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Uncovering molecular mechanisms of muscle atrophy caused by different factors through a comprehensive transcriptome analysis

Hanbi Lee[1], No Soo Kim[2], Aeyung Kim[3], Haeseung Lee[4,*] and Hyuniin Shin[1,*]

[1] *MOGAM Institute for Biomedical Research, Seoul 06730, Republic of Korea*
[2] *KM Convergence Research Division, Korea Institute of Oriental Medicine, Daejeon 34054, Republic of Korea*
[3] *KM Application Center, Korea Institute of Oriental Medicine, Daegu 41062, Republic of Korea*
[4] *College of Pharmacy, Pusan National University, Busan 46241, Republic of Korea*

**Corresponding author: haeseung@pusan.ac.kr and hyunjin.shin@mogam.re.kr*

Skeletal muscle atrophy, also known as muscle wasting, is a physical condition in which muscle mass and strength significantly decrease. Muscle atrophy can occur for various reasons, including aging, drug treatment, and other chronic diseases such as cancer. It has a serious impact on both the quality of life and treatment outcomes for patients. However, the molecular mechanisms causing muscle atrophy are not fully understood yet. Therefore, we designed this study to identify possible molecular mechanisms by running a comprehensive transcriptome analysis on three types of muscle atrophy models induced by aging, dexamethasone treatment, and cancer cachexia. Interestingly, several molecular changes were commonly found from these models. For example, genes involved in extracellular matrix (ECM) and collagen pathways were downregulated, which may reflect weakened muscle and nearby tissue structures. On the other hand, each model demonstrated distinct expression patterns in immune signaling pathways. This indicates that immune signaling pathways may contribute to muscle atrophy in a context-dependent manner. In conclusion, developing more tailored therapeutic strategies for each type of muscle atrophy is important, because muscle atrophy can be caused by different factors even though similar symptoms are observed.