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Advancement of Network Pharmacology in Multi-targeted Therapeutic Evaluation of Medicinal Plants

Gaurav Gautam

Senior Researcher, Department of Pharmacognosy and Phytochemistry, IIMT College of Medical Sciences, IIMT University, 'O' Pocket Ganga Nagar-250001, Meerut, Uttar Pradesh, India.

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***Corresponding Author:** Gaurav Gautam, Senior Researcher, Department of Pharmacognosy and Phytochemistry, IIMT College of Medical Sciences, IIMT University, 'O' Pocket Ganga Nagar-250001, Meerut, Uttar Pradesh, India.

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Abstract

In recent years, network pharmacology has emerged as a powerful approach for understanding the complex interactions between various bioactive components of medicinal plants and their targets within biological systems [1,2]. This approach plays a pivotal role in evaluating the multi-targeted therapeutic potential of medicinal plants, making it a promising tool for drug discovery and development. The integration of traditional knowledge with modern analytical techniques and computational methods has enabled the comprehensive exploration of the pharmacological properties of medicinal plants [3–6]. Medicinal plants have been an essential part of traditional medicine systems worldwide for centuries. These plants contain a wide array of bioactive compounds, such as alkaloids, flavonoids, terpenoids, and polyphenols, which exert therapeutic effects through interactions with specific molecular targets [7,8]. However, elucidating the intricate relationships between these compounds and their targets has proven challenging [2].

Network pharmacology offers a holistic approach to this problem by incorporating techniques from network science, systems biology, and chemoinformatics. It allows researchers to construct complex interaction networks that connect bioactive compounds to their target proteins. By analyzing these networks, it becomes possible to predict how different compounds from medicinal plants may exert their therapeutic effects on various disease pathways [9,10]. One of the major advantages of network pharmacology is its capacity to explore the potential multitargeted effects of medicinal plants. Unlike single-target drugs, many diseases involve a network of interconnected molecular pathways. Medicinal plants, with their multiple bioactive components, can influence multiple points within these networks, providing a holistic approach to treatment [3,7,11,12]. In a recent study conducted on network pharmacological based exploration of therapeutic targets of *Boerhaavia diffusa and Tinospora cordifolia* herbal combination in chronic kidney disease, it has been reported that the major constituents of these plants such as quercetin, ferulic acid, gallic acid, ameliorates the different pathophysiological targets in treatment of kidney disease [4]. Ekbbal et al reported that effect of rosmarinic acid in regulation of Proto-Oncogene c-Fos, Interleukin 2 and Poly (ADP-Ribose) Glycohydrolase, lymphocyte-specific protein tyrosine kinase (LCK), an inhibitor of nuclear factor kappa B kinase subunit beta (IKBKB), C-C motif chemokine receptor 3 (CCR3), Protein C Receptor (PROCR), etc Genomic Expression in attenuation of diabetes and associated complications [13]. Gautam (2022) reported traditional therapeutic claim of *Momordica Charantia* in alleviation of diabetic nephropathy using neptrok pharmacological approaches. The results showed that polyphenols present in *Momordica Charantia* play a significant role in the etiology and treatment of diabetic neuropathy by regulating numerous genomes includes AKTs, CASPs, MAPKs, ILs, NOs, etc [6].

In a study published in Biomedicine journal, multi-mechanistic and therapeutic targets were determined of a India's polyherbal formulation "NEERI KFT" using network pharmacological approaches and reported that gallic acid, quercetin, ferulic acid, etc exhibits a significant role in alleviation of nephrotoxicity induce by cisplatin [3,14]. Tinospora cordifolia is one of the most india's famous medicinal plants used for several therapeutic effect. Gaurav et al reported that it plays a significant effect in alleviation of kidney disease via regulating several pathophysiological targets involved in kidney disease. Furthermore, it was reported that five fatty acids were identified by network pharmacological interaction analysis as having a significant impact on genes including AGTR1, ATG, RELA, NOS3, NOS2, REN, INS, IL6, TNF, MAPK1, and CASP3. These genes may be able to regulate a number of pathophysiological conditions, including insulin resistance, hypertension, oxidative and inflammatory stress, and electrolyte homeostasis, thus supporting normal kidney function [5].

Additionally, network pharmacology helps identify critical hubs or key target proteins within the interaction network [13,15,16]. These hubs often play essential roles in disease development and progression. By targeting these hubs, researchers can develop more effective therapeutic strategies and prioritize compounds with the highest potential for clinical success. Furthermore, network pharmacology assists in the identification of drug-repurposing opportunities. Many medicinal plants have been traditionally used for specific conditions, but network pharmacology may reveal their potential efficacy in treating other diseases. This approach minimizes the time and cost required for developing new drugs by repurposing existing natural remedies [13,17,18]. It has been reported that [19].

In conclusion, the advancement of network pharmacology has provided a robust platform for the multi-targeted therapeutic evaluation of medicinal plants. It combines the knowledge of traditional medicine with modern techniques to uncover the intricate interactions between bioactive compounds and their molecular targets. This approach enhances our understanding of the therapeutic potential of medicinal plants, making them valuable sources of new drug candidates and treatment strategies. As we continue to unveil the full potential of network pharmacology, we can expect more effective and holistic approaches to addressing various health challenges.

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