# Glucose ingestion before and after resistance training does not augment ribosome biogenesis in healthy moderately trained young adults

###### Kristian Lian1, Daniel Hammarström1, Håvard Hamarsland1, Sara Christine Olsen Moen1, Stian Ellefsen1

1Section for Health and Exercise Physiology, Department of Public Health and Sport Sciences, Inland Norway University of Applied Sciences, Lillehammer, Norway

Correspondance: Kristian Lian ([kristian.lian@inn.no](mailto:kristian.lian@inn.no)), Stian Ellefsen ([stian.ellefsen@inn.no](mailto:stian.ellefsen@inn.no))

ORCID: Kristian Lian <https://orcid.org/0000-0002-5169-5960>, Daniel Hammarström <https://orcid.org/0000-0001-8360-2100>, Håvard Hamarsland <https://orcid.org/0000-0002-7343-2774>, Stian Ellefsen <https://orcid.org/0000-0003-0467-2018>

## Abstract

**Purpose:** Muscle hypertrophy, induced by resistance training, is determined by ribosomal biogenesis. High-glucose treatment may augment the transcription of ribosomal RNA, as evident from in vitro studies. However, its effect on resistance training-induced adaptations remains unexplored.

**Methods:** Sixteen healthy, moderately trained individuals (male/female, n = 9/7; age, 23.7 (1.8)/24.6 (4.8)), participated in a within-participant trial with unilateral resistance training with glucose- and placebo supplementation on alternate days over six sessions per condition. Participants remained fasted overnight, receiving glucose/placebo and protein supplementation only before and after RT sessions (3 sets of 10 repetitions maximum unilateral leg press and knee extension). Micro biopsies were sampled from m. vastus lateralis before and after the intervention.

**Results:** Between conditions, there were no significant differences in increases of total RNA and ribosomal RNA (mean difference 7.6%, [-7.2, 24.9], *p* = 0.337, 47S, 37.9%, [-28.4, 131.6], *p* = 0.400; 18S, -7.6%, [-34.0, 29.8], *p* = 0.652; 28S, -2.5%, [-37.7, 53.2], *p* = 0.915; 5.8S, -7.7%, [9.8, 98.0], *p* = 0.644; 5S, -0.4%, [-31.1, 44.2], *p* = 0.982), or levels of cellular myelocytomatosis oncogene, upstream binding factor and ribosomal protein S6 (*p* = 0.094-0.292). There was a linear relationship between upstream binding factor and total RNA, where an increase of 1 standard deviance unit of upstream binding factor equated to a 14% increase in total RNA (*p* = 0.003).

**Conclusion:** Glucose supplementation before and after RT does not augment RT-induced ribosome biogenesis after two weeks of heavy RT in moderately trained young adults.

**Keywords:** Glucose; hypertrophy; resistance training; ribosome; skeletal muscle.

### Statements and Declarations

This study was financed through research funds from the Inland Norway University of Applied Sciences. There were no economical vested interest and everyone participating as researchers and associates, received only a regular salary during this study.

### Author contributions

Data was collected at the sports science lab at the Inland Norway University of Applied Sciences, with all analyses except for serum blood samples were performed at the university. Serum blood samples were performed at Innlandet Hospital Trust. S.E., H.H. and D.H. conceived and designed the study; K.L., S.C.M., D.H. and H.H. performed experiements; K.L. and D.H. interpreted the results; K.L. and D.H. prepared figures; K.L. drafted the manuscript; D.H., H.H. and S.E. edited and revised the manuscript; D.H., H.H. and S.E. approved the final version of the manuscript.

### Acknowledgements

Gratitude are in order to Henriette Spilhaug Bollandsås, Nora Lerdalen Bonsak and Thea Bøhn Nyløkken for their dedication and hard work in the training intervention. The authors would also like to express their gratitude to all the participants, staying commited to this demanding protocol in an impressive way. We also thank Håvard Nygaard for lending your expertise and technical skills to improve this project.

**Abbreviations**

|  |  |
| --- | --- |
| AMP | Adenosine monophosphate |
| AMPK | Adenosine monophosphate-dependent protein kinase |
| ATP | Adenosine triphosphate |
| cDNA | complementary deoxyribonucleic acid |
| CI | Confidence intervals |
| c-Myc | Cellular myelocytomatosis oncogene |
| Ct | Cycle threshold |
| DXA | Dual-energy x-ray absorptiometry |
| ECL | Enhanced chemiluminescence |
| ERK1/2 | Extracellular signal-regulated kinase 1/2 |
| GLU | Glucose |
| mTORC1 | Mammalian target of rapamycin complex 1 |
| PIC | Preinitiation complex |
| PLA | Placebo |
| qPCR | Quantitative polymerase chain reaction |
| rDNA | Ribosomal deoxyribonucleic acid |
| RM | Repetition maximum |
| rRNA | Ribosomal ribonucleic acid |
| RT | Resistance training |
| S6K1 | Ribosomal protein S6 kinase beta-1 |
| SD | Standard deviance |
| SIRT1 | Sirtuin 1 |
| TBS | Tris-buffered saline |
| UBF | Upstream binding factor |

## Introduction

Responses to systematic resistance training (RT) vary widely between individuals, with as much as 10-15% showing impaired skeletal muscle growth in response to standardized training interventions (Thalacker-Mercer et al. 2013; Mann et al. 2014; Álvarez et al. 2018). While there certainly may be differences in the genetic predisposition in terms of readiness to adapt to exercise (Thalacker-Mercer et al. 2013), there are also recent studies showing that epigenetic factors such as ribosomal DNA (rDNA) availability may also impact the ability to mount an anabolic response to RT (Figueiredo et al. 2021). Indeed, the ability to synthesise ribosomes following a period of RT is connected to the magnitude of RT-induced responses in an individual (Hammarström et al. 2020). For instance, increasing training volume generally induce greater ribosome biogenesis and thus, greater benefits of RT (Krieger 2009; Schoenfeld et al. 2017; Hammarström et al. 2020). However, as evident from Hammarström et al. (2020), not all participants experienced increased muscle mass and -strength despite increasing training volume. Therefore, other means than modification of RT variables alone seem necessary to optimise individual responses to RT.

Nutritional supplements such as protein and creatine effectively optimise RT adaptations (Cermak et al. 2012; Lanhers et al. 2015, 2017; Morton et al. 2018). However, it remains unknown if other nutritional adjuvants such as glucose can increase the efficacy of RT. This is surprising since glucose is the preferred energy substrate of the contracting skeletal muscle during strenuous exercise and a major energy supplier to cells via adenosine triphosphate (ATP) synthesis (Mul et al. 2015; Tanaka and Tsuneoka 2018). Furthermore, energy availability is a decisive factor in the *de novo* synthesis of ribosomes (Moss et al. 2007; Kusnadi et al. 2015; Tanaka and Tsuneoka 2018) which in turn determines muscle growth by increasing the muscle’s translational capacity (Stec et al. 2016; Tanaka and Tsuneoka 2018; Figueiredo and McCarthy 2019; Walden 2019; Hammarström et al. 2020). Therefore, investigating the effects of combined RT and glucose ingestion may provide valuable insight into the potential additive effect of glucose and RT on ribosome biogenesis.

