UTJMS 2025 October 15, 14(S1):e1-e1

doi:10.46570/utjms-2025-1521

## Identifying Repurposable Drugs for Schizophrenia using Transcriptomic Datasets

Roshan Sirole<sup>1</sup>, Ali Imami<sup>1</sup>, Robert E. McCullumsmith<sup>2\*</sup>

<sup>1</sup>College of Medicine and Life Sciences, 3000 Arlington Avenue, The University of Toledo, Toledo OH 43615 <sup>2</sup>Professor, Chair of Department of Neurosciences and Psychiatry, 3000 Arlington Avenue, The University of Toledo, Toledo OH 43615

Email: robert.mccullumsmith@utoledo.edu

Received: 12/6/2024

Accepted: 12/13/2024

Published: 10/15/2025

**Background:** Schizophrenia (SCZ) is a neuropsychiatric disorder that significantly affects cognition, behavior, and emotional regulation in approximately 0.45% of adults worldwide. Identification of effective treatment is critical to address the diverse and persistent symptoms of SCZ, particularly cognitive deficits and treatment-resistant cases.

**Objectives:** This study aims to identify repurposable drugs capable of reversing the dysregulated gene expression patterns associated with SCZ using a bioinformatics-driven approach, leveraging transcriptomic data from SCZ patient samples.

**Methods:** Differential gene expression data from the PsychENCODE database were analyzed to identify SCZ-specific molecular signatures. These were systematically compared to drug-induced transcriptomic profiles from public repositories. Utilizing the computational tool DrugFindR, candidate drugs with established safety profiles were prioritized for their potential to counteract SCZ-associated gene dysregulation.

**Results:** The analysis identified multiple candidate drugs, including FDA-approved medications and those in clinical trials, with transcriptomic profiles discordant to SCZ-associated molecular changes. These drugs demonstrated the ability to reverse key dysregulated gene expression patterns, suggesting potential therapeutic benefits. Computational methodologies ensured an efficient, cost-effective approach, highlighting both validated and novel compounds that warrant further experimental exploration.

**Conclusion:** This study underscores the potential of computational bioinformatics in drug repurposing for psychiatric disorders. By identifying drugs that target SCZ-associated gene dysregulation, we provide a promising avenue for precision medicine in SCZ treatment. The findings not only validate existing candidates but also introduce new therapeutic options that could significantly improve outcomes for patients with SCZ.

Keywords: Schizophrenia, SCZ, Treatment-resistant Schizophrenia, Gene Dysregulation, Drug Repurposing