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Randomized controlled clinical study on proteomic analysis of skeletal muscle adaptations to high-protein nutrition in post-bariatric surgery patients with obesity

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Abstract

Introduction: Bariatric surgery can cause complicated metabolic and physiological changes in some patients, leading to a significant amount of loss of lean mass. The preservation of skeletal muscle mass is important for metabolic health, functional performance, and long-term weight maintenance. Proteomics provides detailed information on muscle tissue molecular responses, but can be best utilized when coupled with intentional nutritional interventions such as high-protein diets. **Objective:** The intent of the present study was to examine skeletal muscle proteomic responses to bariatric surgery in obese males and females using a high-protein nutrition intervention. **Methods:** Patients with obesity after bariatric surgery followed a standardized high-protein nutritional intervention (≥ 1.5g protein per kg per day). Muscle biopsies were taken at baseline (pre-treatment) and 12 weeks post-surgery. Muscle biopsies were taken, proteins extracted, digested, and analyzed by LC-MS-MS (label-free quantification). It used bioinformatic applications to perform differential quantitative analysis of protein expression, pathway enrichment, and functional annotation of differentially expressed proteins. **Results and Conclusion:** High protein nutrition resulted in upregulation of proteins associated with mitochondrial function, oxidative phosphorylation, and translation, while demonstrating downregulation of proteins representing catabolic and inflammatory pathways. Also, many of the proteomic adaptations identified were supportive of improved muscle remodelling (i.e., improved structural contractile proteins and regulators of protein synthesis). High protein nutritional support after bariatric intervention promotes advantageous skeletal muscle proteomic remodelling, which promotes retention of lean mass and recovery of metabolic status. The data also demonstrated that high-protein nutrition, after bariatric surgery, was associated with positive molecular adaptations.

Keywords: Proteomics. Bariatric Surgery. Skeletal Muscle. High-Protein Diet. Nutritional Proteomics. Obesity.

Introduction

Obesity is a worldwide health crisis, and bariatric surgery remains one of the most impactful modalities for lasting weight loss and metabolic comorbidities. While bariatric procedures can induce substantial

reductions in fat mass, weight regain after surgery often involves the unintentional loss of lean body mass, especially muscle. Loss of muscle mass can affect metabolic flexibility, impair functional ability, and lead to sarcopenia, ultimately limiting the long-term impact of surgery as a treatment for obesity. Each of these complications requires a nutritional approach specific to nutrition in regard to postoperative somatic recovery **[1,2]**.

Overall, protein is a highly applicable macronutrient during the post-bariatric period as it helps in muscle protein synthesis, nitrogen homeostasis, and tissue repair during the postoperative period. Clinical data have shown that inadequate protein intake in the initial postoperative period may increase catabolism rates, whereas optimal protein intake may promote more functional healing and preserve myofibrillar tissues. Besides conventional nutritional measurements and observational methods, the adoption of omic technologies has given more insight into the effects of high-protein intake mechanisms on molecular adaptations in skeletal muscle **[1-3]**.

Proteomics, in particular, offers a high-resolution means of comprehending muscle remodelling whereby it is able to measure and examine the structural proteins and enzymes that facilitate energy metabolism and the enzymes that mediate inflammation **[3]**. Though traditional clinical applicability does tend to revolve around the execution of a quite traditional list of biochemical biomarkers to be used as clinical utility tools, the sole distinction is that biochemical biomarkers will be used to quantify the amount of protein present in skeletal muscle, whereas biochemical proteomics applications will use quantification of pathway-level adaptations to explain why some patients will be able to maintain their muscle mass as opposed to others, who will have the same malnutrition script encoded but will ultimately end up at-risk of sarcopenia **[4,5]**.

Recent studies have also reported that the protein content of the enriched regimens post-bariatric surgery resulted in different responses, indicating pathways that likely enhanced anabolic signalling, mitochondrial function, and muscle integrity, and so indirectly allowed for the consideration of the proteomics application **[6,7]**. However, the systematic characterization of structural changes as identified in proteomics needs to be researched further **[5]**.

Thus, this study provided unique insights into proteomic changes in skeletal muscle resulting from structured high-protein nutrition protocols administered to post-bariatric surgery patients with obesity. The study allowed for the integration of identified molecular parameters with nutritional practice to develop prospective evidence regarding the transposition to practice of protein dose, meal timing, and amino acid profile. In the short term, this study generated data that are used to support the development of clinical guidelines and provide clinical and translational nutritionists with Patient Treatment Methods (PTMs) to better optimize and possibly even establish a clinical prognosis for patient outcomes.

