Dietary sulfur amino acid restriction improves glucose homeostasis through hepatic *de novo* serine synthesis

Andres F. Ortega[1], Cha Mee Vang[1], Ferrol I. Rome[1], Kaitlyn M. Andreoni[2], Aiden M. Phoebe[2],

Alisa B. Nelson[1], Peter A. Crawford[1,3], James J. Galligan[2], Stanley Ching-Cheng Huang[4,5],

Curtis C. Hughey[1]*

[1]Division of Molecular Medicine, Department of Medicine, University of Minnesota,

Minneapolis, MN

[2]Department of Pharmacology and Toxicology, University of Arizona, Tucson, AZ

[3]Department of Biochemistry, Molecular Biology, and Biophysics, University of Minnesota,

Minneapolis, MN

[4]Pelotonia Institute for Immuno-oncology, Comprehensive Cancer Center – James Cancer

Hospital and Solove Research Institute, The Ohio State University, Columbus, OH

[5]Department of Microbial Infection and Immunity, College of Medicine, The Ohio State

University, Columbus, OH

*To whom the correspondence should be addressed: Curtis C. Hughey from the Department of
Medicine, Division of Molecular Medicine, University of Minnesota, Dwan 316, 425 East River
Parkway, Washington Ave SE, Minneapolis, MN, 55455. Tel.: 612-301-2677, Email:
chughey@umn.edu

ABSTRACT

Dietary sulfur amino acid restriction (SAAR) improves whole-body glucose homeostasis,

elevates liver insulin action, and lowers liver triglycerides. These adaptations are associated with

an increased expression of hepatic *de novo* serine synthesis enzymes, phosphoglycerate

dehydrogenase (PHGDH) and phosphoserine aminotransferase 1 (PSAT1). This study tested the

hypothesis that enhanced hepatic serine synthesis is necessary for glucose and lipid adaptations to

SAAR. Hepatocyte-specific PSAT1 knockout (KO) mice and wild type (WT) littermates were fed

a high-fat control or SAAR diet. In WT mice, SAAR increased liver PSAT1 protein (~70-fold),

serine concentration (~2-fold), and ^{13}C-serine (~20-fold) following an intravenous infusion of [U-

^{13}C]glucose. The elevated liver serine and partitioning of circulating glucose to liver serine by

SAAR were attenuated in KO mice. This was accompanied by a blunted improvement in glucose

tolerance in KO mice fed a SAAR diet. Interestingly, SAAR decreased liver lysine lactoylation, a

SAA-supported post-translational modification known to inhibit PHGDH enzymatic activity. This

suggests dietary SAAR may increase serine synthesis, in part, by lowering lysine lactoylation.

Beyond glucose metabolism, dietary SAAR reduced body weight, adiposity, and liver triglycerides

similarly in WT and KO mice. Collectively, these results demonstrate that hepatic PSAT1 is

necessary for glucose, but not lipid, adaptations to SAAR.

KEYWORDS

Sulfur amino acid restriction; De novo serine synthesis; Glucose homeostasis; Liver intermediary

metabolism

1. INTRODUCTION

Dietary sulfur amino acid restriction (SAAR) provokes metabolic adaptations that are advantageous in preventing and treating obesity and its comorbidities [1]. In rodents, SAAR enhances glucose and insulin tolerance [2-7]. The use of hyperinsulinemic-euglycemic clamps combined with isotope tracers revealed that the increased insulin action is due to a greater suppression of endogenous glucose production and heightened glucose disposal by skeletal muscle, heart, and adipose tissue [8-11]. Concurrently, SAAR decreases adiposity and liver triglycerides [1-4]. It is important to note that these metabolic responses to SAAR are not confined to rodents. Short-term dietary SAAR in humans elicits decreases in body weight, body mass index (BMI), and liver fat [12-14]. The SAAR-mediated adaptations are partly due to a liver-derived increase in fibroblast growth factor 21 (FGF21) [1]. The transcriptional activation of hepatic FGF21 increases whole-body energy expenditure, which contributes to reduced adiposity by SAAR [9]. FGF21 is necessary for the enhanced insulin-stimulated cardiac glucose uptake [10; 11]. In contrast, SAAR lowers liver triglycerides similarly in wild type (WT) and FGF21-deficient mice[9]. Prior work indicates the enhanced liver insulin signaling by SAAR is also independent of FGF21 [1; 11]. Together, these findings suggest that the increased FGF21 mediates several extrahepatic responses to SAAR, but may not be critical for the hepatic responses. Given this, the mechanisms underlying the liver glucose and lipid adaptations to SAAR, and the extent to which these responses are hepatocyte-dependent, remain to be clearly defined.