Transcription of ribosomal RNA (rRNA) by RNA Polymerase I is considered the rate-limiting step in synthesising new ribosomes (Moss and Stefanovsky 1995). Multiple signalling pathways converge to regulate rRNA transcription, including the mammalian target of rapamycin (mTORC1) signal-transduction pathway and c-Myc (Kusnadi et al. 2015; West et al. 2016; Tanaka and Tsuneoka 2018; Walden 2019; Mori et al. 2021). mTOR receives input from growth factors, hormones, mechanical loading, and nutrients to balance protein synthesis through multiple mechanisms based on cellular energy levels (Hoppe et al. 2009). Importantly, mTOR and its downstream target ribosomal protein S6 kinase beta-1 (S6K1) serve as a mediator for insulin signalling in skeletal muscle (Hillier et al. 2000). The mTORC1 pathway contributes to ribosome biogenesis through the regulation of the translation of ribosomal proteins and to forming of the preinitiation complex (PIC) that marks the initiation of rRNA transcription (Figueiredo and McCarthy 2019; Walden 2019). Parallel to mTORC1 (West et al. 2016; Mori et al. 2021), c-Myc increases ribosomal biogenesis directly and through transcriptional control of the upstream binding factor (UBF) (Sanij et al. 2008; Poortinga et al. 2011). Additionally, UBF phosphorylation, required for interaction with the rDNA promoter, is increased by high glucose in a mTORC1 dependent manner (rapamycin sensitive) in kidney glomerular epithelial cells(Mariappan et al. 2011). Independently from UBF and mTORC1, high glucose was shown to lead to chromatin remodelling, which promoted rRNA transcription in cell cultures(Zhai et al. 2012). Together these observations indicate a potential role of glucose in positively affecting muscle rRNA synthesis.

The purpose of this investigation was to test the hypothesis that glucose supplementation before and after RT increases markers of ribosomal abundance following five RT sessions. Secondly, we aimed to describe the association between UBF and total RNA abundance in human skeletal muscle. There have been multiple studies recently suggesting translational capacity to be as important, if not more important than, translational efficiency with regard to long-term skeletal muscle adaptations to RT (Figueiredo 2019; Hammarström et al. 2020, 2022). Previously, *in vitro* studies have shown UBF and c-Myc to be important factors in the PIC, c-Myc as a general transcription factor and UBF as a specific transcription factor for rDNA transcription initiation (Mariappan et al. 2011; Walden 2019). Coupled with the recent observations by Hammarström et al. (Hammarström et al. 2020, 2022), understanding underlying factors regulating and affecting ribosome biogenesis seems key to furthering our understanding of the optimisation of RT to individual phenotypes.

## Materials and methods

All participants gave their written informed consent prior to study enrollment. The study was approved by the regional ethical committee (REK, ID nr. 153628), pre-registered at clinicaltrials.gov (Identifier: NCT04545190), and conducted according to the Helsinki declaration.

### Participants

Sixteen healthy male and female participants (20-33 years, Table 1) were recruited to the study through social media advertisement and word of mouth. The eligibility criteria were non-smokers and moderately trained (i.e. 2-8 RT sessions per 14 days for the last six months). Exclusion criteria were previous injury leading to impaired strength, inability to perform resistance exercise training, symptoms, and a medical record of metabolic disorders including hyperglycemia. Of the sixteen participants that commenced the intervention, three participants dropped out. One due to sickness and inability to resume, two participants experienced muscular discomfort related to heavy resistance training. Lean mass (Table 1) was measured using Dual-Energy X-ray Absorptiometry (DXA, Prodigy Advance PA+302047, Lunar, San Francisco, CA, USA) on Day -1, the last day preceding the RT intervention.

### Experimental design

The study was designed as a 12-day double-blinded randomized controlled trial, with an alternating unilateral RT protocol (Figure 1A). Participants were randomly allocated to exercise one leg with a glucose condition and one leg with a placebo condition (Figure 1A). One person was exclusively responsible for the randomisation code and supplement distribution, blinding both investigators and participants regarding which leg exercised with glucose/placebo conditions. Glucose (Glucosum monohydricum, Merck KGaA, Darmstadt, Germany) and placebo (Steviosa, Soma Nordic AS, Oslo, Norway) were masked by mixing with 300ml Fun Light (Orkla, Oslo, Norway). A blinded taste test revealed that the participants were not able to disclose the contents of the provided boluses (30g glucosum monohydricum vs. ~0.3g Stevia rebaudiana extract). To ensure equal conditions during training sessions and strength testing, participants exercised and tested at the same time of day, +/- 1hr with the same supervisor on pairwise consecutive days (i.e. on days 1-2, 3-4, etc.). To further standardise this, participants also recorded and repeated their daily macronutrient intake (protein, fat, carbohydrate) and total calories on pairwise consecutive days.

All participants completed six RT sessions with glucose and six with placebo, allowing a within-subjects analysis of the effects of glucose ingestion before and after RT. Data from the first five RT sessions was used to investigate main outcome measures (total RNA, rRNA and protein) and leg muscle strength, whereas data from the sixth RT session was used to explore secondary outcomes (muscular recovery, plasma glucose and -c-peptide levels). Participants were asked to avoid resistance- or high-intensity training of the legs from Day -7 (Figure 1A) and onwards, until completion of the intervention and post-testing, to ensure the reliability of pre-intervention strength data and minimal interference from external exercise sources.

### Dietary intervention

The dietary intervention spanned the whole day, divided into three periods: I) From awakening until 2.5 hours (hrs) after RT, II) from 2.5hrs after RT until 2200hrs, and III) from 2200hrs until awakening. During period I, participants ingested protein and glucose **or** protein and placebo only. Glucose/placebo was ingested three times in period I: 30 minutes before RT (0830hrs, 30g vs 0g glucose), immediately before RT (0900hrs, 30g vs. 0g glucose), and immediately after RT (~0930hrs, 30g vs. 0g glucose). Whey Protein Isolate (Proteinfabrikken, Stokke, Norway) was ingested 2hrs before RT (0700hrs) and immediately after RT (~0930hrs), in boluses of 25 g mixed with 150 ml water. In the afternoon (1800hrs-1900hrs, period II) participants ingested glucose or placebo (3x30g vs. 3x0g glucose) opposite to the supplement they received during RT, to ensure a balanced daily intake of glucose. Apart from this, participants ingested a self-chosen diet during period II, registered in MyFitnessPal or similar applications. The self-chosen diet was repeated on pairwise consecutive days, to ensure similar premises for resistance training responses between conditions. During period III (2200-0700hrs), participants remained in an overnight fasted state. The daily onset of the dietary intervention (i.e., first ingestion of protein supplement) varied between participants, from 0600hrs to 0900hrs to allow multiple participants to complete the protocol simultaneously. During sessions, participants were free to ingest water ad libitum.