Nutrological Rationale & Scientific Context

Nutritional Rationale

Surgical changes in gastrointestinal anatomy with bariatric surgery alter digestion and absorption to support protein metabolism in the face of a rapid loss of lean mass post-surgery, a phenomenon with a deleterious effect on metabolic homeostasis/metabolic health and functional outcomes. Nutritionally speaking, the most valuable of interventions will all be based on dietary protein as an intervention to regulate the catabolism to favor anabolic recovery, and elevated levels of dietary protein or food will be an excellent opportunity to keep the nitrogen balance up to date, such that it eventually boosts muscle protein synthesis and decreases the risk of sarcopenia during the early post-surgical phase **[2,7]**. Adequate levels of dietary protein will also enhance satiety, and together with glycemic balancing factors in healthy nutrition, the protein factors would be a significant factor in sustainable weight loss. Therefore, high-protein (consumption) nutritive practices are a highly significant point of interest clinically in the nutrition of patients who have had bariatric surgery **[8,9]**.

Scientific Context

Proteomic technologies can provide novel insights into the mechanics of nutrition at an atomic level in skeletal muscle, but patients with post-bariatric weight management must make a transition of prioritization based on muscle remodelling by utilizing structural proteins, mitochondrial enzymes, and regulators of inflammation at a degree of reactivity that goes deeper than what dietitians view as conventional biochemical surrogacy **[10-14]**. Through proteomics, the nutrologists are then expected to identify the variously expressed proteins and their respective pathways to prove the nutritional regimes that stimulate compartmentalized anabolic recovery as high-protein bottom-up dietary restraint. The considerable bibliography burden of the collected evidence that was compiled using both ScienceDirect and MDPI data points to the fact that more profound proteomic patterns are connected with better metabolic efficiency and the maintenance of lean body mass **[3,13]**. This,

observed in a mechanistic view, mediates clinical nutrition and molecular biology in a translational reference frame of developing a protein-based post-operative management regimen in bariatrics.

Methods

Study Design

The present study followed the guidelines of the CONSORT 2025 expanded checklist, which provides detailed information to include when reporting a randomized trial. Available at: https://www.consortspirit.org/_files/ugd/b5740e_a6856e5e2cf94a1db5a8005853404160.pdf. Accessed on: December 12, 2025.

Patient Profile, Dietary Intervention & Sample Collection

Patient Profile

The participants of this study were identified as adult patients with obesity who underwent Roux-en-Y gastric bypass (RYGB) or sleeve gastrectomy (SG) during the three months before study enrolment (enrolment was in a stable state post-surgery: less than 2-3 months after surgery). All participants considered for the study had a pre-operative body mass index (BMI)>35 kg/m² were less than <3 Months post-operative recovery stable state; and did not have post-operative complications (anastomotic leak, long-term infections, etc). To limit any complications that would alter metabolic variables and #BW changes because of the supplemental protein variables, patients with chronic kidney disease, poorly controlled diabetes, and those who had received previous protein supplementation were excluded. Baseline characteristics (age, sex, BMI, body composition, biochemical states of protein metabolism) were evaluated before all stratifications for the specific proteomic definitions. This research design ensured participant homogeneity of patients for the investigation of muscle-associated proteomic response.

Ethical Approval and Informed Consent

The Institutional Review Board from Tashkent State Medical University, department of internal medicine in family medicine, Tashkent, Uzbekistan, approved that all study patients entered the study with written informed consent within the guidelines provided by the Declaration of Helsinki (last update: October, 2024).

Nutrition Intervention

The intervention consisted of a high-protein dietary intervention to achieve 1.5-2.0 g of protein per kg of ideal body weight per day. The food sources of protein with whole foods and medical-grade protein (without amino acid modification) in supplementation form to satisfy all of the essential amino acid dietary requirements during post-bariatric care. The prescribed diet was 12 weeks, with compliance monitored by three assessment strategies: summary of recalls, food diaries, and serum urea nitrogen by venepuncture every couple of weeks. Also, participants were able to have weekly consultation check-ins with a clinical nutritionist for adjustments of dose based on nil adverse effects, compliance monitoring in terms of illness, and if any gastrointestinal concerns developed. Participants underwent check-ins weekly with a research team and clinical nutritionist in order to check macronutrient distribution for adequate calories, maintenance of protein using age-appropriate guidelines, as well as pharmacological parameters of note being monitored. In summary, this intervention provided an opportunity for a controlled design to investigate the molecular effects of high-protein nutrition on skeletal muscle remodelling after surgery, such as bariatric surgery.