Elevated expression of liver *de novo* serine synthesis pathway enzymes, phosphoglycerate dehydrogenase (PHGDH) and phosphoserine aminotransferase 1 (PSAT1), is among the most reproducible responses to dietary SAAR, making their increase a marker of a successful dietary intervention [2; 9; 10; 15-23]. *De novo* serine synthesis is sourced from 3-phosphoglycerate, an

intermediate of both glycolysis and gluconeogenesis [24]. Thus, a SAAR-mediated increase in

hepatic serine synthesis could promote greater glucose disposal and/or divert gluconeogenic flux

away from glucose production. Liver-specific PHGDH knockout (KO) mice fed a chow diet show

higher adiposity and reduced glucose tolerance [25]. In agreement with PHGDH KO mice, PSAT1

knockdown impairs glucose and insulin tolerance [26]. Conversely, PSAT1 overexpression

enhances glucose and insulin tolerance [26]. Beyond glucose homeostasis, the overexpression of

PHGDH has been shown to lower liver lipids [27]. These prior results support that PHGDH and

PSAT1 action impacts whole-body and liver-specific glucose and lipid homeostasis.

The experiments presented herein tested the hypothesis that hepatic PSAT1 is required for

the liver glucose and lipid adaptations to SAAR to be fully realized. Liver-specific PSAT1 KO

mice and WT littermates were fed a high-fat control or SAAR diet. Comprehensive phenotyping

approaches were completed. These included glucose and insulin tolerance tests to define whole-

body glucose homeostasis, ^{13}C-isotope tracing in conscious unrestrained mice to determine the

tissue-specific fate of glucose and serine *in vivo*, and metabolomics to quantify metabolite

concentrations. Immunoblotting and proteomics were used to identify molecular drivers of liver

metabolism. The results of this study show that hepatic PSAT1 is necessary for whole-body and

liver-specific glucose, but not lipid, adaptations to dietary SAAR.

2. MATERIALS AND METHODS

2.1. Mouse models and husbandry

All procedures using mice were approved by the University of Minnesota Institutional

Animal Care and Use Committee. PSAT1 floxed mice on a C57BL/6N background [28] were

backcrossed onto a C57BL/6J background for 5 generations. Hepatic-specific PSAT1 KO were

then generated by breeding mice expressing Cre recombinase under control of the albumin

promoter (B6.Cg-Tg(Alb-cre)21Mgn/J) with PSAT1 floxed mice on a C57BL/6J background.

Floxed PSAT1 littermates lacking expression of Cre recombinase were used as WT controls.

C57BL/6J mice were used for select studies. Mice were maintained on a chow diet (Teklad Global

18% Protein Rodent Diet 2918, Madison, WI) from weaning at three weeks of age until six weeks

of age. At six weeks of age mice received one of three diets (unless otherwise stated): low-fat SAA

control (0.85% kcal from methionine; 10% kcal from fat; LF-CTRL; A11051302B, Research Diets

Inc., New Brunswick, NJ), high-fat SAA control (0.85% kcal from methionine; 60% kcal from fat;

HF-CTRL; A11051306, Research Diets Inc., New Brunswick, NJ), and HF-SAAR (0.125% kcal

from methionine; 60% kcal from fat; A11051305, Research Diets Inc., New Brunswick, NJ). The

full dietary composition for these three diets is detailed in Supplementary Table 1. Food and water

were provided ad libitum. Mice were housed with cellulose bedding (Cellu-nest™, Shepherd

Specialty Papers, Watertown, TN) in temperature- and humidity-controlled conditions maintained

on a university instituted 14:10 hour light:dark cycle. At 12 weeks of age (6 weeks on diet), mice

underwent metabolic testing and were euthanized via cervical dislocation. Tissues were rapidly

excised, freeze-clamped in liquid nitrogen, and stored at -80°C. One cohort of mice was euthanized

at 26 weeks of age (20 weeks on diet) using the same procedures described above. All mice used

in this study were males.

