## Dynamic proteome profiling of individual proteins in human skeletal muscle after a high-fat diet and resistance exercise

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Aim: We used Dynamic Proteome Profiling (DPP) to estimate the contributions of synthesis and degradation to changes in protein abundance in human skeletal muscle following a diet-exercise intervention.

Methods: Following preliminary exercise testing, age-matched, overweight, sedentary males consumed 9 days of a high-fat diet (77% fat, 8% Carbohydrate, 15% protein; HFD) or HFD + resistance exercise (REX, 3 sessions). Participants ingested deuterium oxide (200 ml/d) during the 9-day intervention period to achieve an appropriate target enrichment of 1-2%. Muscle biopsies from the *vastus lateralis* were obtained prior to and post the HFD, as well as on Days 3 and 6 of the HFD. Venous blood samples were also collected daily during the HFD intervention. Blood and muscle samples were analyzed by mass spectrometry to determine precursor enrichment and the rate of incorporation of deuterium into newly synthesized protein, respectively.

Results: Of the 90 proteins included in the DPP analysis, 28 exhibited differences in either rates of synthesis or abundance after REX. The most common pattern of response was an increase in turnover. Several enzymes of the glycolytic pathway were less abundant in exercise-trained muscle despite elevated rates of synthesis, suggesting protein degradation was increased to a greater extent than the increase in synthesis.

Conclusion: Our findings provide empirical evidence that contributions of synthesis and degradation to overall changes in protein abundance induced by resistance exercise differs on a protein-by-protein basis. We also highlight the importance of the degradation of individual muscle proteins after exercise in human skeletal muscle.