### Assessment of muscular strength

Strength tests were performed prior to (Days -7 and -5, and -1, both legs) and during the intervention (Figure 1A, on days 4 and 8 for leg 1, and days 5 and 9 for leg two), after session 5 and after finalization of intervention (Figure 1A, on days 11/12 for leg 1 and days 12/13 for leg 2). Maximal isometric and isokinetic knee extension torque was measured with a Humac Norm Dynamometer (CSMi, Stoughton, Massachusetts, USA). Individual positions were recorded and standardized from pre-intervention tests (Figure 1A, days -7 and -5). Isokinetic peak torque was measured concentrically from 90 to 0 degrees knee angle (extended knee was set to 0 degrees) at angular velocities of 60- and 240 degrees per second, 2x3 repetitions each, with the first set of each exercise as a sub-maximal warm-up. Isometric knee extensor peak torque was measured at a knee-angle of 60 degrees, for a maximum og 10 seconds and two repetitions per test. The isometric tests were ended when the participants reached a plateau or peak torque development decreased, which on average occurred between 2-4 seconds into the test. During days 4, 5, 8 and 9 (Figure 1D, days 4 and 5 = Post 2RT, days 8 and 9 = Post 4RT), humac tests were conducted one hour before RT on the leg performing RT the previous day. During days 11 and 12, humac tests were performed four times: I) 45min before the last RT session (Figure 1D, Post 5RT), II) 30min after the last RT session (Figure 1D, 30 min post 6RT), III) 2hrs after the last RT session (Figure 1D, 2h post 6RT), and IV) 23hrs after the last RT session (Figure 1D, 23h post 6RT). Test I on day 12/13 included testing of both legs, representing 23hrs post-RT session test of one leg and post-session 5 test of the other leg. The highest peak torque values from the respective angular velocities and time points were summarized in an index. The index was calculated by dividing the average peak torque value by the highest observed peak torque value per angular velocity, and summarizing this new index per angular velocity to a mean strength index.

Assessment of unilateral one repetition maximum (1RM) leg press and knee extension was conducted at pre-intervention testing during familiarization (Figure 1, Ddays -7 and -5). The participants performed a general warm-up with 10min cycling on an indoor exercise bicycle. A protocol consisting of 1x10, 1x6 and 1x3 repetitions with a load equivalent to ~50-75% of assumed max repetitions, was used as a specific warm-up before each of the tests. All positions were controlled and recorded at the first 1RM test and repeated for the RT sessions. Maximal leg press strength was defined as the maximal load lifted in a controlled fashion, starting from a knee angle of 90 degrees. To find a reproducible 90 degree knee angle for each participant, centimeter markings on the side panels of the leg press machine was used to record were to find 90 degrees for each separate leg and participant. Attempts where participants did not reach 90 degrees during the eccentric phase, were not approved. Maximal knee extension testing followed the same specific warm-up was defined as maximal load lifted in a controlled fashion, reaching full extension of the knee joint. Attempts with exaggerated hip movement or beneath full extension were not approved. Two minutes of rest were given during the specific warm-up, and three minutes of rest were given between 1RM attempts.

### Resistance training protocol

Resistance training consisted of three sets of unilateral leg presses and three sets of knee extensions, with an intensity of 10 repetitions maximum (10RM). As a general warm-up, the participants cycled on an indoor exercise bicycle for 5-10 minutes (min). In addition, before the respective exercises, two 10-repetition warm-up sets were completed at ~50% and ~70% of 10RM. To ensure an adequate exercise stimulation throughout the intervention, the exercise load was increased the following set if the participants lifted more than 12 repetitions, as a progressive loading strategy. If the participants lifted fewer than 8 repetitions per set, the load was reduced in the following set. Rest between working sets was two minutes. For safety and standardisation purposes, all sessions were monitored by trained personnel. Lastly, training volume (load and repetitions) was logged for every session.

### Sampling of muscle tissue and blood

Muscle biopsies were sampled from m. vastus lateralis using well-established procedures (Hammarström et al. 2020). Briefly, muscle biopsy sampling was performed under local anaesthesia (Xylocaine, 10 mg ml-1 with adrenaline 5 μg ml−1, AstraZeneca AS, Oslo, Norway) using a 12-gauge needle (Universal Plus, Mermaid Medical AS, Stenløse, Denmark), operated with a spring-loaded biopsy gun (Bard Magnum, Bard, Rud, Norway). After the biopsy sampling, muscle tissue was divided into two aliquots for determination of total RNA/expression of rRNA and two aliquots for protein content measurement. Aliquots were snap-frozen in isopentane (-80°C) and stored at -80°C until further analyses. Muscle biopsies were collected at four time points: I/II) Pre-intervention (Figure 1A, 2hrs before training, Day 1 = leg 1, Day 2 = leg 2), and III/IV) after the fifth RT session, two hours before the sixth RT session (Figure 1A, Day 11 = leg 1, Day 12 = leg 2). At each time point, two samples were taken from the same incision. To standardize this procedure, all individual participants had biopsies taken at the same time of day, in an overnight fasted state.

To measure blood glucose levels with and without glucose ingestion/training, capillary blood was collected from finger draws on days with biopsy sampling. One capillary blood sample was collected on day 1 (Figure 1A) to serve as a baseline. On days 11 and 12 (Figure 1A), capillary blood samples were collected seven times: I) Immediately prior to protein ingestion (0700hrs) II) 45 minutes after protein ingestion (0745hrs) III) 1.5hrs after protein ingestion (0830hrs, i.e., immediately before GLU/PLAC intake), IV) 2hrs after protein ingestion (0900hrs, i.e., immediately before training), IV) in the middle of RT (~0915hrs), V) immediately after training (~0930hrs), and VI) 2hrs after completion of training (~1130hrs). Capillary blood samples were analysed with in-house equipment (BIOSEN C-Line, EKF diagnostic GmbH, Barleben). Venous blood samples were collected from the antecubital vein, coinciding with the capillary samples except 45min after protein ingestion and in the middle of the RT session, to analyse endocrine variables.

### Total RNA extraction and real-time reverse transcription polymerase chain reaction

Two muscle biopsy aliquots were used for total RNA extraction per leg and resulting in a total of eight RNA samples per participant. Total RNA was extracted using TRIzol with muscle tissue homogenized using 0.5mm RNase-free Zirconium beads (~50 ul; Next Advanced, Averill Park, NY, USA) and mechanical agitation (Bullet Blender, Next Advanced, Averill Park, NY, USA). Chloroform (Sigma-Aldrich, Oslo, Norway) was used for phase separation, and the RNA pellet was precipitated with isopropanol (VWR International, Oslo, Norway). To enable analysis of target gene expression per unit tissue weight (Ellefsen et al. 2008; Ellefsen et al. 2014), an exogenous RNA control (λ polyA External Standard Kit, Takara Bio Inc., Shiga, Japan) was added at a fixed amount to each sample (0.04 ng ml-1 of Trizol reagent). For assessment of RNA content and purity, RNA was eluted in TE-buffer (1:2) and assessed via spectrophotometry. All samples had a 260 nm to 280 nm ratio > 1.9. The RNA stock was stored at -80°C until further analyses. Before quantitative analyses of total RNA, samples with known loss of RNA during extraction (n = 9) or a deviation from the observed RNA to muscle tissue weight relationship larger than 3 residual SD while accounting for training status (n = 1) were removed from the data set. Total RNA was normalized to wet muscle weight and log transformed before statistical analyses.

Five-hundred ng of RNA was reverse transcribed using Super Script IV Reverse Transcriptase (Invitrogen, Oslo, Norway), according to the manufacturer’s instructions using anchored oligo-dT and random hexamer primers (Thermo Scientific, Oslo, Norway). All samples were reverse transcribed and diluted to 1:50 before quantitative real-time polymerase chain reaction (qPCR). qPCR reactions were run over 40 cycles (3 s 95°C denaturing and 30 s 60°C annealing) on a fast-cycling real-time detection system (Applied Biosystems 7500 fast Real-Time PCR Systems, Life Technologies AS), with a total reaction volume of 10 µl consisting of 2 µl of complementary DNA (cDNA), gene-specific primers (0.5 µM final concentration) and a commercial master mix (2X SYBR Select Master Mix, Applied Biosystems, Life Technologies AS, Oslo, Norway). An overview of the primers may be found in table 2. Raw fluorescence data was modelled with a best-fit sigmoidal model using the qPCR package (Ritz and Spiess 2008) written for R (R Core Team 2020; Hammarström et al. 2020). qPCR data was normalized to wet muscle weight using the external reference gene (Ellefsen et al. 2008; Ellefsen et al. 2014) and analyzed on the log scale on a target-by-target basis.

