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RESEARCH ARTICLE

A network pharmacology approach for investigating the multi-target mechanisms of Betanin in the treatment of Colon cancer (CC)

Tekou Marie [a,*], Alex Stephane Ndjip Ndjock[b], Chahinez Amira Dahmani[c], Elaf A. Basha[d]

[a] Department of Research, Paul Services and Consulting, Douala, Littoral, Cameroon
[b] Department of Public Health, Universite des Montagnes, Bangangte, Cameroon
[c] Department of Biology, University of Mostaganem, Mostaganem, Algeria
[d] Omdurman Islamic University, Khartoum, Sudan

***Corresponding Author:** Tekou Marie
Department of Research, Paul Services and Consulting, Douala, Littoral, Cameroon
Email: marie.tekou@gmail.com

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Abstract

Betanin, a natural pigment derived from beetroot, has demonstrated promising anticancer properties, particularly in colon cancer (CC). In this study, we employed a network pharmacology approach to elucidate the molecular mechanisms of betanin in CC treatment. Potential targets of betanin were identified through online databases and compared with CC-related genes to determine key overlapping targets. A protein-protein interaction (PPI) network was constructed, and core hub targets were analyzed. Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analyses highlighted key biological processes and signaling pathways involved in CC treatment, such as apoptosis regulation, oxidative stress modulation, and inhibition of cell proliferation. Our findings suggest that betanin exerts anticancer effects by modulating critical molecular targets and signaling pathways, providing a basis for further experimental validation and therapeutic development.

1. Introduction

Colon cancer (CC) remains one of the leading causes of cancer-related mortality worldwide (Feng et al., 2021), with increasing incidence attributed to dietary habits, genetic predisposition, and lifestyle factors (Banerjee et al., 2017). Despite advancements in surgical techniques, chemotherapy, and targeted therapy, resistance to treatment and recurrence remain significant clinical challenges. A deeper understanding of the molecular mechanisms underlying CC progression is essential for developing effective therapeutic strategies. Natural compounds have gained considerable attention due to their multi-target therapeutic potential (Makhoba et al., 2020). Among these, betanin, a betalain pigment found in beetroot (Beta vulgaris), has been widely recognized for its antioxidant, anti-inflammatory, and anticancer properties (Fu et al., 2020). Previous studies have shown that betanin can induce apoptosis, suppress tumor growth, and modulate oxidative stress responses (Silva et al., 2022). However, the precise molecular targets and mechanisms through which betanin exerts its anticancer effects in CC remain largely unexplored. Network pharmacology is an emerging field that integrates bioinformatics, systems biology, and pharmacology to analyze drug-target interactions within complex biological networks (Joshi et al., 2024). By employing a network pharmacology approach, we aim to uncover the multi-target mechanisms of betanin in CC, identifying key pathways and molecular targets that contribute to its therapeutic effects.

2. Materials and Methods

2.1 Identification of Targets for Betanin and Colon Cancer

Betanin-associated targets were obtained from databases such as PubChem (https://pubchem.ncbi.nlm.nih.gov/) and SwissTargetPrediction (https://www.swisstargetprediction.ch/). CC-related genes were retrieved from GeneCards (https://www.genecards.org/), DisGeNET (https://disgenet.com/), and OMIM databases (https://www.omim.org/). The overlapping targets between betanin and CC were identified using Venn diagram analysis (Lin et al., 2024).

2.2 Protein-Protein Interaction (PPI) Network Construction

The identified targets were analyzed using the STRING database to construct a PPI network. Core hub targets were determined based on degree centrality, betweenness centrality, and closeness centrality (Ahmad et al., 2022).

2.3 GO and KEGG Pathway Enrichment Analysis

GO analysis was conducted to examine biological processes, molecular functions, and cellular components associated with the identified targets. KEGG pathway analysis was performed to identify key signaling pathways involved in CC treatment (Chen et al., 2017).

2.4 Visualization of Core Targets

Cytoscape software was used to visualize core targets and analyze their role in CC progression and treatment (Doncheva et al., 2019).

3. Results

3.1 Overlapping Targets of Betanin and Colon Cancer

A total of overlapping targets was identified, indicating potential therapeutic targets for betanin in CC treatment. These targets include proteins involved in apoptosis regulation, oxidative stress response, and tumor suppression (Figure 1).

3.2 PPI Network Analysis

The PPI network revealed the direct and indirect interactions among identified targets, highlighting their significance in CC pathophysiology (Figure 2).