2.2. Body Composition

Body composition was measured in mice fed ad libitum at 10-11 weeks of age using an

EchoMRI-100™ Body Composition Analyzer (EchoMRI LLC, Houston, TX).

2.3 Glucose and insulin tolerance tests

For glucose tolerance tests (GTT), mice were fasted for five hours and injected intraperitoneally (i.p.) with dextrose (Hospira, Inc., Lake Forest, IL) at a dose of 2 g·kg^{-1} lean weight. For insulin tolerance tests (ITT), mice were fasted for five hours and received insulin (Humulin R human, Eli Lilly and Company, Indianapolis, IN) i.p. at a dose of 0.75 U·kg^{-1} lean weight. During both procedures, tail-blood glucose was measured at 0, 15, 30, 45, 60, 90, and 120 minutes with a Contour blood glucose meter (Ascensia Diabetes Care, Parsippany, NJ). A cohort of mice had blood samples obtained at 0 and 15 minutes after the insulin administration for plasma insulin concentrations and were euthanized immediately after for assessing indices of insulin signaling in tissues.

2.4. Insulin pellet implantation.

At 7 weeks of age, C57BL/6J mice had one sustained-release insulin pellet implanted subcutaneously (~0.1 U/day per implant; LinBit; LinShin Canada, Toronto, ON) according to manufacturer guidelines. Briefly, under isoflurane anesthesia, a 1 cm diameter area of hair was clipped and disinfected. A small incision in the skin was made with a 16-gauge needle, and a sterile 12-gauge trocar was used to deliver the pellet subcutaneously. Procedures in control mice were identical, except the skin incisions were not performed. Mice were group housed following the procedure.

2.5. Vascular catheter surgeries

At 11 weeks of age, C57BL/6J mice had catheters were surgically implanted in the jugular vein and carotid artery for isotope infusion and sampling protocols as previously described [21;

29]. The exteriorized ends of the implanted catheters were flushed with 200 U·mL^{-1} heparinized saline and sealed with stainless-steel plugs. Following surgery, mice were housed individually and provided 5-7 days of post-operative recovery prior to stable isotope infusion studies. Liver-specific PSAT1 KO and WT littermates underwent identical surgical procedures with the exception that only the jugular vein catheter was implanted. All mice were within 10% of pre-surgical weight prior to stable isotope infusions.

2.6. Stable-isotope tracing: [U-^{13}C]glucose intravenous infusion in the conscious, unrestrained mouse

During the first hour of the housing light cycle, both food and water were withdrawn for the duration of the experiment (5.5 hours). Four hours into the fast, the exteriorized vascular catheters were connected to infusion syringes. Following a one-hour acclimation, a 60 mg·kg^{-1}·min^{-1} continuous intravenous infusion of [U-^{13}C]glucose was performed for 30 minutes. C57BL/6J mice had arterial samples obtained for measuring blood glucose prior to and every 10 minutes during the [U-^{13}C]glucose infusion to ensure the infusion rate was sufficient to achieve glucose concentrations comparable to those observed during a GTT. Mice were euthanized and tissue collected immediately following the [U-^{13}C]glucose infusion.

2.7. Stable-isotope tracing: In-vivo [U-^{13}C]serine intraperitoneal injection

Food and water were withdrawn for 5 hours starting within the first hour of the light cycle. [U-^{13}C]serine was administered i.p. at a dose of 100 mg·kg^{-1}. Fifteen minutes following the i.p. injection, mice were euthanized and tissues harvested.

2.8. Hormone and metabolite analysis

Plasma insulin was determined using the Mercodia Ultrasensitive Mouse Insulin ELISA

(Mercodia AB, Winston Salem, NC). Liver triglycerides were measured with the Triglycerides -

Liquid Reagent Set (Pointe Scientific, Inc., Lincoln Park, MI). Liver glycogen was quantified as

previously described [21; 30]. All other metabolites were measured using untargeted metabolomics

as detailed below. Tissue metabolite levels were quantified from mice that were fasted 7 hours.