### Protein extraction and immunoblotting

Total protein was extracted using the Minute Total Protein Extraction Kit for Muscles (Invent Biotechnology), according to the manufacturer’s protocol, optimised for our lab. Wet muscle was freeze-dried for 24 hrs and dissected before extraction. The tissue was homogenized with a plastic rod in 80 mg protein extraction powder (Invent Biotechnology) and 100 ul ice cold cell lysis buffer (Denaturing Buffer, Invent Biotechnology), and centrifuged at 19 000 g for 1 min. The supernatant was divided into aliquots to run samples in duplicates, and total protein concentrations were determined in a 1:10 dilution (Pierce Detergent Compatible Bradford Assay Reagent, Thermo Fisher Scientific, Oslo, Norway). The protein samples were diluted to 20.25 µg µl−1 total protein with lysis buffer and 4X Laemmli sample buffer (Bio-Rad Laboratories AB, Oslo, Norway) containing 2-mercaptoethanol. All protein samples were incubated at 95°C and stored at -20°C until further analysis. The protein samples (20.25 µg total protein) were separated at 250V on 4-20% Tris-Glycine gels (Bio-Rad Laboratories) for 50 min and then transferred to PVDF membranes with wet transfer at 300 mA for 3 hrs. Both gel electrophoresis and protein transfer were performed at 4°C. Following the wet transfer, membranes were stained with a reversible total protein stain (Thermo Fisher Scientific) and then blocked for 1hr at room temp with a blocking buffer of Tris-buffered saline (TBS; 20 mM Tris, 150 mM NaCl) with 5% non-fat dry milk and 0.1% Tween-20. Primary and secondary antibodies were purchased from Santa Cruz Biotechnology (Texas, USA): UBF, UBF F-9, sc-13125; rpS6, Ribosomal protein S6 C-8, sc-74459; and Thermo Fisher Scientific (Oslo, Norway): c-Myc, 9E10; goat anti-mouse (for c-Myc), goat anti-mouse IgG1 (y1) horseradish peroxidase conjugate; and anti-mouse (anti-mouse IgG1 horseradish peroxidase conjugate). Antibodies were diluted in blocking buffer to concentrations corresponding to 1:25 000 (UBF, rpS6) and 1:5000 (c-Myc).

Membranes were incubated overnight with primary antibodies, and for 1 hr with secondary antibodies. Between blocking and primary antibody staining, membranes were washed 5 min, between primary and secondary staining, and after secondary staining, membranes were washed 3 x 5 min with TBS-Tween (TBS; 20mM Tris, 150mM NaCl, 0.1% Tween). Following the last wash, membranes were incubated 5 min with enhanced chemiluminescent substrate (ECL, SuperSignal West Femto Maximum Sensitivity Substrate, Thermo Fisher Scientific). Membrane blocking, secondary antibody incubation, washing and ECL incubation were performed at room temp. Primary antibody incubation was performed at 4°C. Chemiluminescence signals were quantified using Image Studio Lite (LI-COR Biotechnology, Lincoln, NE, USA), and total protein content was quantified using ImageJ (Rueden et al. 2017), where total protein content was defined as mean grey value of the whole well with between-well values subtracted as background. A pooled sample was used as a control on each gel to allow for between gel comparisons and quantified protein signals were subsequently normalized to the pooled control sample and total protein.

### Statistics and data analysis

A priori power calculations showed that 20 participants would grant a statistical power of 80% (alpha = 0.05), accounting for an expected dropout of 20%. This power calculation was based on an assumption that the effects of glucose ingestion on ribosome biogenesis (measured as within-participant differences in total RNA) may equate to the effects of increasing RT volume from low to moderate (Hammarström et al. 2020). Total RNA, protein and qPCR data were analyzed by mixed-effects models with fixed effects included as *supplement time*. To decrease the risk of Type I errors, random effects were selected from step-wise elimination of terms from the most complex structure (random slopes for time and supplement and their interaction) to less complex. The most complex random effects structure that converged was chosen as the final model(Matuschek et al. 2017). Plasma glucose, c-peptide, training volume, and the strength index were analyzed by multiple time-point log-fold change score comparisons, using mixed-effects model with baseline values, time and supplement, and the interaction between time and supplement as fixed effects. These data only supported a random intercept per participant. The linear mixed-effects models were fitted with the lmer function from the lme4 package using the lmerTest package to procure p-values (Satterthwaite’s method for approximating degrees of freedom)(Bates et al. 2014; Kuznetsova et al. 2017), written for R(R Core Team 2020). Log-transformed values were expressed as fold changes in visualisations. Descriptive data are presented as mean and (SD). Inferential statistics are presented as means with 95% confidence intervals and *p*-values unless otherwise stated. *p* < 0.05 was considered statistically significant.

## Results

There was no difference in mean change of total training session volume between exercising with placebo or glucose, with an increase of 18 and 16% from session 1 to session 6, respectively (*p* > 0.05). There were no differences in mean macronutrient intake (protein, fat, carbohydrates) or total calorie intake between glucose and placebo on pairwise consecutive days (*p* > 0.05 for all).

Glucose ingestion before and after RT led to significant increases in plasma glucose levels by 38% immediately before RT (Figure 1B, 0 min), by 31% during RT (Figure 1B, 15 min) and by 32% immediately after RT (Figure 1B, 30 min; all : *p* < 0.001), compared to placebo. Two hours after the session, RT with glucose measured 8% lower plasma glucose levels compared to RT with placebo (Figure 1B, 270min: *p* = 0.029). Similarly, levels of c-peptide increased with glucose ingestion over placebo, by 95% immediately before (Figure 1C, 0 min) and 87% after RT (Figure 1C, 30 min; both *p* < 0.001).

After 5 RT sessions (Figure 1D, Post 5RT), there was a significant difference in strength between glucose and placebo, where placebo decreased strength by 7% more than glucose (Figure 1D, *p* = 0.039). At the other time points, there were no significant differences in mean change between exercising with glucose and placebo (Figure 1D, Post 2RT: *p* = 0.514, Post 4RT: *p* = 0.735, 30min post 6RT: *p* = 0.178, 2h post 6RT: *p* = 0.245, 23h post 6RT: *p* = 0.96). Both RT with glucose and placebo led to significantly reduced strength post-fifth session compared to baseline, by 11 and 18% respectively (Figure 1D, Post 5RT: *p* = 0.000). Comparisons of the acute data gathered from the post-fifth session until and including 23hrs post-sixth session showed a significant mean increase in strength of 5-9% after RT with glucose and placebo 30min after the sixth RT session (Figure 1D, 30min post 6RT: *p* = 0.01) and two hours after the sixth RT session (Figure 1D, 2h post 6RT: *p* = 0.004). Twenty-three hours after the last (sixth) RT session, strength was unchanged compared to after the fifth RT session (Figure 1D, 23h post 6RT: *p* = 0.117).