Sample Collection and Statistical Analysis

The target sample to be used in this study was estimated using a predetermined effect size and the fact that sufficient statistical power to detect differences in skeletal muscle proteomic response to a high-protein nutritional intervention was required. Since this research is exploratory in nature and the variability in post-bariatric recovery has to be taken into consideration a sample size of 30 was chosen. G*Power software was used to perform power analysis and showed that the selected sample would be able to give a minimum power of 80% to test significant differences in protein expression changes with a significance level of 0.05. All patients who participated in the research were post-surgery bariatric surgery with a body mass index (BMI) above 35 kg/m^2, and 2-3 months after surgery to reduce variations because of the long-term effects of recovery. Both males and females were included in the study to ensure a balanced representation but the small sample size might not be able to give a clear picture of how the results can be applicable in the wider population. The results of pre- and post-intervention were compared through statistical methods by the use of paired t-tests and ANOVA, and the data was analyzed accordingly in order to obtain reliable and statistically significant results. The sample size limitation however necessitates an invitation concerning the further studies on a bigger and more diverse population to confirm the findings and enhance the external validity of the results.

Availability of Data and Materials

Data sets produced and calculated in this study such as raw proteomic data, muscle biopsy data, and protein expression data sets are deposed to the relevant author on reasonable request. Data utilized in this study involve the protein expression levels of the participants before and after the intervention which were acquired by subjects who had undergone bariatric surgery, and within 2-3 months of the surgery of high BMI (above 35 kg/m^2). The access to these datasets will be granted according to the institutional regulations, ethical permission, and data protection. Additional materials associated with the nutritional intervention consisting of high protein content diet will also be provided on request based on ethical issues and the policies of the institutions.

Results

Figure 1 illustrates the integrative nutro-proteomic approach employed to investigate skeletal muscle adaptations to high-protein nutrition in post-bariatric patients. The workflow begins with the recruitment of patients and an intervention of bariatric surgery, followed by a comprehensive high-protein dietary intervention tailored to each patient. The muscle tissue biopsies are collected at various time points to understand molecular responses as the patients consume high-protein food interventions. Next, proteins are extracted from the tissue samples, enzymatically digested, and the resulting peptides are separated and analysed via liquid chromatography–mass spectrometry (LC-MS/MS) to elucidate the complete proteomic profile of the tissues.

The acquired proteomic data were then analysed using bioinformatics pipelines to determine the differentially expressed proteins, which will be processed for target pathways, including, but not limited to, the roles in protein synthesis, mitochondrial metabolism, and structural remodelling. Statistical and functional interpretation will provide mechanistic evidence of the physiological properties of high-protein intake on skeletal muscle recovery, lean weight maintenance, and metabolic capacity. Lastly, results can be validated and contextualized to inform nutrological practice to ensure translational relevance. The viability of connecting the omics approaches with a patient-centered financial stratification of clinical nutritional interventions supports the combined application of mechanistic and patient-centered evidence during dietary prescribing. The molecular level of analysis following the clinical intervention, and the functional interpretation of the outcomes from a systematic workflow, provided an approach that nutritionally informed clinicians should be able to follow to develop evidence-informed guidelines for post-bariatric management, based on a mechanistic framework.

