

Abstract

Pharmacological Network Study on the Effect of Quercetin on Gastric Cancer Using Computerized Databases [†]

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Abstract: Gastric cancer (GC) is the second most common cause of death of any cancer-related cases in the world, and is also in the top 5 most common malignancy cancers in general. There are plenty of well-distributed treatments, offering better hygiene, more robust and complete nutrition, and the eradication of pathogens such as *Helicobacter pylori*. Currently, there is still the need for more treatments, especially those of lower cost, like those coming from already easily available products. Quercetin (QRC) is a natural phenolic compound present in a wide variety of products, e.g., in plants like *Hibiscus sabdariffa*, onions, grapes, broccoli, and citrus fruits. This product has been shown to have great potential therapeutic effects, and it has also been suggested that it could be useful in combating different types of cancer; however, information regarding the targets or mechanisms that QRC has on cancer cells is still unclear. Therefore, this study aims to identify the targets that QRC has, like anti-cancer treatment for GC using different bioinformatic tools and databases. From MalaCards and SwissTargetPrediction, both QRC and GC molecular targets were defined, and then they were matched with the Venny 2.1.0 platform. From this, 31 genes were gathered, and then they were analyzed using the ShinyGo0.77 and DAVID-Bioinformatic Resources. Furthermore, StringDB was used to identify the protein–protein interactions, and Cytoscape 3.6.0 12 hub genes were obtained. Those hub genes were then subject to Gene Expression Profiling Interactive Analysis and TISIDB. Finally, molecular docking studies were performed using the SwissDock database. The results suggest that, according to the gene ontology data, QRC has a relationship with the regulation of cell death, response to stress, cell motility, response to amyloid-beta, cellular response to reactive oxygen species, and apoptotic processes. Some genes like EGFR were correlated with an abundance of CD8 and Neutrophil infiltration but didn't show to improve the survival rate. Furthermore, molecular docking results show that QRC can bind to multiple molecules of interest. These results complement some of the currently available information alluding to the effectiveness of plants rich with QRC as part of the treatment used for different kinds of cancer, but it also suggests a plethora of new targets that this molecule has in GC, while at the same time giving a clearer idea of the mechanisms that are affected in GC by QRC. However, as with any other study that primarily uses bioinformatic tools, these final results are to be used for more direct and precise research, especially if experimental protocols are used.

Keywords: quercetin; network; gastric cancer; bioinformatics



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