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Short Communication

Evaluation of Herbal Components of Chrysanthemum in Fatty Liver Disease

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DESCRIPTION

Metabolic dysfunction-associated fatty liver disease represents an expanding global health concern, shaped by sedentary lifestyles, caloric excess and complex metabolic disturbances involving lipid accumulation, insulin resistance, oxidative damage and inflammatory signaling. The disorder evolves across a spectrum that includes simple steatosis, steatohepatitis, fibrosis and eventually cirrhosis or hepatocellular carcinoma in advanced cases. While existing treatments emphasize lifestyle changes and symptom management, a deeper understanding of cellular and molecular events is essential for identifying more effective therapeutic candidates.

Zebrafish present significant advantages as a biomedical model for metabolic research due to their genetic similarity to humans, transparent larvae, rapid development and capacity for high-throughput screening. Their liver structures, lipid metabolism processes and inflammatory responses resemble those found in mammals, making them ideal for studying hepatic disorders. When zebrafish larvae are fed a high-fat diet or exposed to lipid-rich compounds, they develop fat accumulation in the liver that closely parallels human steatosis. Observable alterations include enlarged hepatocytes, accumulation of lipid droplets, increased reactive oxygen species production and dysregulation of genes responsible for lipid synthesis and breakdown. These features allow clear visualization and quantification of disease progression as well as response to therapeutic compounds in a relatively short time frame.

The biological activities observed in the zebrafish model can be further explained through network pharmacology, which integrates systems biology, bioinformatics and cheminformatics to predict interactions between compounds and biomolecular targets. This approach allows for the mapping of multiple compounds present in Chrysanthemum to potential protein targets associated with metabolic dysfunction-associated fatty liver disease. Rather than focusing on a single molecule or receptor, network analysis considers how numerous compounds interact with a wide range of targets, producing coordinated biological effects.

One major pathway affected involves the regulation of fatty acid synthesis and oxidation. Normally, an imbalance between these two processes contributes to hepatic lipid overload. In the presence of Chrysanthemum-derived compounds, expression levels of genes involved in lipid synthesis, such as sterol regulatory element-binding proteins and fatty acid synthase, tend to decrease. At the same time, genes responsible for fatty acid breakdown and mitochondrial beta-oxidation show elevated expression. This coordinated activity contributes to a healthier lipid balance inside liver cells, allowing excess fat to be removed more efficiently.

Mitochondrial health is another significant factor in liver cell stability. Mitochondria serve as primary regulators of energy conversion and fatty acid oxidation. In a diseased state, mitochondrial structure becomes fragmented and energy conversion declines. Observations in zebrafish reveal that treated groups display improved mitochondrial morphology and more efficient energy metabolism. Network analysis supports interactions between Chrysanthemum components and mitochondrial enzymes and membrane proteins responsible for maintaining membrane potential and enzymatic function.

The multi-component nature of Chrysanthemum is particularly beneficial when addressing complex disorders driven by multiple interacting factors. Rather than targeting a single receptor or biochemical step, the plant's phytochemical profile allows for systemic modulation. This broad spectrum activity matches the complexity of metabolic dysfunction-associated fatty liver disease, which involves endocrine, inflammatory and metabolic disturbances simultaneously. The integrated zebrafish and network pharmacology method therefore provides a comprehensive way to observe how these compounds perform both at the organismal level and within intracellular networks.

CONCLUSION

The integration of a zebrafish model with network pharmacology analysis creates a powerful framework for exploring the therapeutic potential of Chrysanthemum in metabolic dysfunction-associated fatty liver disease. The model

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demonstrates improvements in lipid clearance, oxidative balance, inflammatory reduction, mitochondrial stability and insulin responsiveness. At a molecular level, network predictions support the involvement of numerous signaling and metabolic proteins that collectively shape disease development and regression. This dual-layered approach provides an efficient and reliable avenue for identifying natural compounds capable of modulating complex metabolic disorders, opening avenues for further research and eventual clinical investigation.

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