

Effectiveness of *Amorphophallus paeoniifolius* hydroalcoholic extract in asthma using network pharmacology and OVA–LPS rat model

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Amorphophallus paeoniifolius hydroalcoholic extract (HAE) possesses reported anti-inflammatory and bronchodilator properties and is traditionally used for asthma and cough. The present study aimed to investigate its anti-asthmatic potential using network pharmacology, followed by experimental validation. Major phytoconstituents of HAE were screened for target prediction and protein–protein interaction analysis. Gene ontology and KEGG pathway enrichment analyses were performed using STRING. Anti-asthmatic activity was evaluated in an ovalbumin–lipopolysaccharide (OVA–LPS)-induced rat model. Haematological parameters, inflammatory markers, Th2 cytokines, and lung histopathology were assessed and analysed using one-way ANOVA ($p < 0.05$). Lupeol, quercetin, resveratrol, stigmaterol, and β -sitosterol were identified as key bioactive compounds targeting asthma-related genes. Enrichment analysis highlighted TNF, Toll-like receptor, NOD-like receptor, and MAPK signalling pathways as major inflammatory regulators. *In vivo*, HAE significantly ($p < 0.05$) reduced total and differential leukocyte counts, Th2 cytokines, mast cell infiltration, airway inflammation, mucus hypersecretion, and bronchial hyperresponsiveness. Histopathology confirmed attenuation of inflammatory cell infiltration and airway remodelling. HAE exerts significant anti-asthmatic effects through multi-target immunomodulatory and anti-inflammatory mechanisms.

Keywords: *Amorphophallus paeoniifolius*, Asthma, Gene ontology, KEGG pathway, Network pharmacology, Th2 cytokines

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