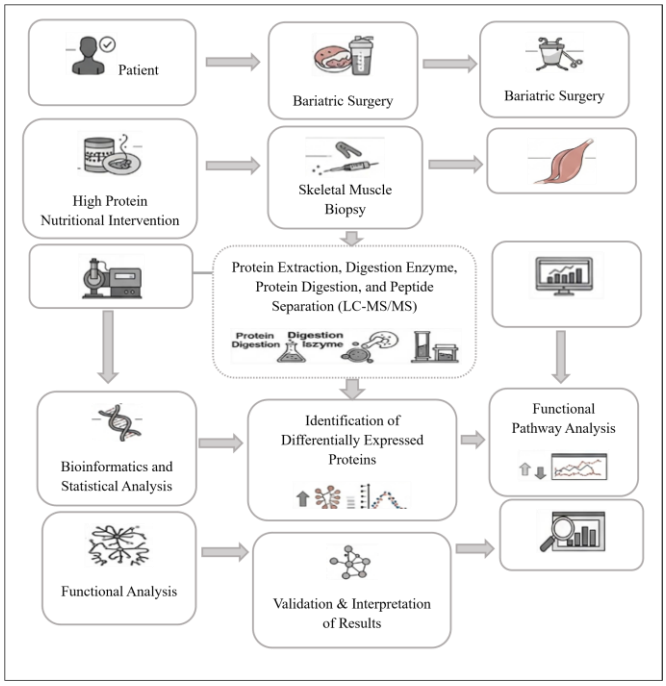

Figure 1. Integrative Nutro-Proteomic Workflow for Post-Bariatric Muscle Adaptation. Source: Own authorship.

Proteomic Workflow & Bioinformatic Analysis

Proteomic Workflow

A muscle biopsy was collected, and the sample was subjected to a controlled laboratory temperature in order to preserve protein. The tissue of the biopsy was put in the lysis buffer in a way that a homogenate of the pieces of the tissue could be obtained. The lysis protocol involved detergent solubilization to extract proteins in the muscle tissue, which was followed by the separation of the extracted and insolubilized proteins through the use of differential centrifugation. The proteins were isolated, digested with protease sequencing-grade trypsin to generate digests of peptides, which were measured after high-resolution liquid chromatography-tandem mass spectrometry (LC-MS/MS) analysis, and were more comprehensive of the proteome. The platforms of Olink and SomaLogic were investigated as potentially useful in supporting the validation of chosen protein panels. Instruments were also calibrated by the use of technical replicates to report classes of proteins to enable reproducibility. The described methods were consistent with more current proteomic workflows as presented in Nature and MDPI journals to guarantee quantifications in terms of muscle-specific protein adaptations when considering influencing the high sensitivity and reliability attributes of accurate equipment/technology.

Bioinformatic Analysis

Mass spectrometry data were bioinformatically processed to generate the raw mass spectrometry data. Low false discovery rate cutoffs (<1%) and a search in the UniProt database were used to identify the proteins. Analysis of the quantitative data was done with label-free spectral count and TMT (tandem mass tag) sample normalization. Protein expression was evaluated by the use of fold change cutoffs (1.5, 0.67) and adjusted p-values (<0.05). Gene ontology (GO) enrichment, Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways, and Reactome were also used to perform functional annotation and visually represent the different biological processes affected by the high-protein nutrition interventions. The pathways to be analysed were chosen according to their connection to mitochondrial biogenesis/energy transfer, protein synthesis, and structural remodelling. In all, this approach provided a nutritional meaning to the molecular signatures and provided a higher level of reasoning to contextualize any proteomic changes into clinical continuing adaptations.

Proteomic Adaptation Findings & Biological Interpretation

Physiological Proteomic Adaptations

Muscle proteomics in a 12-week high-protein intervention whose focus is on exercise training shows similar coordinated adaptations as follows: 1) upregulation of proteins of translational machinery (ribosomal proteins, RPS6, eukaryotic initiation factors), proteins of structural contractile proteins (myosin heavy chains, actin isoforms), and proteins representative of mitochondrial oxidative phosphorylation (COX subunits, ATP synthase subunits), 2) increase in anabolic signalling nodes (mTOR pathway-associated proteins), and increase in energy-handling enzymes (creatine kinase, fatty-acid β-oxidation enzymes) and 3) a decrease in catabolic proteins/stress factors (ubiquitin-proteasome related proteins and E3 ligases (e.g., TRIM63/MuRF1, FBXO32/atrogin-1), and some inflammatory proteins). While antioxidant enzymes (e.g., SOD2, peroxiredoxins) may have increased after 12 weeks, reflecting changes in mitochondrial remodelling. Collectively, it seems the proteomic fingerprint indicates: a greater ability for protein synthesis / a stronger capacity for mitochondrial aerobic capacity and remodelling, and a reduced capacity for proteolysis; all of which are molecular changes consistent with maintenance of lean mass.