3.3 GO Enrichment Analysis

GO analysis showed significant enrichment in biological processes such as apoptosis regulation, oxidative stress response, and immune modulation (Figure 3).

3.4 KEGG Pathway Analysis

KEGG analysis identified pathways such as PI3K-Akt signaling, Wnt signaling, and oxidative phosphorylation as key mechanisms through which betanin exerts its anticancer effects (Figure 4 & 5).

3.5 Core Targets Analysis

Visualization of core targets emphasized their role in disrupting CC progression by interfering with key cellular pathways (Figure 6).

4. Discussion

The network pharmacology approach provides a comprehensive understanding of betanin's pharmacological mechanisms in CC. The identification of core hub targets highlights their significance in mediating anticancer effects. Enrichment analyses further confirm betanin's role in regulating apoptosis, oxidative stress response, and immune modulation.

KEGG pathway analysis highlights the critical role of PI3K-Akt and Wnt signaling in CC, pathways known to mediate survival, proliferation, and resistance mechanisms. Betanin's ability to modulate these pathways suggests its potential in overcoming drug resistance and enhancing treatment efficacy. Additionally, betanin's antioxidant and anti-inflammatory properties provide further therapeutic benefits in CC management.

Future research should focus on experimental validation through in vitro and in vivo models. Additionally, exploring betanin's synergistic effects with existing CC treatments could pave the way for integrative therapeutic approaches.

5. Conclusion

This study elucidates the pharmacological mechanisms of betanin in colon cancer treatment using a network pharmacology approach. By identifying key molecular targets and pathways, our findings provide a scientific basis for further experimental validation and clinical applications. The study underscores the potential of natural compounds like betanin in addressing complex diseases such as CC.

Declarations

Ethics approval statement

No ethical approval was required for the current study as it did not deal with any human or animal samples.

