## Signaling Pathways-based Approach for Identifying Mechanisms of Herbal Medicines

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## Abstract

Indonesian Herbal Medicine (IHM) has been recognized as one of the most important strategies in complementary and alternative medicine. In Indonesia, many of this herbal knowledge were passed down from one generation to the next through oral tradition and daily rituals. Nowadays, IHM is developed to meet the requirement of Indonesian Healthcare System. However, understanding its mechanism of action in the treatment of disease remains unknown due to its numerous complex compound mixtures that often bound transiently to multiple therapeutic targets. Investigating the mechanism of action of the IHM formula is key to the modernization of IHM. Identifying which are the active compound(s) of IHM formulas, which biological entities they target, and through which signaling pathway(s) they act to modify disease symptoms, can be studied with multiple approaches including network pharmacology, pharmacogenomics, proteomics, and metabolomics. The concept of network pharmacology is built on the belief that targeting multiple nodes in interconnected molecular systems rather than individual molecules, which could lead to better efficacy and fewer adverse effects. A network pharmacology approach can integrate prediction of ingredients, target exploration, network construction, module partition and pathway analysis. This approach successfully helped to identify several active ingredients of IHM, interacting with several important key targets. Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analysis indicated that IHM-regulated pathways were mainly classified into several systems. The present work may help to illustrate the mechanism(s) of action of IHM, and it may provide a better understanding of herbal formula effects.

Keywords: action mechanism, Indonesian Herbal Medicine, pathways analysis, targets prediction