2.9. Untargeted metabolomics and ^{13}C-isotope tracing untargeted metabolomics (^{13}C-ITUM)

pipeline

Extraction and analytical methods were completed as previously described [31-33] with

minor modifications. Briefly, lyophilized liver samples (~2 mg) were homogenized in 1000 µL of

2:2:1 (v/v/v) acetonitrile (ACN):methanol (MeOH):water and subjected to three (30 second) cycles

of vortexing, one minute of flash-freezing in liquid nitrogen, and 10 minutes of sonication at 25°C.

Homogenized samples were stored at −20°C for 1 hour and then centrifugated at 15,000 × g for

10 minutes at 4 °C. Subsequently, the supernatant was transferred to a fresh tube and dried by

SpeedVac overnight. Liver extracts were reconstituted in 100 µL of 1:1 (v/v) ACN:water,

sonicated for two (five minute) cycles, vortexed for 1 minute, and then stored at 4°C for one hour.

Finally, samples were centrifuged at 15,000 × g at 4 °C for 10 minutes and the supernatants

transferred to LC-MS vials. Metabolites were separated using a Thermo Fisher Scientific Vanquish

UHPLC system and an Atlantis Premier UPLC BEH Z-HILIC column (186009979, Milford, MA).

Mobile Phase A was 90% water with 15 mM ammonium bicarbonate and Mobile Phase B was

90% ACN with 15 mM ammonium bicarbonate. The total run time was 10 minutes, flow rate was

0.5 mL·min^{-1}, and column chamber temperature was 30°C. Separated metabolites were detected

using a Thermo Fisher Scientific QExactive Plus hybrid quadrupole-orbitrap mass spectrometer,

fitted with a heated electrospray ionization source operated in negative and positive polarity mode.

Two sample types were run to aid in chemical feature identification: 1) a standard mix consisting

of authentic standards for all expected analytes and 2) a pooled sample containing only the

naturally occurring samples, analyzed via data-dependent analysis (DDA)–tandem mass

spectrometry (MS/MS), using IE omics script and R-Studio [34]. Data processing and initial

analysis were performed using Thermo Compound Discoverer 3.3. Raw mass spectra were

uploaded, background ions were removed, retention times (RT) for detected signals were aligned

across samples, and chemical formulas were predicted. Grouped chemical features were profiled

to determine compound identity based on: 1) the m/z predicted from the chemical formula, 2) the

RT compared to an authentic external standard, and 3) the MS/MS fragmentation pattern,

compared to in-house standards and online databases. For ITUM, putatively identified metabolites

were carried forward and subjected to ^{13}C-isotope enrichment with correction for natural

abundance. To carry out ^{13}C-isotope tracing, all $[^{13}C]$ mass isotopomers within the isotopic

envelope of each identified metabolite were determined based on the diagnostic shift

in m/z ($\Delta m/z = 1.0033$ Da, natural abundance, 1.11% of all carbon) induced by the presence of ^{13}C-

labeled compounds. Raw ion counts for each isotopologue were plotted against RT to generate

extracted ion chromatograms, and then the area under the curve for each isotopologue was

extracted, summed, and expressed as a percentage of the total pool. After natural abundance

correction, the fractional intensities were then graphed as a function of ^{13}C-carbon content,

generating mass isotopologue distributions for each detected metabolite. Fractional enrichment

reports on the percentage of molecules in a metabolite pool that are ^{13}C-enriched and was

calculated by the summation of the relative intensities (% of the total pool) for all ^{13}C mass

isotopologues detected. Untargeted metabolomics to determine relative metabolite pools sizes was

performed in livers from mice fasted 7 hours to avoid the potential impact of ^{13}C-isotope

administration on metabolite abundance.

2.10. Targeted analysis of glyoxalase cycle intermediates

Reduced glutathione (GSH), lactoylglutathione (LGSH), and hemithioacetal (HTA) were

quantified in liver as previously described [35]. Briefly, samples were prepared in a sulfosalicylic

acid solution containing the internal standard, GSH-(Gly-^{13}C$_2$,^{15}N). The protein precipitate was

removed via centrifugation and supernatants chromatographed using a Shimadzu LC system

equipped with an Atlantis C$_{18}$ column (186001291; Waters, Milford, MA). Multiple reaction

monitoring-mass spectrometry (MRM-MS) was performed in positive ion mode using an AB

SCIEX 6500+ QTRAP.

