POSTER - RNA AND TRANSCRIPTOMICS

IDENTIFICATION OF TISSUE-SPECIFIC LONG NON-CODING RNAS ASSOCIATED WITH SKELETAL MUSCLE AND ADIPOSE TISSUE WASTING IN CANCER CACHEXIA

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Cancer cachexia is a multifactorial syndrome characterized by progressive weight loss in cancer patients, with specific losses of skeletal muscle and adipose tissue. Despite its impact on cancer patients, the exact mechanisms underlying skeletal muscle and adipose tissue wasting have not yet been fully elucidated. Recent research has shown that long non-coding RNAs (lncRNAs), a class of non-coding RNAs that are > 200 nt in length, play a significant role in metabolic abnormalities. The objective of this study was to identify lncRNAs associated with the complex mechanisms underlying the metabolic alterations of tissues severely affected by cancer cachexia. We searched for all microarray datasets publicly available in the GEO datasets (NCBI). Then, each dataset was

analyzed using GEO2R to identify the differentially expressed genes (DEG) between control and cachectic groups. The 24 datasets covered a range of tumor types and models, as well as different tissue types including muscle, adipose, brain, and liver samples from both humans (n = 176) and mice (n = 80). We found 128 tissue-specific lncRNAs in humans, with 67 been expressed in abdominal muscles and 26 in intra-abdominal adipose tissue. Only six lncRNAs (ADAMTSL4-AS1, BAALC-AS2, MIR100HG, DIO3OS, VLDLR-AS1, MIRLET7BHG) were shared between two or more human tissues. In mice, abdominal muscles also showed a high number of differentially expressed lncRNAs (44), with only 66 being shared between tissue. These tissue-specific features of lncRNAs make them potential mediators or therapeutic targets for cancer-associated cachexia. In conclusion, we identified tissue-specific lncRNAs associated with cachexia in humans and mice by analyzing microarray datasets from different tissue types. The tissue-specific features of lncRNAs make them potential mediators or therapeutic targets for the syndrome. The identification of specific lncRNAs associated with cachexia in different tissues can guide future co-expression studies and lead to the development of targeted treatments for cancer patients with cachexia.