International Journal of Biotechnology and Clinical Medicine ISSN 2583-4665
Vol.3, No.4, Oct - Dec 2024, pp. 92~94

THE ROLE OF NETWORK PHARMACOLOGY IN TARGET IDENTIFICATION

KM. Saravanan[1]*
[1]B Aatral Biosciences Private Limited, Bengaluru - 560091, Tamil Nadu, India

Article Info

Article history:

Received October 24th, 2024
Revised October 30th, 2024
Accepted November 15th, 2024

Keyword:

Network biology
Pharmacology
Brain Disorders
Neurology
Disease target

ABSTRACT

As the pharmaceutical landscape shifts toward precision medicine, network pharmacology offers a revolutionary approach to understanding the complex interplay of biological systems. It moves beyond the traditional "one-drug, one-target" paradigm to a more holistic "multi-target" strategy. This paradigm shift holds immense promise for addressing diseases with multifactorial etiologies, such as cancer, neurodegenerative disorders, and metabolic syndromes.

Corresponding Author:

Dr. KM. Saravanan,
B Aatral Biosciences Private Limited, Bengaluru - 560091,
Karnataka, India.
Email: saravananbioinform@gmail.com

How to Cite:

Saravanan KM. The role of network pharmacology in target identification. IJBTCM. 2024; Volume 3 (Issue 4): Page 92-94.

EDITORIAL

Drug discovery traditionally relied on identifying single molecular targets implicated in a disease pathway. While this approach has yielded success, it often fails to address the complexity of diseases influenced by interconnected biological networks [1]. Single-target drugs can lead to suboptimal efficacy or unintended side effects due to their narrow scope and inability to account for compensatory mechanisms within the biological system. Network pharmacology addresses these limitations by leveraging advances in systems biology, computational modeling, and data integration [2]. It views diseases as the result of perturbations in biological networks rather than isolated molecular anomalies. This perspective allows for identifying key nodes or hubs within these networks that can serve as potential therapeutic targets. By considering the interdependencies and redundancies inherent in biological systems, network pharmacology provides a more comprehensive framework for target identification [3].

The application of network pharmacology relies on a suite of advanced tools and methodologies: Biological Network Construction: Using high-throughput omics data (genomics, proteomics, transcriptomics), researchers construct disease-specific networks that map interactions between genes, proteins, and metabolites [4]. Tools like Cytoscape and STRING enable visualization and analysis of these networks. Network Analysis: Techniques such as centrality analysis, modular analysis, and pathway enrichment help identify critical nodes or subnetworks associated with disease progression [5]. These nodes often represent potential drug targets. Data Integration: Combining data from multiple sources, such as public databases, patient cohorts, and literature mining, enhances the robustness of network models. Resources like KEGG, Reactome, and DrugBank provide invaluable information for constructing comprehensive networks. Computational Drug Repurposing: Network pharmacology facilitates the identification of existing drugs that can modulate multiple nodes within a disease network [6]. This repurposing strategy accelerates the drug development timeline and reduces costs. Multi-Omics Integration: Advances in artificial intelligence and machine learning enable multi-omics data integration

to refine network models, ensuring that they reflect the dynamic and context-dependent nature of biological systems [7].

Network pharmacology has already demonstrated its potential in various therapeutic areas. For example, In cancer In oncology, network pharmacology has been used to identify synergistic drug combinations that target multiple pathways simultaneously [8]. This approach helps overcome resistance mechanisms often encountered with monotherapies. Neurological Disorders: For diseases like Alzheimer's and Parkinson's, network-based strategies have identified novel targets by focusing on the interplay between genetic mutations, protein aggregation, and metabolic dysfunction. Cardiovascular Diseases: Network pharmacology has enabled the discovery of multi-target drugs that modulate interconnected pathways involved in atherosclerosis and hypertension. Infectious Diseases: The COVID-19 pandemic underscored the value of network pharmacology in rapidly identifying potential drug targets and repurposing existing therapies to address emerging threats [9].

