A novel deep proteomic approach unveils molecular signatures affected by aging and resistance training

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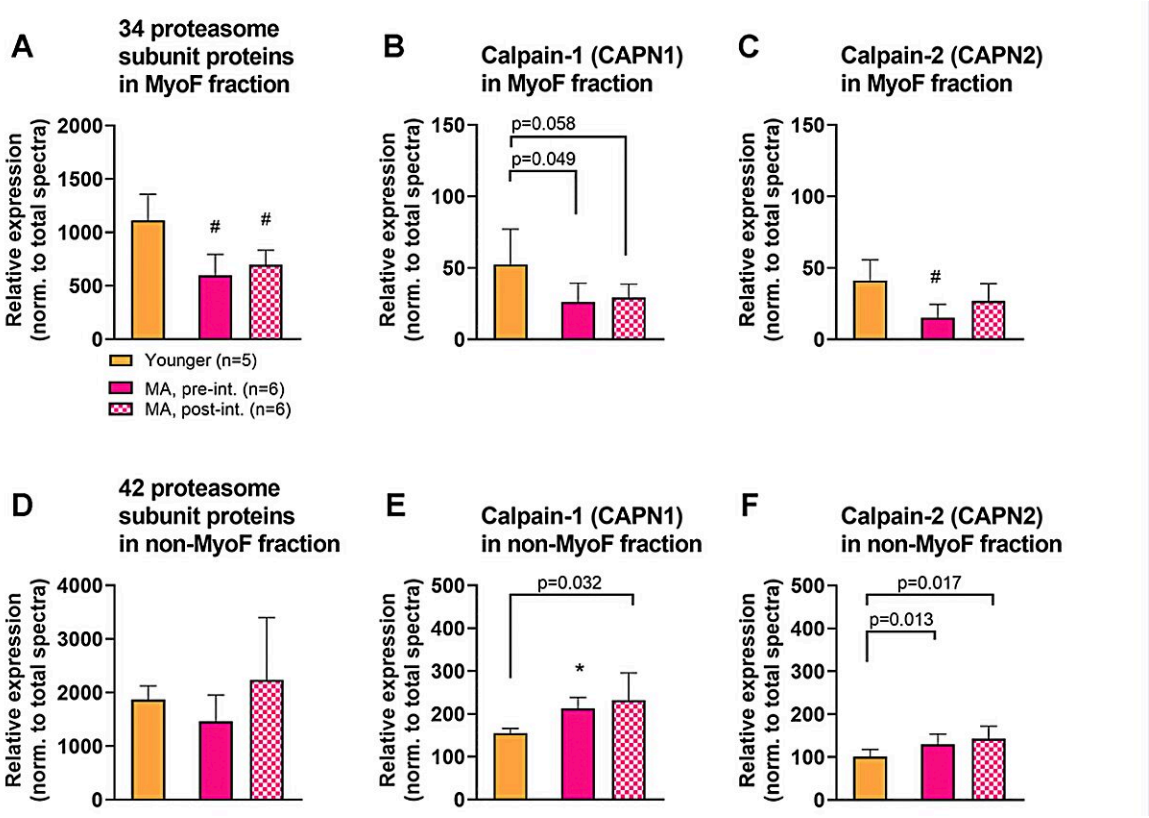

MyoF and non-MyoF proteasome and calpain proteins. Credit: *Aging* (2024). DOI: 10.18632/aging.205751

A new research paper was published in *Aging* titled, "A novel deep

proteomic approach in human skeletal muscle unveils distinct molecular signatures affected by aging and resistance training."

The skeletal muscle proteome alterations to aging and resistance training have been reported in prior studies. However, conventional proteomics in skeletal muscle typically yields wide protein abundance ranges that mask the detection of lowly expressed proteins.

In this new study, researchers from Auburn University, Seer, Inc., and The Center for Applied Health Sciences adopted a novel deep proteomics approach whereby myofibril (MyoF) and non-MyoF fractions were separately subjected to protein corona nanoparticle complex formation prior to digestion and Liquid Chromatography Mass Spectrometry (LC-MS).

"Specifically, we investigated MyoF and non-MyoF proteomic profiles of the vastus lateralis muscle of younger (Y, 22±2 years old; n=5) and middle-aged participants (MA, 56±8 years old; n=6). Additionally, MA muscle was analyzed following eight weeks of resistance training (RT, 2d/week)," the researchers write.

Across all participants, the number of non-MyoF proteins detected averaged to be 5,645±266 (range: 4,888–5,987) and the number of MyoF proteins detected averaged to be 2,611±326 (range: 1,944–3,101). Differences in the non-MyoF (8.4%) and MyoF (2.5%) proteomes were evident between age cohorts, and most differentially expressed non-MyoF proteins (447/543) were more enriched in MA versus Y.

Biological processes in the non-MyoF fraction were predicted to be operative in MA versus Y including increased cellular stress, mRNA splicing, translation elongation, and ubiquitin-mediated proteolysis. RT in MA participants only altered ~0.3% of MyoF and ~1.0% of non-MyoF proteomes.

"In summary, aging and RT predominantly affect non-contractile proteins in skeletal muscle. Additionally, marginal proteome adaptations with RT suggest more rigorous training may stimulate more robust effects or that RT, regardless of age, subtly alters basal state skeletal muscle protein abundances," the authors conclude.

More information: Michael D. Roberts et al, A novel deep proteomic approach in human skeletal muscle unveils distinct molecular signatures affected by aging and resistance training, *Aging* (2024). DOI: 10.18632/aging.205751

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