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Review Article

A Novel Molecular Pathway Linking BRCA1 Dysfunction To High Risk for Cardiac Disease

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Abstract

Cardiovascular disease is a collection of pathologies related to the heart and surrounding blood vessels. A recent study demonstrated a link between BRCA1 gene mutation and the pathogenesis of cardiovascular disease, but the molecular mechanism is not understood. African American women with BRCA1 mutations tend to develop aggressive TNBC associated with a high mortality rate. Our previous work showed BRCA1 to bind to a downstream target Ubc9 resulting in increased SIRT1 expression which facilitated BRCA1 and SIRT1 to translocate to the nucleus and activate ER- α . However, BRCA1 mutations in TNBC impaired tethering to Ubc9 resulting in cytoplasmic localization of these proteins. Loss of Ubc9 function as seen in myocardial ischemia translates to the development of myocardial infarction, cardiovascular disease, and tumorigenesis. Furthermore, a deleterious effect of Ubc9 further manifests as increased activity of VEGF and endothelial cells which influences the progression of cardiovascular disease. VEGF activity is also influenced by the down regulation of Caveolin-1 and SIRT1 which translates to hypertension and tumorigenesis. In healthy individuals, SIRT1 works to prevent arterial stiffness and regulates the apoptosis of cardiomyocytes. SIRT1 also works to localize BRCA1 within the nucleus, and its repression has been linked to cardiovascular dysfunction. Both ER- α and ER- α contribute to cardiovascular function by upregulating protective effects against infarction and reperfusion injury. Specifically, mutation to cardiovascular disease and proposes potential novel targets to treat BRCA1-associated TNBC with heart dysfunction.

Keywords: BRCA1; Ubc9; Caveolin-1; VEGF; SIRT1

Introduction

Cardiovascular disease is a category of diseases characterized by abnormal pathology in the heart or circulatory system; these diseases include arterial disease, heart failures, and cardiac dysrhythmias. Based on National Health and Nutrition Examination Survey data collected from 2016, approximately 48% of Americans over the age of 20 years were diagnosed with cardiovascular disease [1]. Considering the recent COVID-19 pandemic, COVID-19 patients with cardiovascular disease had a higher mortality risk compared to COVID-19 patients without cardiovascular disease [2].

These findings highlight the role of expanded treatment options for cardiovascular disease to lower mortality risk and increase patient quality of life. In our study, we worked to increase treatment options by understanding the relationship between the Breast Cancer Gene (BRCA1) mutation and cardiovascular disease. In understanding the interplay between the onset of cardiovascular disease and the BRCA1 gene, we highlighted the role of several mediators involved in this relationship including vascular endothelial growth factor, small ubiquitin-like modifier proteins, Ubc9, Caveolin-1, and SIRT1.

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BRCA1

Breast cancer is the leading cause of death in American women. In 2022, it is expected that there will be over 280,000 new invasive breast cancer diagnoses, equivalent to 15% of all new cancer cases [3]. Breast cancer is often associated with mutations in tumor suppressor genes such as BRCA1 and BRCA2. and sensitivity to hormones in response to its quantity of receptors. BRCA1 is a human tumor suppressor gene associated with the etiology of breast and ovarian cancers. It is located on chromosome 17q21 and plays a role in DNA repair, regulation of cellular proliferation, and cardiovascular disease [4,5]. The BRCA1 gene codes for an 1863 amino acid full-length BRCA1 protein [6]. Our lab has identified two splice variants BRCA1a/p110 and BRCA1b/p100 in breast carcinoma [7]. BRCA1 is an essential mediator for homologous recombination by the recruitment of recombinases and double-strand break repairs [8]. Studies have shown that mutations in BRCA1 contribute to genetic instability, dysfunctional DNA repair mechanisms, and an increased risk for developing chronic diseases such as cancers and cardiovascular disease [9,10].

BRCA1 mutation leads to the highest mortality for cardiovascular disease

Breast cancer genes have been shown to be a gatekeeper in cardiovascular health. A recent study has shown that functional BRCA1 proteins have a protective effect on cardiomyocytes by reducing cardiac hypertrophy [11]. BRCA1 is known to be involved in DNA double-strand recombination repair. Studies have also shown that BRCA1 may be associated with other proteins involved in DNA repair mechanisms such as oxidative DNA repair [12]. In a BRCA1 +/+ mouse model treated with induced DNA damage, BRCA1 promoted the shuttle of subnuclear RAD51 foci and homologous recombination repair mechanisms [13]. Upregulated BRCA1 promoted increased RAD51 nuclear localization and recombination repair in cardiovascular tissue [5]. On the other hand, ablation of the BRCA1 gene led to adverse cardiovascular function [5]. Faulty DNA repair mechanisms are a hallmark of various chronic diseases such as cancer and cardiovascular disease. In addition to cancer progression, BRCA1-haploinsufficiency has been shown to cause an increase in epithelial progenitor cells and subsequent vascular dysfunction [14]. Correspondingly, BRCA1 mutations induce suppression of vascular remodeling and increase mortality due to cumulative DNA damage and the induction of p53 apoptotic pathways in cardiomyocytes [5].