### Markers of ribosome biogenesis

*Total RNA and ribosomal RNA*

From baseline to post-intervention total RNA and rRNA per unit muscle weight increased on average by ~20-27% and ~25-57%, respectively (Figure 2). However, RT with glucose did not induce increased accumulation of total RNA (Figure 2A, mean difference 7.6%, [-7.2, 24.9], *p* = 0.337) or rRNA (Figure 2B; 47S, 37.9%, [-28.4, 131.6], *p* = 0.400; 18S, -7.6%, [-34.0, 29.8], *p* = 0.652; 28S, -2.5%, [-37.7, 53.2], *p* = 0.915; 5.8S, -7.7%, [9.8, 98.0], *p* = 0.644; 5S, -0.4%, [-31.1, 44.2], *p* = 0.982) compared to RT with placebo.

*Protein*

Overall, RT led to robust increases from pre- to post-intervention in all measured proteins (Figure 3A). RT with glucose resulted in estimated levels of c-Myc, UBF and RPS6 being -40, -21 and -17% lower compared to placebo, respectively, without showing statistical significance (*p* = 0.094-0.292; Figure 3A). There was a linear relationship between UBF and total RNA, where an increase of 1 SD unit of UBF equated to a 14% increase in total RNA (*p* = 0.0002; Figure 3C).

## Discussion

The main findings of the present study were that heavy resistance training with glucose did not affect markers of ribosome biogenesis, measured as total RNA, rRNA, and rDNA transcription initiation-associated proteins, compared to RT with placebo. Similarly, RT with glucose in general did not affect markers of skeletal muscle functionality such as strength and recovery, or total training session volume. At one time point, RT with glucose led to less reduction in strength compared to placebo. Levels of plasma glucose and c-peptide were significantly higher before, during and after the RT sessions with glucose. Importantly, there were no differences in daily macronutrient intake on pairwise consecutive days. These findings suggest that the effects of high vs. low glucose/glucose starvation condition on rDNA transcription initiation observed in previous *in vitro* studies (Mariappan et al. 2011; Tanaka et al. 2015) are not translatable to acute effects in human skeletal muscle *in vivo*. Notably, the present study was specifically designed to investigate differences in pre to post changes within participants, and is as such also quite limited to this perspective. Hence, the observed effects of time serve as supplementary to the efficiency of the design, without a negative control group to compare with.

To our knowledge, no previous study has investigated the effects of glucose compared to placebo ingestion with RT on ribosome biogenesis in human skeletal muscle previously, making our hypotheses exploratory and comparisons few. *In vitro* studies on mice glomerular epithelial cells (Mariappan et al. 2011) and human breast cancer cells (Tanaka et al. 2015) have observed glucose-induced UBF-dependent augmentation of ribosome biogenesis (Mariappan et al. 2011), and reduced rRNA transcription by glucose starvation (Tanaka et al. 2015). These findings do imply an important role for glucose in the initiation of rDNA transcription, the rate-limiting step of ribosome biogenesis (Mariappan et al. 2011; Tanaka et al. 2015). In addition, Hillier et al. found physiological hyperinsulinemia to stimulate p70S6K phosphorylation in human skeletal muscle (Hillier et al. 2000). Moreover, robust increases in markers of ribosome biogenesis such as 47S pre-rRNA and mature rRNA can be expected after an acute bout of RT (Figueiredo et al. 2016) or a short period of RT (Hammarström et al. 2020, 2022). Therefore, we hypothesized that if glucose can, directly or indirectly via insulin, stimulate the initiation of rDNA transcription, five sessions of RT with glucose compared to placebo will elicit this effect. Further, glucose ingestion increases energy levels, leading us to hypothesize that high glucose vs. placebo condition would stimulate energy-sensitive pathways such as mTORC1, PIH1, extracellular signal-regulated kinase 1/2 (ERK1/2), AMP-dependent protein kinase (AMPK) and Sirtuin 1 (SIRT1) (Mariappan et al. 2011; Zhai et al. 2012; Kim et al. 2013; Tanaka et al. 2015). Despite previously reported upregulation in PIC assembly due to high-glucose mediated mTORC1, ERK1/2 and PIH1 or low-glucose mediated AMPK and SIRT1 activation (Hoppe et al. 2009; Mariappan et al. 2011; Zhai et al. 2012; Kim et al. 2013; Tanaka et al. 2015), the present study showed no signs of such effects of glucose vs. placebo conditions. Resistance training, irrespective of condition, yielded a robust accumulation of total RNA and expression of rRNA, in line with previous observations (Hammarström et al. 2020, 2022). Due to the exploratory nature of our hypotheses, this was hardly a very surprising result. Indeed, previous studies have used cell cultures from yeast (Zhai et al. 2012), rodent (Hoppe et al. 2009; Mariappan et al. 2011) or human cells (Tanaka et al. 2015) and are, as such, not directly comparable to human skeletal muscle cells. Importantly, previous studies investigated high vs. low glucose conditions (Mariappan et al. 2011), or high glucose vs. glucose starvation (Hoppe et al. 2009; Tanaka et al. 2015), while the present study aimed to compare high glucose condition to placebo, with a matched daily macronutrient and energy intake. Therefore, the comparison made in the present study was high plasma glucose levels vs. normal plasma glucose levels, to investigate the effect of glucose *per se* and not intracellular energy status. Thus, while glucose ingestion presumably is important in supplying energy for growth-inducing processes such as ribosome biogenesis (Kusnadi et al. 2015; Tanaka and Tsuneoka 2018; Figueiredo and McCarthy 2019) there is no apparent effect of ingesting glucose *per se* on markers of ribosome biogenesis.

In the present study, despite not measuring the activity in central pathways mediating anabolic signalling (mTORC1, ERK1/2), analyses of the downstream target UBF and the ribosomal protein S6 (rpS6), as well as the general transcription factor c-Myc, further supported observations from the RNA data. UBF has previously been described as a master regulator of rDNA transcription *in vitro* (Russell and Zomerdijk 2005; Kusnadi et al. 2015; Figueiredo and McCarthy 2019), while rpS6 is proposed as a valid and reliable means to measure ribosome biogenesis (Chaillou et al. 2012; Nakada et al. 2016). Lastly, c-Myc has previously been described as a potent regulator of ribosome biogenesis, independent of mTORC1, and a direct regulator of UBF (Poortinga et al. 2011; West et al. 2016; Mori et al. 2021). Hence, it seems quite reasonable to observe similar changes in these three proteins. The linear relationship found exclusively between UBF content and total RNA accumulation, and neither c-Myc nor rpS6, support the importance and specificity of UBF content in human skeletal muscle ribosome biogenesis. While this is not a novel finding, it has only recently been observed in human skeletal muscle following RT (Hammarström et al. 2022). As such, UBF also seems to respond to mechanical loading in human muscle cells in line with responses seen in cell cultures and synergist ablation models (Mariappan et al. 2011; Walden et al. 2012), in addition to the previously reported response to hormonal, nutritional, and cellular energy signals (Russell and Zomerdijk 2005; Kusnadi et al. 2015; Figueiredo and McCarthy 2019).

