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Transcriptomic Analysis of Frequently Prescribed Herbal Medicines

Heeseon Jo[1], and Haeseung Lee[1,*]

[1] *Department of Pharmacy, College of Pharmacy and Research Institute for Drug Development,*
Pusan National University

**Corresponding author: haeseung@pusan.ac.kr*

Samul-tang and Sagunja-tang are representative prescriptions in oriental medicine that are used to regulate 'Blood' (血) and 'Qi' (氣) for treating various diseases. However, due to their complex compositions, it remains challenging to determine which mechanisms are predominantly involved and which components are responsible for these effects.

To address this challenge, we conducted a systematic transcriptomic analysis across multiple cell lines treated with Samul-tang and Sagunja-tang. We found both prescriptions modulated several common biological pathways, particularly those involved in VEGFA-VEGFR2 Pathway, glycolysis and gluconeogenesis, mitochondrial electron transport chain, supporting their shared therapeutic effects. A comparative analysis revealed a unique effect of Sagunja-tang, specifically downregulating a liver-specific pathway essential for cholesterol biosynthesis on HepG2 liver cells. Further compound-target network analysis identified eight potential bioactive compounds from Sagunja-tang that may contribute to this pathway modulation.

This study provides proof of concept for identifying bioactive compounds within complex herbal formulations, offering a foundation for further investigation into their mechanisms of action in traditional medicine.