cells. Journal of Cancer Research and Treatment; 6(3), 60-69, Aug 2018.

[9] Dean M, Boland J, Yeager M, Im KM, Garland L, Rodriguez-Herrera M et al. Addressing health disparities in Hispanic breast cancer: accurate and inexpensive sequencing of BRCA1 and BRCA2. GigaScience; 4:50, Nov 2015.

[10] Fackenthal JD, Olopade OI. Breast cancer risk associated with BRCA1 and BRCA2 in diverse populations. Nat Rev Cancer.; 7(12): 937-48, Dec 2007.

[11] Huo D, Ikpatt F, Khramtsov A, Dangou JM, Nanda R, Dignam J, et al. Population Differences in Breast Cancer: Survey in Indigenous African Women Reveals Over-Representation of Triple-Negative Breast Cancer. J Clin Oncol,; 27(27): 4515-21, Sep 2009.

[12] Capo-Chichi CD, Aguida B, Gnangnon F, et al. Altered expression of BRCA1/2 proteins in breast cancer in Benin. Conference: 6ème Colloque de l'Université d'Abomey-Calavi (UAC), Benin. 25-30 sept 2017.

[13] Hounguè S, Totah T, George S, Jean-Léon Olory-Togbé JL, Capo-chichi CD. BRCA1 Protein Deficiency in Breast Cancer Microbiopsy Lysate Delineates Patient Survival Time. Journal of Cancer Research and Treatment.; 9(1), 1-11.

[14] Tkocz D, Crawford NT, Buckley NE, Berry FB, Kennedy RD, Gorski JJ, Harkin DP, Mullan PB. BRCA1 and GATA3 corepress FOXC1 to inhibit the pathogenesis of basal-like breast cancers. Oncogene; 31, 3667–3678, Aug 2012.

[15] Arnold JM, Choong DY, Thompson ER, Waddell N, Lindeman GJ, Visvader JE et al. Frequent somatic mutations of GATA3 in non-BRCA1/BRCA2 familial breast tumors, but not in BRCA1-, BRCA2- or sporadic breast tumors. Breast Cancer Res Treat.; 119(2): 491-6, Jan 2010.

[16] Lara K, Consigliere N, Pérez J, Porco A. BRCA1 and BRCA2 mutations in breast cancer patients from Venezuela. Biol Res.; 45(2): 117-30, 2012.

[17] Yoon NK, Maresh EL, Shen D, Elshimali Y, Apple S, Horvath S et al. Higher levels of GATA3 predict better survival in women with breast cancer. Hum Pathol.; 41(12): 1794-801, Dec 2010.

[18] Xu AP, Xu LB, Smith ER, Fleishman JS, Chen ZS, Xu XX. Cell death in cancer chemotherapy using taxanes. Front Pharmacol.; 14: 1338633, Jan 2024.

[19] Jivani A, Shinde RK. A Comprehensive Review of Taxane Treatment in Breast Cancer: Clinical Perspectives and Toxicity Profiles. Cureus.; 16(4): e59266, Apr 2024.

[20] Chen MC, Hsu SL, Lin H, Yang TY. Retinoic acid and cancer treatment. Biomedicine (Taipei).; 4(4): 22, 2014.

[21] Esposito M, Kang Y. RAI2: linking retinoic acid signaling with metastasis suppression. Cancer Discov.; 5(5): 466-8, May 2015.