As in the biological data, there was generally no difference in the change of strength as an index between the conditions. Generally, skeletal muscle strength decreased from baseline to post-fifth and -sixth RT sessions, with a significantly less reduction in glucose compared to placebo at post-fifth session measurement. This could suggest that the RT protocol fatigued the participants, as both training frequency and intensity were quite high. Another promising explanation might be the biphasic recovery pattern, as described by Raastad & Hallén (Raastad and Hallén 2000), where the participants experienced a rapid recovery during the initial 11hrs post-exercise, followed by a levelling off or drop until 22hrs post-exercise. Herein, inflammation and phagocytic activity were proposed to be involved in the performance drop between 11-22hrs (Raastad and Hallén 2000). Indeed, this pattern seems quite similar to what was observed in the present study, with a rapid recovery at 30min and 2hrs post-sixth RT session and a drop at 23hrs. Further, strength testing during the intervention was conducted 23hrs after RT, meaning that these tests also may have been influenced by the biphasic recovery. However, this does not explain the difference between conditions at post-fifth RT session, or the great drop in strength from post 4RT to post 5RT sessions. A possible argument could be that exercising without glucose may have caused more stress compared to exercising with glucose, as glucose is the preferred energy source during strenuous exercise (Mul et al. 2015), thus increasing performance with glucose compared to placebo. Notably, training volume showed that the total training session volume was equal on pairwise consecutive days, i.e. no difference between days 1-2, days 3-4 and so on. Hence, there were no differences in mechanical loading to induce a higher stress between conditions. Arguably, an increased energy availability via glucose ingestion during RT may induce less acute stress on the exercised skeletal muscle, therefore less fatigue, and perhaps less performance reduction, compared to placebo during RT (Westerblad et al. 1998; Kent-Braun 1999) Unfortunately, we did not conduct measurements of markers of metabolic stress such as inorganic phosphate, H+, Mg2+ and the ADP/ATP ratio (Westerblad et al. 1998; Kent-Braun 1999). Therefore, discussing the potential effect of differences in metabolic stress between conditions would only be speculation, however probable. Lastly, these inconclusive observations may also reflect our limited sample size, despite using a within-subjects design. Initially, we met our minimum limit of 16 participants. Unfortunately, three dropped out during the intervention, leaving our statistical power slightly underpowered according to the a priori calculation. Furhter, we did not measure the intramuscular glycogen storage, representing another limitation to our design. Hence, we cannot know for certain whether there were actual differences within the exercising skeletal muscles between the glucose and placebo condition. The participants did indeed match their macro nutrients on pairwise consecutive days, and the plasma glucose measurements did not show any differences in blood sugar until ingestion of placebo/glucose. Thus, it may stand to reason that the participants had similar levels of intramuscular levels before ingesting any supplement and that the glucose supplement led to higher glucose availability during exercise, as by design. However, even if the leg exercising with glucose supplement did in fact take up the extra glucose, it did not seem to affect any of our outcome measures.

*Conclusion*

In conclusion, ingestion of glucose immediately before and after resistance exercise training does not acutely augment ribosome biogenesis after two weeks of heavy resistance exercise training, in moderately trained young adults. Neither does it acutely enhance muscular performance during the exercise period or after five sessions, nor recovery within 23hrs of the last session. The observations in total RNA, rRNA and rDNA transcription initiation-associated proteins support the key role of UBF in ribosome biogenesis regulation in human skeletal muscle following resistance training. If future investigations are to be made on this topic, a greater sample size coupled with a negative control group and analyses of the intramuscular glycogen storage may provide higher-resolution results.

### DATA AVAILABILITY

Complete data sets and scripts are downloadable here; <https://github.com/Kristianlian/ribose-paper>

### SUPPLEMENt MATERIAL

Extended methods can be found here; <https://github.com/Kristianlian/ribose-paper>

## References

Álvarez C, Ramírez-Vélez R, Ramírez-Campillo R, et al (2018) Interindividual responses to different exercise stimuli among insulin-resistant women. Scandinavian Journal of Medicine & Science in Sports 28:2052–2065. <https://doi.org/10.1111/sms.13213>

Bates D, Mächler M, Bolker B, Walker S (2014) Fitting Linear Mixed-Effects Models using lme4. <https://doi.org/10.48550/ARXIV.1406.5823>

Cermak NM, Res PT, Groot LC de, et al (2012) Protein supplementation augments the adaptive response of skeletal muscle to resistance-type exercise training: A meta-analysis. The American Journal of Clinical Nutrition 96:1454–1464. <https://doi.org/10.3945/ajcn.112.037556>

Chaillou T, Koulmann N, Simler N, et al (2012) Hypoxia transiently affects skeletal muscle hypertrophy in a functional overload model. American Journal of Physiology-Regulatory, Integrative and Comparative Physiology 302:R643–R654. <https://doi.org/10.1152/ajpregu.00262.2011>

Ellefsen S, Stensløkken K-O, Sandvik GK, et al (2008) Improved normalization of real-time reverse transcriptase polymerase chain reaction data using an external RNA control. Analytical Biochemistry 376:83–93. <https://doi.org/10.1016/j.ab.2008.01.028>

Ellefsen S, Vikmoen O, Zacharoff E, et al (2014) Reliable determination of training-induced alterations in muscle fiber composition in human skeletal muscle using quantitative polymerase chain reaction: Muscle fiber typing using qPCR. Scandinavian Journal of Medicine & Science in Sports 24:e332–e342. <https://doi.org/10.1111/sms.12185>

Figueiredo VC (2019) Revisiting the roles of protein synthesis during skeletal muscle hypertrophy induced by exercise. American Journal of Physiology-Regulatory, Integrative and Comparative Physiology 317:R709–R718. <https://doi.org/10.1152/ajpregu.00162.2019>

Figueiredo VC, McCarthy JJ (2019) Regulation of Ribosome Biogenesis in Skeletal Muscle Hypertrophy. Physiology 34:30–42. <https://doi.org/10.1152/physiol.00034.2018>

Figueiredo VC, Roberts LA, Markworth JF, et al (2016) Impact of resistance exercise on ribosome biogenesis is acutely regulated by post-exercise recovery strategies. Physiological Reports 4:e12670. <https://doi.org/10.14814/phy2.12670>

Figueiredo VC, Wen Y, Alkner B, et al (2021) Genetic and epigenetic regulation of skeletal muscle ribosome biogenesis with exercise. The Journal of Physiology 599:3363–3384. <https://doi.org/10.1113/JP281244>

Hammarström D, Øfsteng SJ, Jacobsen NB, et al (2022) Ribosome accumulation during early phase resistance training in humans. Acta Physiologica 235: <https://doi.org/10.1111/apha.13806>

Hammarström D, Øfsteng S, Koll L, et al (2020) Benefits of higher resistance‐training volume are related to ribosome biogenesis. The Journal of Physiology 598:543–565. <https://doi.org/10.1113/JP278455>

Hillier T, Long W, Jahn L, et al (2000) Physiological Hyperinsulinemia Stimulates p70 Phosphorylation in Human Skeletal Muscle . The Journal of Clinical Endocrinology & Metabolism 85:4900–4904. <https://doi.org/10.1210/jcem.85.12.7036>

Hoppe S, Bierhoff H, Cado I, et al (2009) AMP-activated protein kinase adapts rRNA synthesis to cellular energy supply. Proceedings of the National Academy of Sciences 106:17781–17786. <https://doi.org/10.1073/pnas.0909873106>

Kent-Braun JA (1999) Central and peripheral contributions to muscle fatigue in humans during sustained maximal effort. European Journal of Applied Physiology and Occupational Physiology 80:57–63. <https://doi.org/10.1007/s004210050558>

Kim SG, Buel GR, Blenis J (2013) Nutrient regulation of the mTOR Complex 1 signaling pathway. Molecules and Cells 35:463–473. <https://doi.org/10.1007/s10059-013-0138-2>

Krieger JW (2009) Single Versus Multiple Sets of Resistance Exercise: A Meta-Regression. Journal of Strength and Conditioning Research 23:1890–1901. <https://doi.org/10.1519/JSC.0b013e3181b370be>

