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Resumo	Propolis is a natural compound with recognized anticancer properties, and its chemical composition varies depending on climatic, botanical, and geographical factors. Among its bioactive compounds, flavonoids are particularly notable for their potential in preventing and treating colorectal cancer (CRC), a disease responsible for over 45,000 new cases in Brazil in 2023, according to INCA. This study applies a network pharmacology approach to investigate molecular interactions between propolis flavonoids and CRC-related targets. Six flavonoids were selected, and their chemical structures and pharmacokinetic properties were analyzed using PubChem and SwissADME. Target genes were predicted using SwissTargetPrediction and intersected with CRC-associated genes from GeneCards, OMIM, and PharmGKB. Protein-protein interaction (PPI) networks were built using STRING and analyzed in Cytoscape to identify top 10 hub genes. Functional enrichment was performed using GO and KEGG databases, revealing that 14 of the 266 therapeutic targets identified are part of the colorectal cancer signaling pathway. IGF1R and EGFR were among the key targets, as they modulate PI3K-Akt and MAPK signaling, promoting cell survival and inhibiting apoptosis via FOXO inactivation. Molecular docking simulations, conducted via DockThor and validated by RMSD values, showed strong interactions between key proteins (TNF, EGFR, CASP3) and candidate flavonoids. Nymphaeol A and Propolin C demonstrated the highest affinity for TNF and CASP3, while Galangin showed notable interaction with EGFR. These findings support the therapeutic potential of propolis flavonoids in modulating CRC-related molecular pathways, offering a basis for further development of natural compound-based strategies for colorectal cancer treatment.

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