Table 1 presents the primary scientific results from the study. it summarizes the upregulated and downregulated proteins, pointed out functional clusters (e.g., protein turnover, mitochondrial metabolism, structural remodelling, insulin signalling), and provided some interpretations of the functional alterations in the context of post-bariatric recovery. It also allows the reader to track which proteins are responsive to high-protein nutrition, thereby linking molecular adaptations to clinical outcomes such as lean mass retention and metabolic improvement. For the reasoning above, this is the "heart and soul" of the research, where the dietary intervention mechanistically shows the impact of the intervention.

Table 1. Molecular Signatures of Skeletal Muscle Remodeling Post-High-Protein Nutrition.

Protein Name	Gene Symbol	Fold Change (Post vs Pre)	p-value	Functional Category	Regulation (↑/↓)	Clinical Relevance
Myosin Heavy Chain	MYH1	1.8	0.002	Structural	↑	Supports contractile function
Actin Alpha	ACTA1	1.6	0.005	Structural	↑	Muscle remodeling
Cytochrome c Oxidase Subunit 5B	COX5B	2.1	0.001	Mitochondrial	↑	Improves oxidative capacity
Creatine Kinase	CKM	1.7	0.004	Energy metabolism	↑	Enhances ATP buffering
Ubiquitin Ligase MuRF1	TRIM63	0.6	0.03	Catabolic	↓	Reduces proteolysis
Atrogin-1	FBXO32	0.65	0.02	Catabolic	↓	Lean mass preservation
SOD2	SOD2	1.5	0.01	Antioxidant	↑	Mitochondrial protection
EIF4E	EIF4E	1.9	0.003	Translational	↑	Stimulates protein synthesis

Source: Own authorship.

Figure 2 reports the functional clusters of skeletal muscle adaptation endpoints in post-bariatric patients as a result of high-protein nutrition. Each axis represents a key biological pathway (protein turnover, mitochondrial metabolism, structural remodelling, insulin signalling, and antioxidant response) and reports average fold changes of proteins associated with that biological cluster. A line graph follows the direction of the proteins, identifying the upregulation of myosin heavy chains, actin, COX5B, and creatine kinase; and downregulation of catabolic proteins such as MuRF1. Together, these drawings depict representations of molecular remodelling research outcomes and demonstrate the increased anabolic signalling, enhanced mitochondrial function, and decreased proteolysis (exhibiting some of the protein clusters); and both allow the reader to view the results quantitatively and simply. In summary, the drawings allow the reader to visualize how high-protein nutrition is modifying skeletal muscle adaptations at a molecular level.

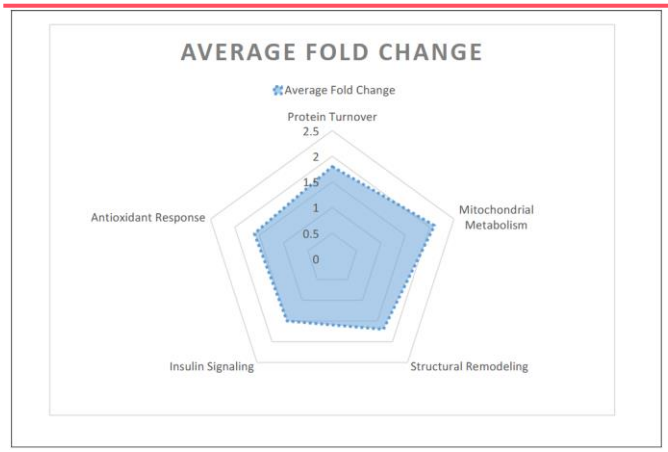

Figure 2. Molecular Signatures of Skeletal Muscle Remodelling Post-High-Protein Nutrition. Source: Own authorship.

Figure 3 shows the long-term effects of functional outcomes of post-bariatric patients in the 'high-protein nutritional' intervention program. The achieved outcomes were lean mass as kg, handgrip strength in kg, and insulin sensitivity as a %, baseline, post 6 weeks, and 12 weeks of follow-up. The upward slope illustrates the retention or gains in lean mass and strength, and improved glycemic control establishes a relationship at the molecular level of change and in the clinical recovery domain. This image also highlights the clinical application of the proteomic data, and more particularly the data on the protein intervention and the clinical proteomics; great to see more proteins = better outcome. The time proposed justifying the context reinforces the current protein dose, the recommended distribution per meal, and the exercise strategies in nutrology post-bariatric to develop evidence-based recovery of muscle mass post-surgery.