Kusnadi EP, Hannan KM, Hicks RJ, et al (2015) Regulation of rDNA transcription in response to growth factors, nutrients and energy. Gene 556:27–34. <https://doi.org/10.1016/j.gene.2014.11.010>

Kuznetsova A, Brockhoff PB, Christensen RHB (2017) lmerTest package: Tests in linear mixed effects models. Journal of Statistical Software 82:1–26. <https://doi.org/10.18637/jss.v082.i13>

Lanhers C, Pereira B, Naughton G, et al (2015) Creatine Supplementation and Lower Limb Strength Performance: A Systematic Review and Meta-Analyses. Sports Medicine 45:1285–1294. <https://doi.org/10.1007/s40279-015-0337-4>

Lanhers C, Pereira B, Naughton G, et al (2017) Creatine Supplementation and Upper Limb Strength Performance: A Systematic Review and Meta-Analysis. Sports Medicine 47:163–173. <https://doi.org/10.1007/s40279-016-0571-4>

Mann TN, Lamberts RP, Lambert MI (2014) High Responders and Low Responders: Factors Associated with Individual Variation in Response to Standardized Training. Sports Medicine 44:1113–1124. <https://doi.org/10.1007/s40279-014-0197-3>

Mariappan MM, D’Silva K, Lee MJ, et al (2011) Ribosomal biogenesis induction by high glucose requires activation of upstream binding factor in kidney glomerular epithelial cells. American Journal of Physiology-Renal Physiology 300:F219–F230. <https://doi.org/10.1152/ajprenal.00207.2010>

Matuschek H, Kliegl R, Vasishth S, et al (2017) Balancing type i error and power in linear mixed models. Journal of memory and language 94:305–315

Mori T, Ato S, Knudsen JR, et al (2021) C-Myc overexpression increases ribosome biogenesis and protein synthesis independent of mTORC1 activation in mouse skeletal muscle. American Journal of Physiology-Endocrinology and Metabolism 321:E551–E559. <https://doi.org/10.1152/ajpendo.00164.2021>

Morton RW, Murphy KT, McKellar SR, et al (2018) A systematic review, meta-analysis and meta-regression of the effect of protein supplementation on resistance training-induced gains in muscle mass and strength in healthy adults. British Journal of Sports Medicine 52:376. <https://doi.org/10.1136/bjsports-2017-097608>

Moss T, Langlois F, Gagnon-Kugler T, Stefanovsky V (2007) A housekeeper with power of attorney: The rRNA genes in ribosome biogenesis. Cellular and Molecular Life Sciences 64:29–49. <https://doi.org/10.1007/s00018-006-6278-1>

Moss T, Stefanovsky VY (1995) [Promotion and Regulation of Ribosomal Transcription in Eukaryotes by RNA Polymerase](https://doi.org/10.1016/S0079-6603(08)60810-7). In: Progress in Nucleic Acid Research and Molecular Biology. Elsevier, pp 25–66

Mul JD, Stanford KI, Hirshman MF, Goodyear LJ (2015) [Exercise and Regulation of Carbohydrate Metabolism](https://doi.org/10.1016/bs.pmbts.2015.07.020). In: Progress in Molecular Biology and Translational Science. Elsevier, pp 17–37

Nakada S, Ogasawara R, Kawada S, et al (2016) Correlation between Ribosome Biogenesis and the Magnitude of Hypertrophy in Overloaded Skeletal Muscle. PLOS ONE 11:e0147284. <https://doi.org/10.1371/journal.pone.0147284>

Poortinga G, Wall M, Sanij E, et al (2011) C-MYC coordinately regulates ribosomal gene chromatin remodeling and Pol I availability during granulocyte differentiation. Nucleic Acids Research 39:3267–3281. <https://doi.org/10.1093/nar/gkq1205>

R Core Team (2020) [R: A language and environment for statistical computing](https://www.R-project.org/). R Foundation for Statistical Computing, Vienna, Austria

Raastad T, Hallén J (2000) Recovery of skeletal muscle contractility after high- and moderate-intensity strength exercise. European Journal of Applied Physiology 82:206–214. <https://doi.org/10.1007/s004210050673>

Ritz C, Spiess A-N (2008) *qpcR* : An R package for sigmoidal model selection in quantitative real-time polymerase chain reaction analysis. Bioinformatics 24:1549–1551. <https://doi.org/10.1093/bioinformatics/btn227>

Rueden CT, Schindelin J, Hiner MC, et al (2017) ImageJ2: ImageJ for the next generation of scientific image data. BMC Bioinformatics 18:529. <https://doi.org/10.1186/s12859-017-1934-z>

Russell J, Zomerdijk JCBM (2005) RNA-polymerase-I-directed rDNA transcription, life and works. Trends in Biochemical Sciences 30:87–96. <https://doi.org/10.1016/j.tibs.2004.12.008>

Sanij E, Poortinga G, Sharkey K, et al (2008) UBF levels determine the number of active ribosomal RNA genes in mammals. Journal of Cell Biology 183:1259–1274. <https://doi.org/10.1083/jcb.200805146>

Schoenfeld BJ, Grgic J, Ogborn D, Krieger JW (2017) Strength and Hypertrophy Adaptations Between Low- vs. High-Load Resistance Training: A Systematic Review and Meta-analysis. Journal of Strength and Conditioning Research 31:3508–3523. <https://doi.org/10.1519/JSC.0000000000002200>

Stec MJ, Kelly NA, Many GM, et al (2016) Ribosome biogenesis may augment resistance training-induced myofiber hypertrophy and is required for myotube growth in vitro. American Journal of Physiology-Endocrinology and Metabolism 310:E652–E661. <https://doi.org/10.1152/ajpendo.00486.2015>

Tanaka Y, Tsuneoka M (2018) [Control of Ribosomal RNA Transcription by Nutrients](https://doi.org/10.5772/intechopen.71866). In: Sebata A (ed) Gene Expression and Regulation in Mammalian Cells - Transcription Toward the Establishment of Novel Therapeutics. InTech

Tanaka Y, Yano H, Ogasawara S, et al (2015) Mild Glucose Starvation Induces KDM2A-Mediated H3K36me2 Demethylation through AMPK To Reduce rRNA Transcription and Cell Proliferation. Molecular and Cellular Biology 35:4170–4184. <https://doi.org/10.1128/MCB.00579-15>

Thalacker-Mercer A, Stec M, Cui X, et al (2013) Cluster analysis reveals differential transcript profiles associated with resistance training-induced human skeletal muscle hypertrophy. Physiological Genomics 45:499–507. <https://doi.org/10.1152/physiolgenomics.00167.2012>

Walden F von (2019) Ribosome biogenesis in skeletal muscle: Coordination of transcription and translation. Journal of Applied Physiology 127:591–598. <https://doi.org/10.1152/japplphysiol.00963.2018>

Walden F von, Casagrande V, Östlund Farrants A-K, Nader GA (2012) Mechanical loading induces the expression of a Pol I regulon at the onset of skeletal muscle hypertrophy. American Journal of Physiology-Cell Physiology 302:C1523–C1530. <https://doi.org/10.1152/ajpcell.00460.2011>

West DWD, Baehr LM, Marcotte GR, et al (2016) Acute resistance exercise activates rapamycin-sensitive and -insensitive mechanisms that control translational activity and capacity in skeletal muscle: Translational activity and capacity in skeletal muscle. The Journal of Physiology 594:453–468. <https://doi.org/10.1113/JP271365>

