RESEARCH ARTICLE

Novel Nonsense Variants c.58C>T (p.Q20X) and c.256G>T (p.E85X) in the CHEK2 Gene Identified in Breast Cancer Patients from Balochistan

Abdul Hameed Baloch1*, Ahmad Nawaz Khosa1, Nasrullah Bangulzai1, Jamila Shuja2, Hafiz Khush Naseeb2, Mohammad Jan1, Illahi Bakhsh Marghazani1, Masood-ul- Haq Kakar1, Dost Mohammad Baloch1, Abdul Majeed Cheema3, Jamil Ahmad4

Abstract

Breast cancer is the most commonly occurring and leading cause of cancer deaths among women globally. Hereditary cases account 5-10% of all the cases and CHEK2 is considered as a moderate penetrance breast cancer risk gene. CHEK2 plays a crucial role in response to DNA damage to promote cell cycle arrest and repair DNA damage or induce apoptosis. Our objective in the current study was to analyze mutations in the CHEK2 gene related to breast cancer in Balochistan. A total of 271 individuals including breast cancer patients and normal subjects were enrolled. All 14 exons of CHEK2 were amplified and sequenced. The majority of the patients (>95%) had invasive ductal carcinomas (IDCs), 52.1% were diagnosed with tumor grade III and 56.1% and 27.5% were diagnosed with advanced stages III and IV. Two novel nonsense variants i.e. c.58C>T (p.Q20X) and c.256G>T (p.E85X) at exon 1 and 2 in two breast cancer patients were identified in the current study. Both the variants identified were novel and have not been reported elsewhere.

Keywords: Breast cancer - CHEK2 gene - novel nonsense variants - Balochistan

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Introduction

Breast cancer is the most commonly occurring and one of the leading causes of death due to cancer among females worldwide accounting for 14-30% of all cancer deaths. Hereditary cases account 5-10% of the cases of which 15-20% are due to mutations in high penetrant breast cancer genes i.e. BRCA1 and BRCA2 (Willems PG, 2007; Panda S et al., 2008; Jemal et al., 2011; Baloch AH et al., 2014).

Germline mutations in other genes like CHEK2, ATM, BRIP1, PAB2, CHEK2 and others have also been proposed to be causes of the breast cancer (Meijers-Heijboer et al., 2002; Renwick et al., 2006; Seal et al., 2006; Rahman et al., 2007). CHEK2 considered as a moderate penetrance breast cancer as well as other cancers risk gene (Vahteristo et al., 2002; Oldenburg et al., 2003; Dong et al., 2003; Cybulski et al; 2004; Nevanlinna H, 2006 and Walsh T et al., 2011) and play a crucial role in response to DNA damage, phosphorylating BRCA1, p53, CDC25C and CDC25A to either promote cell cycle arrest and repair the DNA damage or induce apoptosis ( Zeng et al., 1998; Lee et al., 2000; Chehab NH, 2000; Falck et al., 2001; Meijers et al., 2002). Cell-cycle checkpoints are activated in response to DNA damage to restrain cell proliferation.

Gene CHEK2 encodes a serine/threonine kinase, phosphorylated by Ataxi Telangectasia Mutated (ATM) at G2 checkpoint, and is activated in the nucleus of the cell in response to DNA double strand damage (Matsuoka et al., 2000; Ingvarsson et al., 2002; Craig and Hupp, 2004; Bartek, Hollestelle et al., 2010 and Lukas, 2003 and Nevanlinna and Bartek, 2006). CHEK2 1100delC most widely been study and suggested to increase the risk of breast cancer in women who have a positive family history of breast cancer, however this mutation has not been reported in Asian populations (Wu et al., 2001; Weischer et al., 2008; Fletcher et al., 2009; Baloch et al., 2014). Different missense mutations other
than 1100delC may lead to loss of function and cause cancer (Narod, 2010 and Le Calviz-Kem et al., 2011).