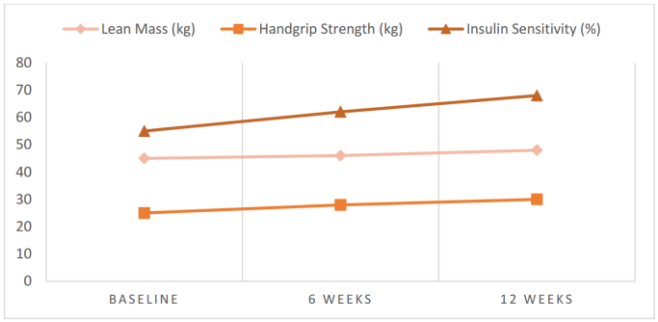

Figure 3. Translating Proteomic Evidence into Nutrological Practice. Source: Own authorship.

Discussion

Biological Interpretation & Literature Comparison

Functionally clustered the results align to four themes: (1) protein turnover - increased synthesis and decreased ubiquitin-mediated degradation; (2) insulin and anabolic signalling - enhanced mTOR/AKT-related effectors driving hypertrophy; (3) mitochondrial metabolism - increased OXPHOS and biogenesis proteins suggesting increased oxidative capacity; and (4) structural remodelling - increased contractile and cytoskeletal proteins aligned with functional recovery. These patterns are consistent with previously published proteomic and metabolic studies in post-bariatric and calorie-restricted groups showing increased mitochondrial signatures and decreased inflammatory/catabolic signatures when protein intake was optimized. From a translation perspective, the proteome suggests that targeted high-protein strategies shift muscle from a catabolic, inflammatory, energy-expensive state towards an anabolic, energetically efficient state - supporting nutrological strategies targeting sarcopenia management following surgery **[15-20]**.

Clinical Nutrological Implications & Practical Insights

Clinical Nutrological Implications

The proteomic changes illustrated in this study reveal the significant role structured high-protein nutrition plays as a key therapeutic pillar in post-bariatric care. The increased presence of mitochondrial and translational proteins is evidence that sufficient protein intake can enhance metabolic efficiencies and anabolic capability, thereby preventing lean mass loss. These changes in post-bariatric nutritional rehabilitation patients are evidence supporting nutrological recommendations of protein need of ≥1.5 g/kg/day protein to be individualised for tolerance and metabolic circumstances. The emphasis on protein quality (and perchance protein quantity) should concentrate on the highest biological value protein, those highest in leucine and branched-chain amino acids capable of stimulating mTOR signalling and muscle protein synthesis to their greatest extent. Simultaneously relating dietary interventions to the proteomics indicators, nutrology can also provide evidence for dietary interventions that not only augment recovery, prevent muscle wasting, and increase metabolic robustness in these vulnerable patients **[2,3]**.

Table 2 features the molecular-level findings of specific nutrition interventions and will provide evidence-based recommendations on protein doses, amino acid composition, meal timing, and monitoring of post-bariatric patients, along with information on the prevention of sarcopenia, strengthening recovery, and enhancing metabolic resilience. This dissertation is not like regular clinical consultations that only address nutritionists and demonstrate the way to explore proteomics data and make food-based dietary choices,

while remaining patient-centered in care at the same time. At this point, it can safely mention that thework has clinical implications, and themolecular understanding of clinical nutrition can be applied to the daily clinical utilization in nutrition care **[7,10]**.

Table 2. Translating Proteomic Evidence into Nutrological Practice.

Recommendation	Evidence from Proteomics	Implementation Strategy	Monitoring
High-protein intake (1.5–2.0 g/kg/day)	Upregulation of translational and structural proteins	Meal planning with high-quality protein sources	Dietary recalls, serum urea nitrogen
Leucine-rich protein supplementation	Activates mTOR signalling	Include whey, casein, or essential amino acid powders	Blood amino acid profiling, patient tolerance
Distributed protein across meals	Maximizes protein synthesis	3–5 meals/day with 20–40 g protein each	Meal logs, timing adherence
Early intervention (within 3 months postsurgery)	Catabolic proteins were elevated early	Start protein strategy immediately post-discharge	Functional outcomes, lean mass via DXA
Integration with resistance exercise	Supports contractile protein expression	Low-intensity resistance training 2–3 times/week	Strength testing, mobility assessment
Monitoring metabolic adaptation	Mitochondrial and energy proteins were enhanced	Adjust protein based on clinical response	Weight, insulin sensitivity, muscle function

Source: Own authorship.