Despite its promise, network pharmacology faces several challenges: Data Quality and Standardization: The accuracy of network models depends on high-quality, standardized data. Variability in experimental conditions and data sources can compromise model reliability. Computational Complexity: Constructing and analyzing large-scale networks require significant computational resources and expertise in bioinformatics. Biological Validation: Computational predictions must be validated experimentally, which can be resource-intensive and time-consuming [10]. To overcome these hurdles, interdisciplinary collaboration is essential. Integrating expertise from computational biology, pharmacology, and clinical research will accelerate the translation of network pharmacology insights into therapeutic innovations. Moreover, developing user-friendly software tools and standardized data-sharing frameworks will democratize access to network pharmacology approaches [11].

Network pharmacology represents a transformative approach to target identification, offering a comprehensive view of disease mechanisms and enabling the development of multi-target therapies. By embracing the complexity of biological systems, this field is poised to address the challenges of modern medicine and deliver solutions for previously intractable diseases.

FUNDING

Nil

COMPETING INTEREST

The authors declare no conflict of interest.

REFERENCES

[1] Sreeraman S, Kannan MP, Singh Kushwah RB, Sundaram V, Veluchamy A, Thirunavukarasou A, Saravanan KM. Drug design and disease diagnosis: the potential of deep learning models in biology. Current Bioinformatics. 2023;18(3):208-20.

[2] Balaji AP, Bhuvaneswari S, Raj LS, Bupesh G, Meenakshisundaram KK, Saravanan KM. A review on the potential species of the zingiberaceae family with anti-viral efficacy towards enveloped viruses. J Pure Appl Microbiol. 2022;16(2):796-813.

[3] Saravanan KM, Zhang H, Hossain MT, Reza MS, Wei Y. Deep Learning-Based Drug Screening for COVID-19 and Case Studies. Methods Pharmacol. Toxicol., 2021, p. 631–60.

[4] Le HT, Murugesan A, Ramesh T, Yli-Harja O, Mani SK, Kandhavelu M. Molecular interaction of HIC, an agonist of P2Y1 receptor, and its role in prostate cancer apoptosis. International journal of biological macromolecules. 2021;189:142-50.

[5] Saravanan KM, Palanivel S, Yli-Harja O, Kandhavelu M. Identification of novel GPR17-agonists by structural bioinformatics and signaling activation. International journal of biological macromolecules. 2018;106:901-7.

[6] Saravanan KM, Selvaraj S. Performance of secondary structure prediction methods on proteins containing structurally ambivalent sequence fragments. Peptide Science. 2013;100(2):148-53..

[7] Vijayaram S, Kannan S, Saravanan KM, Vasantharaj S, Sathiyavimal S, Palanisamy SP. Preliminary phytochemical screening, Antibacterial potential and GCMS analysis of two medicinal plant extracts. Pakistan journal of pharmaceutical sciences. 2016;29(3): 819-822.

[8] Saravanan KM, Krishnaswamy S. Analysis of dihedral angle preferences for alanine and glycine residues in alpha and beta transmembrane regions. Journal of Biomolecular Structure and Dynamics. 2015;33(3):552-62..

[9] M. Saravanan K, Selvaraj S. Search for identical octapeptides in unrelated proteins: Structural plasticity revisited. Peptide Science. 2012;98(1):11-26.

[10] Zhang H, Zhang T, Saravanan KM, Liao L, Wu H, Zhang H, et al. DeepBindBC: A practical deep learning method for identifying native-like protein-ligand complexes in virtual screening. Methods 2022;205:247–62.

[11] Saravanan KM, Zhang H, Zhang H, Xi W, Wei Y. On the Conformational Dynamics of β-Amyloid Forming Peptides: A Computational Perspective. Front Bioeng Biotechnol 2020;8:00532.