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BIBLIOMETRIC ANALYSIS: CHEK2 GENE AND BREAST CANCER

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Abstract

Cancer has become one of the main problems for health organizations around the world. The risk of developing cancer during a lifetime (up to 75 years of age) is approximately 20%, and the risk of dying from cancer is 10% [1]. One in every five people will be diagnosed with cancer during their lifetime, and one out of ten patients with the disease will die from it. In 2020, 2.26 million new cases of cancer were reported [2]. Breast cancer is the most commonly diagnosed type of cancer in women worldwide and is the leading cause of death among women with the disease[3]. If the current trend in breast cancer continues, it is estimated that by 2040, over 3 million new cases and 1 million deaths will be recorded, solely due to population growth and aging. As of today, various levels of penetrant mutations associated with the risk of developing breast cancer, including mutations in the CHEK2 gene (checkpoint kinase gene), are known [4]. It has been determined that the CHEK2 gene is a susceptibility gene for breast cancer in several populations. In 2002, it was reported that a mutation in the CHEK2 gene could lead to the development of breast cancer, and numerous subsequent studies have confirmed this [5–7].

Objective of the study: A bibliometric analysis of articles published between 2018 and 2022 on the relationship between breast cancer and the CHEK2 gene.

Materials and Methods: The most highly cited articles on CHEK2 gene mutations were sourced from the Scopus database, with a total of 550 articles included. The results were analyzed using VOSviewer and other online bibliometric analysis platforms, with graphical analyses performed.

Keywords: CHEK2 gene, breast cancer, mutation.

Results: The number of published articles showed an increase mainly in the years 2018-2019 and 2020-2021. The majority of scientific research and publications were

conducted by scientific research institutions in the United States. [8]. The United Kingdom and Canada hold the next positions. This can be attributed to the fact that economically developed countries have the ability to allocate more funding for scientific research [9]. When relating our topic to the field of science, we can see that research is primarily linked to the medical field (49%). We conclude that this is due to the close connection of our topic to human health. The journal "Redox Biology" has published the highest number of articles on this subject. [10–13]. It should also be noted that the correlation between the journal's impact factor (IF) and the number of citations for articles is not particularly significant.

Conclusion: Recent research indicates that the CHEK2 gene plays a crucial role in the hereditary types of cancer development. Investigations in this area are increasing year by year. Studying mutations in the CHEK2 gene is essential not only for accurate diagnosis but also for selecting appropriate treatment methods for patients.

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