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Association of FGFR2 rs2981582 polymorphism and breast cancer susceptibility: An updated systematic review and meta-analysis

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Abstract

The present meta-analysis aims to determine whether Fibroblast Growth Factor Receptor 2 (FGFR2) rs2981582 gene polymorphism is associated with mammary carcinoma risk in Asians and Caucasians based on case-control studies. Among women worldwide, mammary carcinoma is the most common type of cancer and the leading cause of death from cancer. Despite the overlap between early-onset and late-onset mammary carcinoma rates, mammary carcinoma incidence profiles increase exponentially until menopause and then decrease. The FGFR2 is crucial to mammary carcinoma progression. The search was conducted on several databases such as Embase, PubMed, Google Scholar, and Science Direct to find the suitable case-control studies. All statistical analyses were conducted using Review Manager 5.4 software and Metagenyo. The present study consists of 23 case-control studies (21,549 controls and 18,906 mammary carcinoma cases) to examine the association between the FGFR2 rs2981582 gene polymorphism and mammary carcinoma risk. PROSPERO (ID 348820) has been used to register the review methodology. The FGFR2 gene polymorphism rs2981582 was associated with a

strong association in all genetic models. In order to estimate the publication bias, the funnel plot was used. However, there did not appear to be any significant bias. As a result, it is essential to conduct more extensive epidemiological studies are needed to confirm this finding and to gain a deeper understanding of the molecular mechanisms underlying this association.

Introduction

Breast cancer is the most commonly diagnosed cancer type in woman by surpassing lung cancer, accounting for 1 in 8 cancer diagnoses worldwide (Melina et al., 2022). In 2020, an estimated 2.3 million cases of female breast cancer were diagnosed globally, and about 685,000 women died from the disease. Fig. 1 bar diagram shows the number of newly diagnosed breast cancer cases and deaths from breast cancer by world region. With over 70% of all new cases and 81% of all deaths observed in women aged 50 and above, the global burden from breast cancer remains concentrated in this age group (Melina et al., 2022). By 2040, the number of newly diagnosed breast cancers is projected to grow by over 40%, to about 3 million cases every year. Similarly, deaths from breast cancer are set out to increase more than 50%, from 685,000 in 2020 to 1 million in 2040 (Melina et al., 2022).

The formation of new blood vessels from existing blood vessels, known as angiogenesis, is a critical step in cancer growth, invasion, and metastasis (Ferrara et al., 2003). The angiogenic process is modulated by a series of catalytic and inhibitory factors (Carmeliet and Jain, 2000). FGFR2 has been shown to inhibit the growth and progression of various tumour types in multiple scientific studies (Turner and Grose, 2010; Park et al., 2016; Wang et al., 2019). However, despite these findings, the specific mechanism through which FGFR2 inhibits tumour gene expression and impedes tumour development is still unclear and warrants further investigation. The single nucleotide polymorphisms (SNPs) in the FGFR2 gene is significantly associated with the development of mammary carcinoma. This genetic variation alters the function or expression of the FGFR2 protein, leading to abnormal signalling pathways involved in cancer development (Martin et al., 2011). Numerous case-control studies have been conducted to investigate the relationship between FGFR2 SNP and mammary carcinoma. These studies have consistently demonstrated that certain variants of the SNP are associated with an increased risk of developing breast cancer (Zhang et al., 2017; Xia et al., 2015). FGFR2 polymorphisms have been examined in numerous studies, but interpretations from related reports remain unconvincing because of differences in ethnicity, region, and other factors (Raskin et al., 2008; Chan et al., 2012a, Chan et al., 2012b). However, differences in results among ethnic groups make it challenging to draw definitive conclusions. Regional variations and other factors like sample sizes and study designs