Consent to participate

Not applicable

Consent to publish

Not applicable

Data Availability Statement

The data are available from the corresponding author upon reasonable request

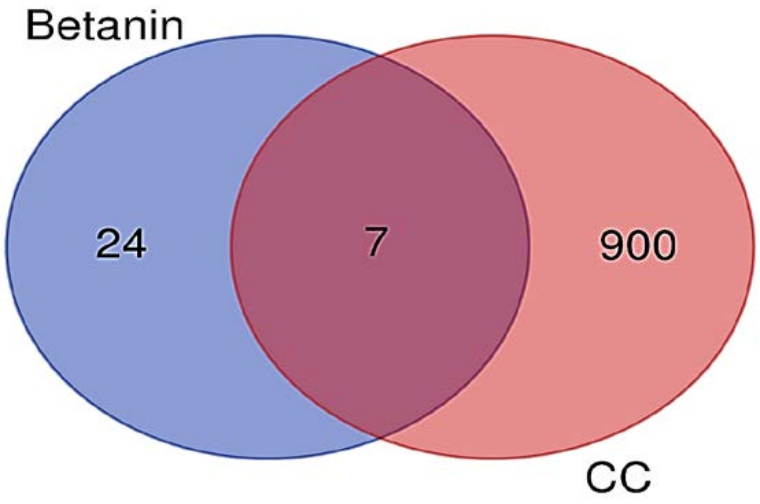

Figure 1: Venn diagram of betanin and CC to detect targets

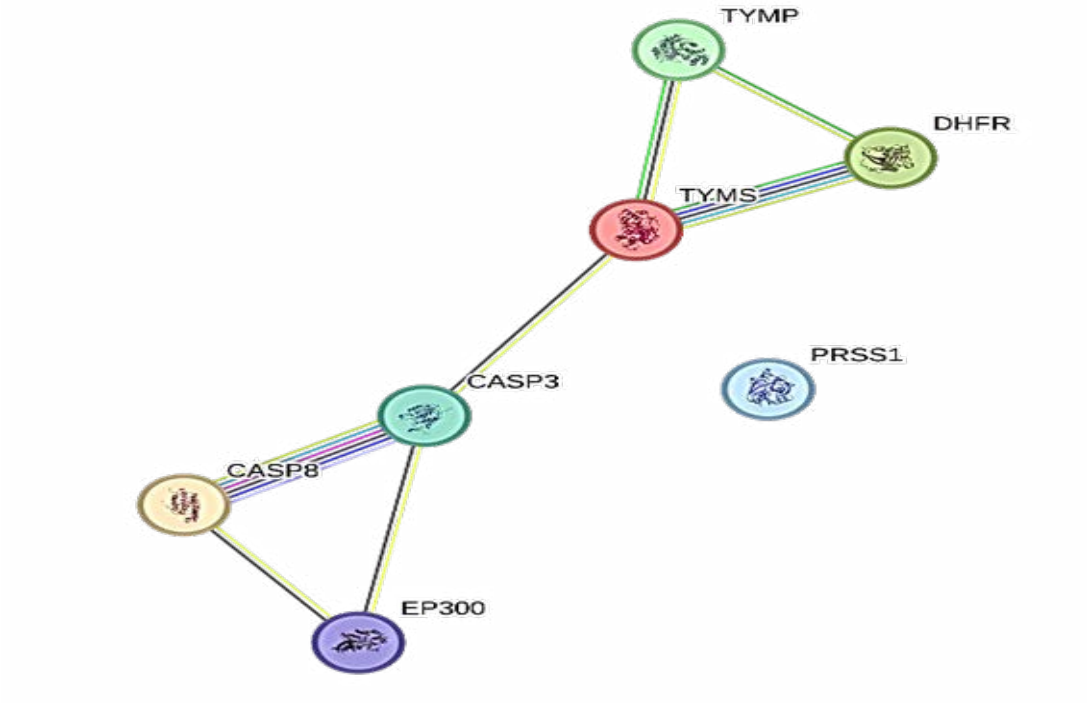

Figure 2: STRING database PPI network

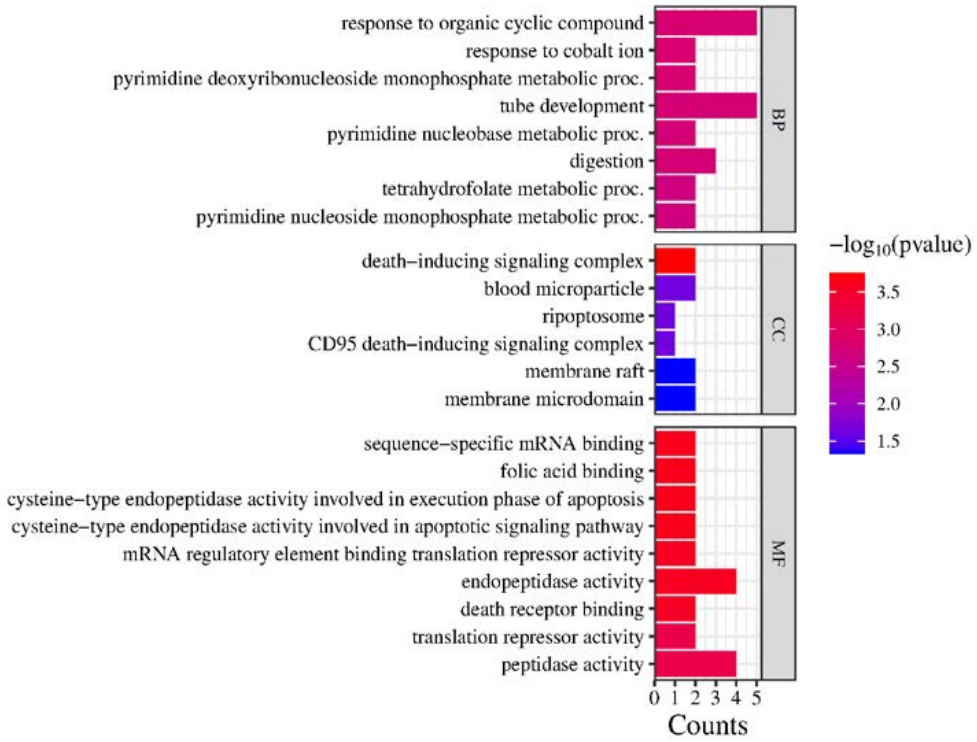