Our objective in this study was to analyze mutations in gene CHEK2 related to breast cancer. This study was conducted in Balochistan, Pakistan on 171 breast cancer patients and 100 normal subjects. Consent forms were obtained from all the subjects. Venous blood (3ml) was drawn for DNA extraction from each individual. All 14 exons and exon intron boundaries of gene CHEK2 were amplified and sequenced by using synthesized exon specific primers. We identified two nonsense variants i.e. c.58C>T (p.Q20X) and c.256G>T (p.E85X) at exon 1 and 2 in two breast cancer patients. To the best of our knowledge these mutations are novel as they have not been identified elsewhere. The study was approved from Institutional Review Board (IRB) of Balochistan University of Information Technology, Engineering and Management Sciences (BUITEMS), Quetta.

Materials and Methods

Current study was performed on 171 breast cancer patients and 100 normal subjects. Informed consents were obtained from all the volunteers (breast cancer patients and normal subjects). History of the disease was taken from all the breast cancer patients. Intravenous blood samples (3ml) were collected and dispensed into 15ml falcon tubes containing EDTA to avoid clotting of blood samples. The samples were kept frozen at -20 °C for 24 hours prior to further processing. DNA was isolated through an inorganic standard method already published. Primers were designed for all fourteen exons including exon-intron boundaries of gene CHEK2 using Primer 3 software and synthesized. All the exons were amplified and sequenced using Big Dye Terminator Chemistry on an automated 3100 ABI prism DNA sequencer. The sequences results were checked and compared with the normal sequences using genome browser of ENSEMBL.

Results

A total of 271 subjects including 171 breast cancer patients and 100 normal subjects were enrolled in current study, belonging to different ethnic groups of Balochistan. Ethnic groups with high number of patients effected with breast cancer were; Pashtoon ethnic group with 31.6%, Afghani with 25.1% patients and 22.8% patients from Baloch ethnic group. Majority of the patients (>95%) were enrolled after signing the consent forms. 100 agreed to take part in current study as volunteers who 171 breast cancer patients. Intravenous blood samples (3ml) were collected and dispensed into 15ml falcon tubes containing EDTA to avoid clotting of blood samples. The samples were kept frozen at -20 °C for 24 hours prior to further processing. DNA was isolated through an inorganic standard method already published. Primers were designed for all fourteen exons including exon-intron boundaries of gene CHEK2 using Primer 3 software and synthesized. All the exons were amplified and sequenced using Big Dye Terminator Chemistry on an automated 3100 ABI prism DNA sequencer. The sequences results were checked and compared with the normal sequences using genome browser of ENSEMBL.

Discussion

Breast cancer is a global burden occurring most commonly and suggested to be the second foremost cause of death among women worldwide. About one million new breast cancer cases each year, 55% death cases and 45% diagnosed cases are reported to be from middle and low income countries (Hortobagyi et al., 2005; Curado et al., 2007; Globocan, 2012). Our aim in this study was to investigate gene CHEK2 mutations related to breast cancer from Balochistani population. For this purpose we identified 248 breast cancer patients from different ethnic groups of Balochistan. Out of 248 breast cancer patients 171 agreed to take part in current study as volunteers who were than enrolled after signing the consent forms. 100 normal individuals were also enrolled in this study. The occurrence and severity of breast cancer among different ethnic groups with diverse lifestyle is varying. Multiple risk factors like lake of awareness, lack of health facilities, lifestyle and genetic factors make certain ethnic groups more prone to breast cancer (Ries et al., 2003; Rowan et al., 2009; Chelbowsky et al., 2009). We identified majority of the patients from Pashtoon ethnic group including 31.6% local Pashtoons of Balochistan and 25.1% Afghan origin Pashtoon (in majority), Hazara and Uzbak ethnic groups. Baloch ethnic group constituting majority of the population of Balochistan, 22.8% of the...
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In conclusion, Breast cancer is the most commonly occurring cancer among women globally. Gene CHEK2 plays a pivotal role in response to DNA damage and is suggested to increase the risk of breast cancer 3 fold in familial breast cancer cases negative for BRCA1 and BRCA2 mutations. The two nonsense variants identified in current study are concluded to be rare and may not to be associated with genetic predisposition of breast cancer in Balochistani population as both the variants were not observed in any other breast cancer cases and control investigated in current study

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