BRCA1 and Triple Negative Breast Cancer

Mutations in tumor suppressor genes such as BRCA1 and BRCA2 are an indicator of a predisposition to certain types of breast, ovarian and other cancers [15]. BRCA1 mutation-associated triple-negative breast cancer (TNBC) is an invasive and highly aggressive type of breast cancer. In TNBC, malignant breast cancer cells lack receptors for progesterone, estrogen, and HER2, thus eliciting proliferation and distant metastasis. African American women have disproportional mortality rates due to BRCA1 mutations,

TNBC, and cardiovascular disease [16,17].

BRCA1 downstream targets Ubc9, Caveolin-1, and VEGF

BRCA1 activity regulates downstream targets Ubc9, Caveolin-1, and vascular endothelial growth factor (VEGF). Small ubiquitin-like modifier proteins (SUMO) are conjugated in a posttranslational modification resulting in the SUMOylation of the lysine residues on the target protein [18]. SUMOylation has been shown to have protective effects against proteasomal degradation in pathological disease manifestations [19]. SUMO proteins are activated, conjugated, and ligated by E1, E2, and E3 ligase enzymes, respectively. SUMO conjugation is catalyzed by the SUMO- conjugating enzyme, Ubc9. The SUMOylation and deSUMOylation processes contributes to the stability and subcellular localization of factors in chronic disease [20]. In addition, these processes were shown to be modulators in breast cancer and cardiovascular disease [18]. In our previous studies, we found the amino-terminal of BRCA1, BRCA1a, and BRCA1b bind Ubc9, a SUMO-E2 conjugating enzyme [21]. In normal conditions, BRCA1 binds Ubc9 in conjunction with the nuclear localization signal, resulting in the nuclear localization of BRCA1 proteins [22]. However, a BRCA1 disease associated mutation fails to bind to Ubc9 resulting in cytoplasmic localization of BRCA1 proteins [22]. Furthermore, BRCA1 was shown to possess a SUMO-1 and Ubc9 - dependent E3 ubiquitin ligase activity on ER-a. Ubc9 binding mutants have repressed growth inhibition found in ER-a negative breast cancer and TNBC. SUMO proteins are also shown to be involved in cardiomyocyte development, protection, and cardiac gene expression [23]. Myocardial ischemia and oxidative stress decreases Ubc9 activity and subsequently, SUMO-specific cysteine proteases (SENP1 and SENP2) are activated. This results in deSUMOylation in ischemic infarction, cardiovascular disease, and tumorigenesis [24,25]. Hypoxia-inducible factor 1-alpha, HIF-1a, is upregulated inducing the expression of pro-angiogenic factors such as vascular endothelial growth factor (VEGF) as well as endothelial cell (EC) activity. VEGF interruption is associated with vascular toxicity, arterial stiffness, blood pressure, and inflammation [26,27]. Decreased Ubc9 activity contributes to pro-apoptotic pathways and activation of endothelial cells (EC) in cardiovascular tissue. EC activation and ischemic stress are regulated by SUMO conjugated-E2 enzymes in the myocardium, influencing the progression of cardiovascular diseases [28]. Sirtuin-1 (SIRT1) is an NAD+ dependent histone deacetylase that plays a major role in metabolism, tumorigenesis, genomic instability, and cancer metastasis [29,30]. BRCA1 binds Ubc9, shuttling BRCA1 proteins to the nucleus. BRCA1 proteins bind to the promoter region of SIRT1 to inhibit Survivin expression thus mediating cellular proliferation. Correspondingly, Caveolin-1 is also activated which regulates vascular endothelial growth factor (VEGF) and angiogenesis [31]. It is observed that SIRT1 activity increases in the normal heart and has protective effects against inflammation, heart disease, and atherosclerotic plaque formation [32]. SIRT1 activation also attenuates arterial stiffness and hypertension [33].

Mutation carriers at higher risk of cardiovascular disease

BRCA1 mutations that are associated with TNBC, impair the tethering of Ubc9 and shuttling of BRCA1 proteins. Consequently, SIRT1 and Caveolin-1 are repressed. Knockdown of Caveolin-1 and SIRT1 are shown to induce the expression of VEGF, increase vascular permeability, decrease vascular remodeling, and increase hypertension [32,34,35]. Recent studies have shown that BRCA1 plays a role in the maintenance of cardiovascular health [5]. BRCA1 mutations have been shown to induce defective cardiomyocyte function, cardiac toxicity, and ischemic stress [5,36]. African American women have a high incidence of BRCA1 mutations, TNBC, and cardiovascular disease [16,17].