Figure 3: GO enrichment analysis

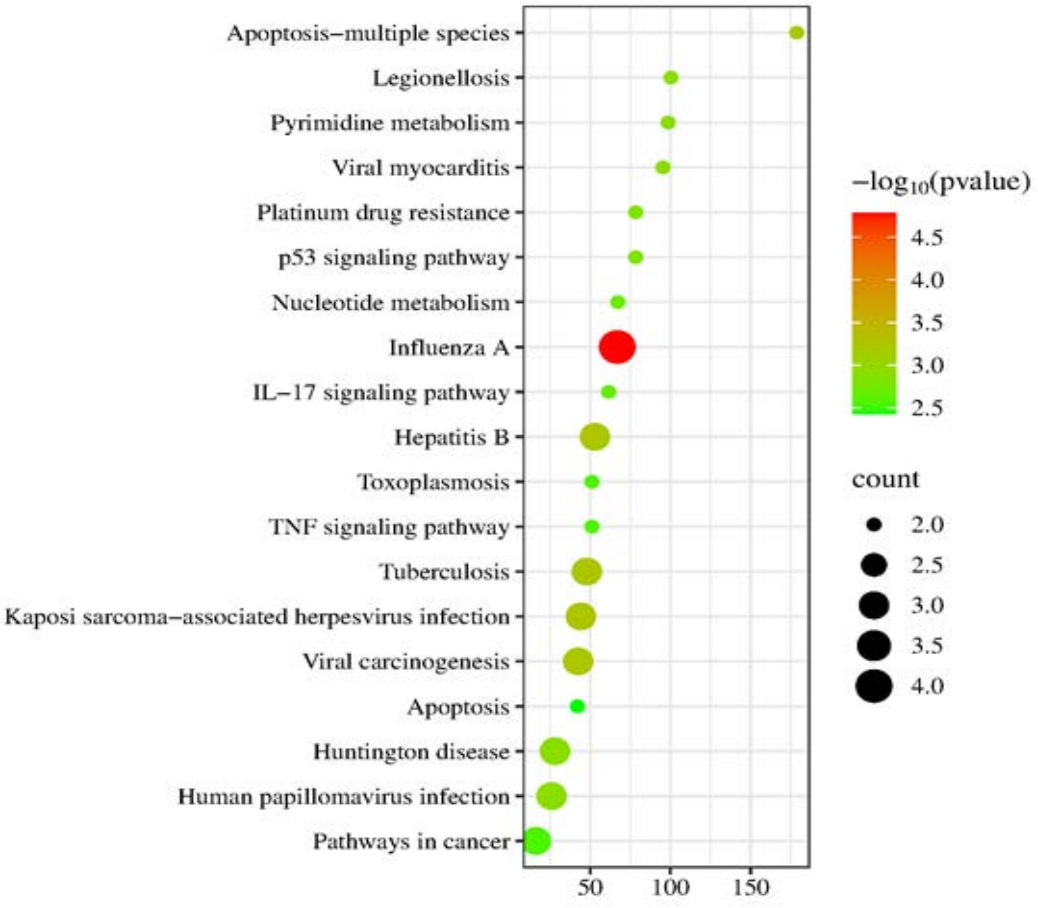

Figure 4: FTIR analysis of HT-Au NPs

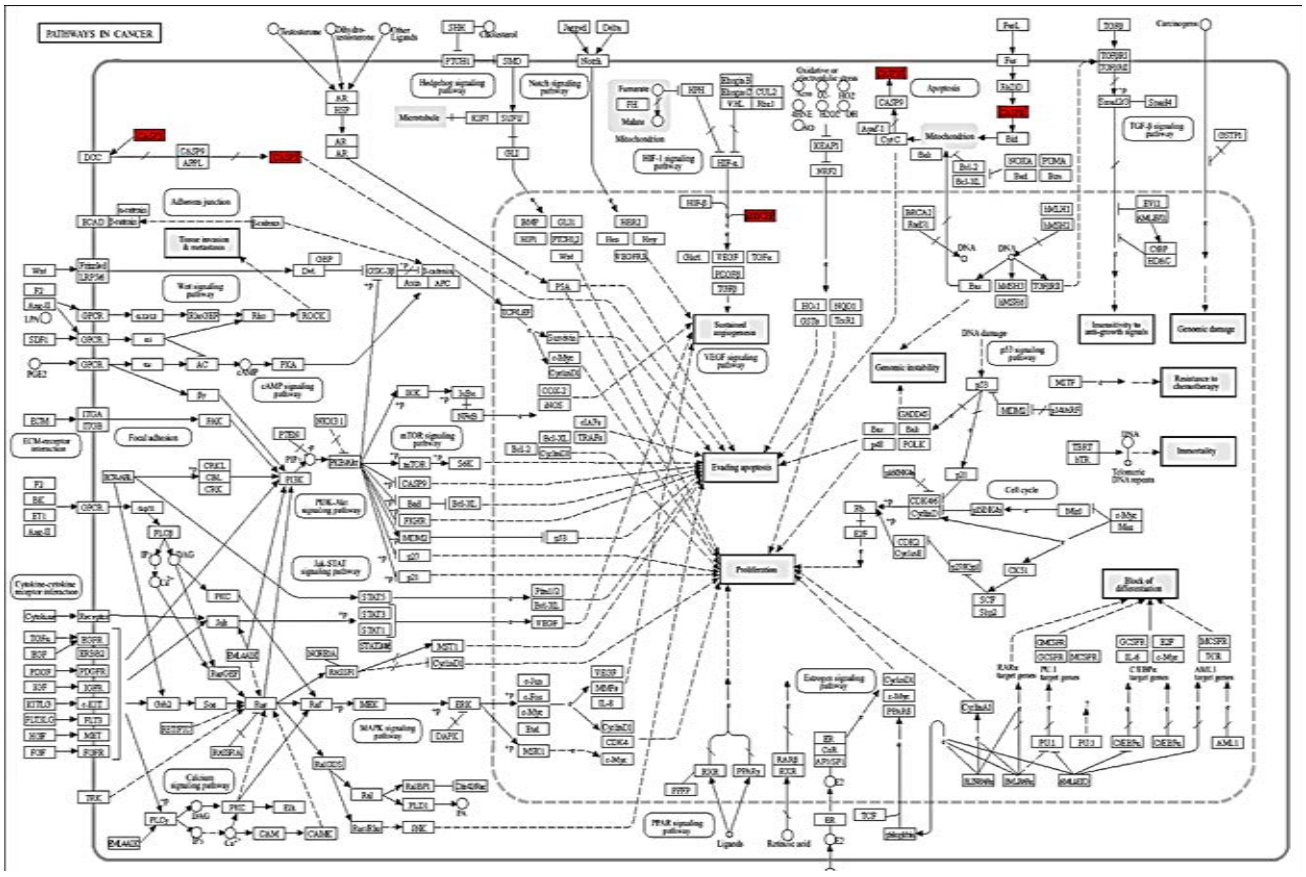

Figure 5: KEGG pathway analysis showing betanin's role in CC treatment

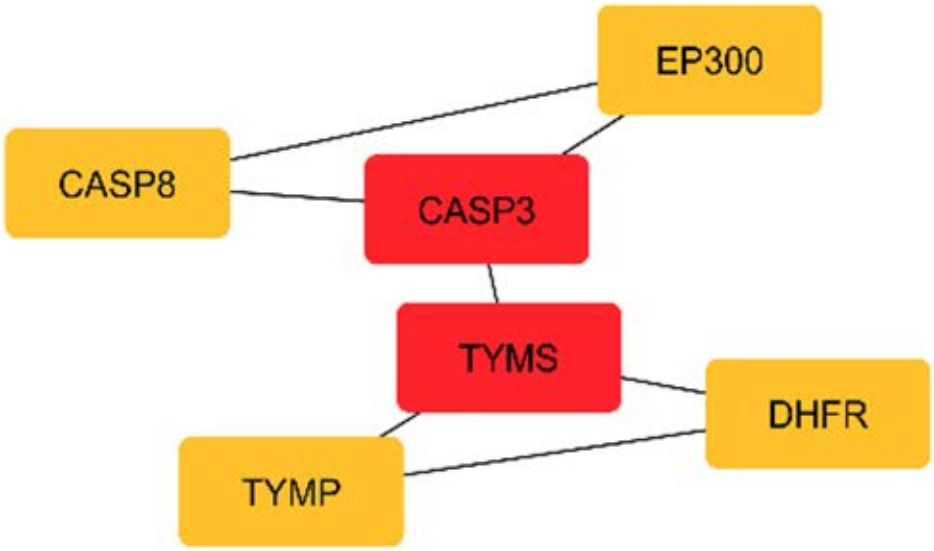

Figure.6: Inverted structures depicting the top core hub targets of betanin in CC

Competing Interests

The authors declare that they have no conflict of interest

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Author contribution

Conceptualization, Data curation, Investigation: T.M, A.S.N.N, C.A.D. Formal analysis: E.B Writing—review and editing: EB. All authors have read and agreed to the published version of the manuscript

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