Westerblad H, Allen DG, Bruton JD, et al (1998) Mechanisms underlying the reduction of isometric force in skeletal muscle fatigue: Causes of force reduction in muscle fatigue. Acta Physiologica Scandinavica 162:253–260. <https://doi.org/10.1046/j.1365-201X.1998.0301f.x>

Zhai N, Zhao Z, Cheng M, et al (2012) Human PIH1 associates with histone H4 to mediate the glucose-dependent enhancement of pre-rRNA synthesis. Journal of Molecular Cell Biology 4:231–241. <https://doi.org/10.1093/jmcb/mjs003>

# Figure/table legends

**Figure 1:** A) An overview of the experimental design with 12 days of concomitant dietary intervention and resistance training (RT), preceded by 7 days involving familiarization. Between days -7 and -1, participants were familiarized to the RT exercises via 1RM leg press and knee extension testing, and to the strength tests via Humac Norm dynamometer (days -7 and -5). Before baseline testing, the participants were randomly allocated to exercise one leg with glucose (GLU) and the other with placebo (PLA), in a unilateral, alternating fashion. Further, non-dominant/dominant + GLU/PLA, and onset with GLU or PLA was also randomized, the figure illustrates an example where the participant was randomized to start RT with GLU. Biopsies were taken from m. vastus lateralis at baseline (Day 1 leg 1, Day 2 leg 2), and after five RT sessions (Day 11 leg 1, Day 12 leg 2). Blood for measurement of plasma glucose and -c-peptide was sampled at baseline (Day 1), and during post testing (Day 11 leg 1, Day 12 leg 2), via finger draws and venous blood samples. Skeletal muscle strength was measured as peak torque in unilateral isometric and isokinetic (at 60 and 240 degrees per second) knee extension before, multiple times during, and after five and six session. . B and C) Changes in plasma glucose (B, mmol/L) and serum c-peptide levels (C, pmol/L). Glucose levels in blood was measured via finger draws 120 (-120), 90 (-90), and 30min (-30) before RT, immediately before RT (0), during RT (15), immediately after RT (30) and 2hrs after RT (120). C-peptide levels were measured simultaneously to these finger draws, except for 90min before and during RT. D) Changes in muscular strength measured as isometric and isokinetic peak torque (60 and 240 d/s) via Humac Norm Dynamometer, conducted at baseline (A: Day -1), after two and four RT sessions (A: Day 4 and 8 leg 1, Day 5 and 9 leg 2), after five RT sessions/before the 6th session (Day 11 leg 1, Day 12 leg 2), as well as 30min, 2hrs and 23hrs after the 6th RT session (A: Day 11/12 leg 1, Day 12/13 leg 2). The index was calculated by normalizing peak torque values to the highest peak torque value at each respective speed, and then summarized and used in change score calculations. Values are presented as changes in estimated marginal means ± 95% confidence intervals (CI). \* = *p* < 0.05 between groups. Glucose n = 13, placebo n = 13.

**Figure 2:** Changes in total RNA and ribosomal RNA. A) Total RNA, B) 47S pre-rRNA, 18S rRNA, 28S rRNA, 5.8S rRNA, 5S rRNA. Baseline = Day 1 leg 1/ Day 2 leg 2, Post = Day 11 leg 1, Day 12 leg 2. Total RNA and rRNA were analyzed in duplicates, with two duplicates per biopsy (two muscle tissue pieces per time point), and normalized to ng x mg wet muscle weight for total RNA and external reference gene (Lambda) for rRNA. Total RNA and rRNA changes were calculated as log-fold change score per mg wet muscle weight. Mean change scores of the duplicates were calculated and transformed to the log-scale before modelling, then reverse-transformed for figure illustration. Values are estimated marginal means fold change per leg per supplement ± 95% CI. Glucose n = 13, placebo n = 13.

**Figure 3:** Changes in protein content. A) Fold-change pre-post in levels of protein in placebo and glucose + fold-change difference 95% CI, with representative western blots of the respective proteins. Protein samples were analyzed in two duplicates per biopsy per time point, loaded on separate gels in an inverted order, e.g. from gel 3 to 6, as shown by the duplicates (1 and 2). Changes in protein levels were calculated as log-fold change scores normalized by pools (pool of all protein samples per gel). Mean log fold-change scores of the duplicates were calculated before modelling and reverse-transformed for figure illustration. Values are estimated marginal means fold change per leg per supplement ± 95% CI. Glucose n = 13, placebo n = 13. B) Representative total protein stain blot. C) Linear relationship between total RNA (ng x mg) and UBF levels (SD units), with time added as a covariate. Total RNA was normalized by wet muscle weight, and UBF was normalized by pools per gel and total protein per lane factor. Values are presented as log-transformed means.

# Tables

**Table 1. Participant characteristics:** Values are means ± SD. 60º sec-1 = 60 degrees per second movement speed (isokinetic), 240º sec-1 = 240 degrees per second movement speed (isokinetic), 0º sec-1 = 0 degrees per second movement speed (isometric).

|  | | | | | | Knee-extension peak torque | | |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Sex | n | Age (yrs) | Stature (cm) | Body mass (kg) | Lean mass (kg) | 60º sec-1 | 240º sec-1 | 0º sec-1 |
| Female | 7 | 24.6 (4.8) | 172.1 (5.8) | 68.5 (3.5) | 49.5 (6.5) | 161.0 (28.8) | 98.9 (9.7) | 231.9 (41.1) |
| Male | 9 | 23.7 (1.8) | 176.7 (5.0) | 78.4 (6.1) | 61.1 (4.5) | 217.4 (19.5) | 140.1 (18.6) | 284.8 (34.4) |

**Table 2. Primer sequences:** Values of Ct are means ± SD. rRNA = ribosomal RNA, E = primer efficiency. Average cycle thresholds (Ct) and priming efficiencies were calculated from all qPCR reactions.

| Gene | Sequence (forward - reverse) | Ct mean (SD) | E |
| --- | --- | --- | --- |
| 18S rRNA | 5’-TGCATGGCCGTTCTTAGTTG-3’ 5’-AACGCCACTTGTCCCTCTAAG-3’ | 9.73 (0.768) | 1.82 |
| 28S rRNA | 5’-TGACGCGATGTGATTTCTGC-3’ 5’-TAGATGACGAGGCATTTGGC-3’ | 11.0 (0.968) | 1.88 |
| 5.8S rRNA | 5’-ACTCTTAGCGGTGGATCACTC-3’ 5’-GTGTCGATGATCAATGTGTCCTG-3’ | 15.8 (0.747) | 1.81 |
| 5S rRNA | 5’-TACGGCCATACCACCCTGAAC-3’ 5’-GGTCTCCCATCCAAGTACTAACC-3’ | 18.4 (0.639) | 1.83 |
| 47s rRNA | 5´-CTGTCGCTGGAGAGGTTGG-3´ 5´- GGACGCGCGAGAGAACAG-3´ | 26.1 (1.90) | 1.81 |
| Lambda F2R2 | 5´-AAGACGACGCGAAATTCAGC-3´ 5´- TGGCATTCGCATCAAAGGAG-3´ | 23.2 (1.50) | 2.02 |
| Lambda F3R3 | 5´-TCGCGGCGTTTGATGTATTG-3´ 5´- TGACGCAGACCTTTTCCATG-3´ | 23.8 (0.890) | 1.81 |