Myocardial distress in response to ischemia and reperfusion are leading risk factors in cardiovascular disease mortality [37,38]. SIRT1 regulates inflammation responses in myocardial ischemia and reperfusion [37]. Thus, SIRT1 regulation is essential for cardiovascular protection and prevention of cardiac cell apoptosis [39]. SUMOylated SIRT1 is localized in the cardiomyocyte nuclei [40]. However, in ischemia, the overproduction of deSUMOylase and SENP2 contribute to reduced nuclear localization of SIRT1. Investigations on the role of Ubc9-deSUMOylation pathways indicate overexpression of SENP2 which contributes to cardiac dysfunction, congenital heart defects, and pro-atherogenesis [41,42]. Therefore, BRCA1 mutation-associated knockdown of SIRT1 expression has

negative implications on cardiovascular health. SIRT1 activation is seen as a novel therapeutic target for cardiac ischemia and reperfusion due to its involvement in essential cardiometabolic processes [40].

Role of ER- α , VEGF, and Caveolin-1 in cardiovascular disease

An increase in SIRT1 expression promotes the subcellular nuclear transport of BRCA1 through Ubc9 tethered pathways which are essential in cardiovascular protection and breast cancer modulation. On the other hand, decreased SIRT1 binding affinity promotes cytosolic localization of BRCA1 proteins and cardiovascular dysfunction. In accordance, there is impaired regulation of HIF1-a, VEGF, and Caveolin-1 in BRCA1 mutation-associated cardiovascular disease. As a result, cardiomyocytes have dysfunctional nucleocytoplasmic shuttle mechanisms and cardiac gene expression, as well as pro-apoptotic pathways that ultimately contribute to cardiovascular disease. Hormonal factors such as estrogen are shown to have cardioprotective effects in ischemia and reperfusion through genomic signaling mechanisms [43]. Two of the most common nuclear estrogen receptors are ER-α and ER-β [44]. Estrogen binding to ER-a results in pleiotropic effects that regulate cardiac function [43,44]. ER-a promotes up-regulation of anti-apoptotic gene expression in cardiomyocytes [45,46]. Likewise, in estrogen receptor-negative cancers such as TNBC, these cardioprotective effects are prospectively decreased.

Conclusions

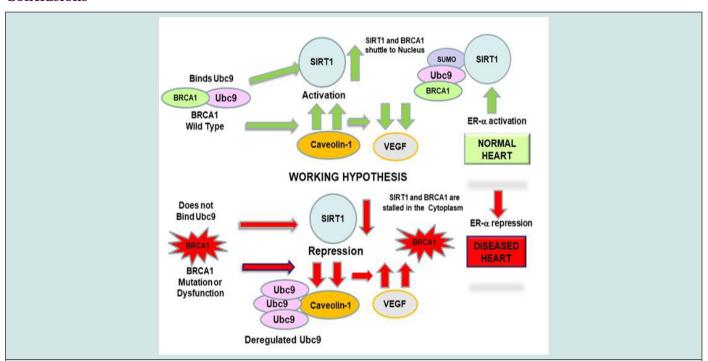


Figure 1: A novel molecular mechanism to show how BRCA1 regulates heart function. BRCA1, by binding Ubc9, facilitates nuclear cytoplasmic shuttling of SIRT1 and ER -α. activation. BRCA1 mutation / dysfunction (as seen in TNBC patients) results in loss of Ubc9 binding cytoplasmic mis-localization of SIRT1, deregulated levels of Ubc9, and ER- α repression resulting in defective heart function.

The BRCA1 tumor suppressor gene has long been affiliated with the differential diagnosis of breast and ovarian cancer; however, there is also an interconnection between BRCA1 gene mutations and a high risk for developing cardiovascular diseases in patients. Along with its many functions, studies have found that the BRCA1 gene has a protective mechanism that contributes to sustaining cardiovascular health, which when disrupted will lead to defective cardiac function. Disturbances in this mechanism are brought about by mutations in the BRCA1 gene, which is unable to bind Ubc9, resulting in down regulation of SIRT1, and Caveolin-1, as well as increasing VEGF levels, thus causing a higher risk for cardiovascular diseases. More research in the future is still needed regarding the mechanism and its implications, which will provide novel ways to treat cardiac diseases as well as TNBC that result from the loss of function of the BRCA1 gene (Figure 1).

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