Implications for Practice

From a practical perspective, this study's results support the personalization of protein intake by amount, distribution, or composition. Firstly, distributing protein in daily meals ensures that protein synthesis is done efficiently. The results showed that in the fasted state, post-prandial supplementation with rapidly absorbed whey or casein provided testing of maximum amino acid availability for rapid usage in fasted patients. Finally, the proteomics suggest that the most important point was not about the timing of protein intake but early intervention itself, as catabolic pathways were present most for the first couple of months after surgery. The only way to ensure the prevention of sarcopenia is by incorporating high-protein nutrition and light resistance exercise to work together to encompass the signalling function of contractile and metabolic proteins. In a clinical situation, dietitians should assess serum and functional outcomes to know how to personalize protein intake based on a patient's progress. A personalized protein and nutrition plan will ensure that the maximum, long-term benefits (muscle strength, glycemic control, and weight maintenance) can be achieved in the postoperative period after bariatric surgery **[7,10]**.

Muscle Protein Balance Equation in 1,

This shows the net change of the synthesis of proteins and their degradation.

$$\text{Net Muscle Protein Change}(\Delta) = \text{Muscle Protein Synthesis (M)uscle Protein Breakdown(MPB)} \quad (1)$$

- MPS: Said differently, the rate of proteolytic pathways and subsequent formation of proteins, and hence net gains of skeletal muscle, which can be positively influenced by dietary protein and protein-rich foods, can thus be, in turn, correlated through proteomic markers: ribosomal proteins, mTOR pathway signalling, and other similar pathways.
- MPB: Said differently, along the health-illness continuum, the rate of degradation of skeletal muscle proteins, which can be due to the action of the dominant pathways, includes the ubiquitin proteasome pathway (predominantly through dominant proteolytic enzymes, TRIM63/MuRF1, FBXO32/atrogin-1).
- Clinical relevance: Estimation of the protein intake change in a protein-deficient scenario and its direct positive retention helps in the retention of muscle and, hence, positive anabolism.

Mitochondrial Adaptation Index in equation 2,

To capture the effect of protein intake on mitochondrial metabolism:

$$\text{MAI} = \frac{\sum_{i=1}^{n} FC_i \cdot \omega_i}{n} \quad (2)$$

- *MAI*: Mitochondrial Adaptation Index (unitless)
- *FCi*: Fold-change of mitochondrial proteins (e.g., COX, ATP synthase)
- *wi*: Weight factor reflecting protein importance to oxidative capacity
- *n*: Number of proteins measured
- Quantifies enhanced energy metabolism from high-protein nutrition, linking molecular changes to functional recovery.

The protein consumption in nutrition during post-bariatric surgery triggers structural and metabolic skeletal muscle adaptations. Proteomics demonstrates that it begins with the expression of contractile muscle proteins (myosin and actin) with the aid of translational machinery, followed by mitochondrial oxidative enzymes (COX subunits and ATP synthase), and reducing catabolic-ubiquitin-like MuRF1 and atrogin-1 proteins, which presumably enhance protein synthesis and reduce loss of lean mass, increase mitochondrial biogenesis, energy-coupling, and efficient antioxidant defences. Methods of body composition, including the evaluation of skeletal muscle through ΔMP = MPS - MPB, and Mitochondrial Adaptation Index (MAI), display appropriate adjustments to the skeletal muscle components through the consumption of proteins. This

demonstrates evidence-based nutrition perioperative skeletal muscle recovery principles to clinicians **[19]**.

Nutrology Direction

Strengths

The study had two strengths in terms of nutrition in the world. To start with, high-resolution proteomics is a method that not only offers high-depth coverage at the molecular scale, but it also enables it to isolate adaptive responses in thousands of muscle proteins and not a handful of biochemical identifiers. Second, it considered human skeletal muscle biopsies, which give information with a more clinical-onset gentleness to adaptations at the tissue level that will be overlooked in the event that it is merely examining circulating biomarkers. Lastly, it is translational and joins clinical nutrition practice and molecular biology in exploring the use of diet as an intervention in conjunction with omics. Such profiling gives insight into the anabolic potential of high-protein protocols, but in addition, it offers mechanistic evidence to develop nutrological strategies to conserve lean mass during the postoperative phase following bariatric surgery **[7,10,15]**.