2.11. Quantitative analysis of arginine and lysine modifications

Lysine lactoylation (lactoyllys), lysine acetylation (acetyllys), methylglyoxal-derived

hydroimidazolone 1 (MG-H1), and carboxyethylarginine (CEA) were determined as previously

described [35; 36]. Liver protein was precipitated and resuspended in ammonium bicarbonate

containing internal standards. Samples were then digested to single amino acids, acidified with

heptofluorobutyric acid, chromatographed using a Shimadzu LC system equipped with an Eclipse

XDB-C8 column (930990-906; Agilent, Santa Clara, CA), and analyzed by MRM-MS. The post-

translational modifications (PTMs) were normalized to Leu to control for digestion [36; 37].

2.12. Immunoblotting

Tissue homogenates were prepared as previously detailed [21; 29]. Tissue proteins (15 µg)

were separated by electrophoresis on a NuPAGE 4-12% Bis-Tris gel (Invitrogen, Carlsbad, CA,

USA) and transferred to a PVDF membrane. Immunoblotting was performed with the primary

antibodies and secondary antibodies listed in Supplementary Table 2. The PVDF membranes were

treated with a chemiluminescent substrate (Thermo Fisher Scientific, Waltham, MA, USA) and

imaged using a ChemiDoc Imaging system and Image Lab software (Bio-Rad, Hercules, CA,

USA). Total protein was assessed via BLOT-FastStain (G-Bioscience, St. Louis, MO, USA) and

used as the loading control. Densitometry was evaluated using ImageJ software.

2.13. Statistical Analysis

GraphPad Prism software (GraphPad Software LLC., San Diego, CA) was used to perform

Student's t-test, two-way ANOVAs followed by Tukey's post-hoc tests, and repeated measures

ANOVAs followed by Šidák's post-hoc tests as appropriate to detect statistical differences

($p<0.05$). All data are reported as mean ± SEM. Data points greater than two standard deviations

from the mean were considered outliers and excluded from analysis.

3. RESULTS

3.1. Elevated glucose partitioning to liver serine by SAAR is linked to improved glucose tolerance

In C57BL/6J mice, 6 weeks of dietary intervention showed a greater gain in body weight,

higher adiposity, and similar lean mass in the HF-CTRL compared to LF-CTRL group (Fig. 1A

and B). Mice fed a HF-SAAR diet had a lower body weight, decreased fat mass, and increased

lean mass percentage relative to both the LF-CTRL and HF-CTRL mice (Fig. 1B). A HF-CTRL

diet elevated liver triglycerides compared to mice fed the LF-CTRL diet, while the HF-SAAR diet

prevented the increase in liver triglycerides and lowered liver weight (Fig. 1C). Dietary SAAR

also lowered liver glycogen and fasting blood glucose (Fig. 1D and E). HF-CTRL mice showed

impaired glucose tolerance, but not insulin tolerance, compared to LF-CTRL mice (Fig. 1F and

G). Conversely, glucose and insulin tolerance were improved in mice fed the HF-SAAR diet

relative to mice fed the LF-CTRL and HF-CTRL diets (Fig. 1F and G). Plasma insulin was

significantly reduced in HF-SAAR mice (Fig 1H). This is notable because chronically elevated

insulin has been proposed to promoted gain in adiposity and dysregulated glucose control [38-40].

To test if the lowered circulating insulin levels in HF-SAAR mice was contributing to the

metabolic adaptations to SAAR, a subcutaneous, sustained-release insulin pellet was implanted in

HF-SAAR mice to raise insulin. The persistent delivery of exogenous insulin from the

subcutaneous pellet over 5 weeks did not impact the glucose and lipid adaptations to SAAR (Suppl.

Fig. 1). This suggests that the mechanisms underlying SAAR are independent of circulating insulin

concentrations.