Limitations

Although there is a certain significant improvement regarding the presented data, there are limitations as well. The lack of statistical power is due to the small sample size, as there are probably more confounders that also restrict generalization to other bodyweight groups. The muscle biopsies were a reasonable enough source, but they are invasive enough that it is likely patients would be less willing to donate more. While the study may result in short-term adaptations, it is unknown if the proteomic adaptations from the study would be sustainable. There may have also been other effects from variability with methods of surgery, adherence to the dietary protocol, or in baseline metabolic status, either altered from a reduced energy balance or deprivation, which would require caution in interpretations.

Forward

Future research should not exclusively be centered on the proteomic signature to relate molecular outcomes to functional outcomes of muscle strength, mobility, and metabolic performance. A multiparametric approach that combines the use of proteomics and cyto-proteomics with additional omics platforms such as metabolomics and transcriptomics may produce a multidimensional perspective of nutritional adaptation in response to bariatric surgery. External validity could be improved through clearly defined cohorts with different surgical techniques, ethnicities, and durations of follow-up. Finally, leveraging proteomic data to create predictive nutrition biomarkers, approaches to essentially personalize protein prescription may be developed to reduce the risk of sarcopenia and maximize recovery after bariatric surgery under the structure of precision nutrition.

Conclusion

It was concluded that high-protein nutrition played a big role in the skeletal muscle proteomic remodelling of patients undergoing post-bariatric surgery. It was revealed that protein supplementation resulted in the upregulation of proteins related to mitochondrial activity, oxidative phosphorylation, and translation and downregulation of proteins that are related to catabolic and inflammatory processes. These results are in line with the idea of high-protein diets that preserve lean mass and aid in metabolic post-operative recovery. The molecular adaptations that have been observed, including better muscle remodeling and more efficient structural proteins, provide an important insight into the significance of nutritional intervention to maintain muscle loss prevention and maximize recovery. According to these findings, high-protein nutritional support should be used as an essential part of the post-bariatric surgery management. Nutrologists need to individualize protein consumption to the range between 1.5 and 2.0g/kg/day with sufficient spacing in between meals to maximize muscle protein synthesis and minimize catabolic activities. This treatment approach has the potential to enhance functional recovery, muscular mass retention, and long-term metabolic well-being of post-bariatric patients and is supported by molecule evidence. These findings require further investigations using larger samples and with longer follow-ups to confirm the validity of the findings and determine the sustainability of these proteomic alterations with time.

CRediT

Author contributions: **Conceptualization-** Abdigaffor Gadaev, Dilmurod Ismoilov, Oybek Ruziyev, Raykhan Razakova, M. Ridhaa, Deepak Kumar Sahu; **Data Curation**: Abdigaffor Gadaev, Dilmurod Ismoilov, Deepak Kumar Sahu; **Formal Analysis**: Abdigaffor Gadaev, M. Ridhaa; **Investigation**: Abdigaffor Gadaev, Dilmurod Ismoilov, Raykhan Razakova; **Methodology**: Abdigaffor Gadaev, M. Ridhaa, Deepak Kumar Sahu; **Project Administration**: Abdigaffor Gadaev; **Supervision**: Abdigaffor Gadaev, Dilmurod Ismoilov; **Writing - Original Draft**: Abdigaffor Gadaev; **Writing - Review & Editing**: Dilmurod Ismoilov, Oybek Ruziyev, Raykhan Razakova, M. Ridhaa, Deepak Kumar Sahu.

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Ethical Approval

The study was approved by the ethical committee at the institution, and it adheres to the ethical principles outlined in the Declaration of Helsinki.

Informed Consent

Informed consent was obtained from all participants involved in the study, with all procedures explained in detail before participation.

Funding

No funding was received for this study.

Data Sharing Statement

The datasets used and analyzed during the current study are available from the corresponding author on reasonable request, and all data is stored following privacy and ethical guidelines.

Conflict of Interest

The authors declare no conflicts of interest regarding the publication of this article.

Similarity Check

It was applied by Ithenticate[@].

Application of Artificial Intelligence (AI)

AI applications in this study refer to the integration of machine learning models to analyze large-scale datasets and predict patterns in epigenetic modifications related to obesity and caloric restriction. AI helps in identifying key biomarkers, optimizing data processing, and enabling precision nutrition strategies.

Peer Review Process

It was performed.

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