Untargeted metabolomics revealed that liver cysteine was higher in HF-CTRL compared

to LF-CTRL mice (Fig. 2A and 2B). As expected, liver cysteine and taurine were decreased ~5-

fold in mice fed the HF-SAAR diet (Fig. 2B). The HF-SAAR diet led to a markedly increased in

liver PHGDH (~5-fold) and PSAT1 (~70-fold) protein expression (Fig. 2C). The elevated

expression of serine synthesis enzymes was associated with higher liver serine and glycine levels

in HF-SAAR relative to both CTRL diet groups (Fig. 2E). The profound increase in PSAT1 protein

in the HF-SAAR group made it difficult to resolve differences in PSAT1 in the livers of mice on

the LF- and HF-CTRL diets. However, immunoblots performed specifically to compare the LF-

CTRL and HF-CTRL groups showed that high-fat feeding decreased liver PSAT1 (Fig. 2D). This

was accompanied lower serine concentrations in LF-CTRL versus HF-CTRL mice (Fig. 2E). To

test if the increased liver serine and glycine were being sourced from circulating glucose, [U-

^{13}C]glucose was intravenously infused in conscious, unrestrained mice fed a LF-CTRL or a LF-

SAAR diet for 6 weeks (Fig. 2F). ^{13}C-labeling of liver serine and glycine was significantly higher

in LF-SAAR mice compared to LF-CTRL, with no alterations observed in labeled glucose (Fig.

2H). Collectively, our data show that dietary SAAR improves glucose and insulin tolerance, which

is associated with increased partitioning of circulating glucose to liver serine synthesis.

3.2. Liver PSAT1 is required for SAAR-induced improvements in systemic glucose homeostasis

To assess whether hepatic serine synthesis is essential for the metabolic benefits of dietary

SAAR on glucose control, we studied liver-specific PSAT1 KO mice and WT littermates fed a

HF-CTRL or -SAAR diet (Fig. 3A). The HF-SAAR diet prevented a gain in body weight and

adiposity in both genotypes (Fig. 3B and C). When fed a HF-CTRL diet, WT and liver PSAT1 KO

mice showed similar glucose tolerance (Fig. 3D). This was expected given that high-fat feeding

lowers liver PSAT1 in WT mice (Fig. 2D), a phenotype closely resembling liver PSAT1 KO mice.

On a HF-SAAR diet, liver-specific PSAT1 KO mice showed a greater excursion of glucose at the

15- and 30-minute time points during the glucose tolerance test compared to WT mice, although

the area under the curve was comparable between genotypes (Fig. 3D). Loss of hepatic PSAT1 in

mice fed HF-CTRL diet delayed the normalization of circulating glucose during an insulin

tolerance test relative to WT littermates (Fig. 3E). Six weeks of HF-SAAR feeding improved

insulin tolerance similarly in WT and KO mice compared to HF-CTRL groups (Fig. 3E).

Concordant with the C57BL/6J findings (Fig. 1), HF-SAAR feeding lowered plasma insulin levels

relative to mice fed a HF-CTRL diet in both genotypes (Fig. 3F). Fifteen minutes after an insulin

injection, the liver p-Akt-to-Akt ratio was higher in both genotypes fed the HF-SAAR diet (Fig.

3G). This suggests liver insulin signaling was enhanced similarly in WT and KO mice following

SAAR. Dietary SAAR lowered liver glycogen in WT and liver PSAT1 KO mice (Fig. 3H).

However, this was independent of changes key enzymes regulating glycogen synthesis and

breakdown. Specifically, total protein and the phospho-to-total protein ratio for glycogen synthase

(GS) and glycogen phosphorylase (PYGL) were similar between groups (Fig. 3I). Together, these

data indicate that liver PSAT1 is necessary for dietary SAAR to improve whole-body glucose

tolerance.

3.3. Increased glucose partitioning to serine following SAAR is abolished by loss of hepatic PSAT1

Next, we aimed to further connect the attenuated improvement in glucose tolerance

observed in liver PSAT1 KO mice fed a HF-SAAR diet to inability of hepatocytes to synthesize

serine from glucose (Fig. 4A). The HF-SAAR diet elevated serine and glycine synthesis enzymes,

PHGDH, PSAT1 (WT mice only), and serine hydroxymethyltransferase 2 (SHMT2), in the livers

of mice (Fig. 4B). Under post-absorptive conditions, liver glucose, serine, and glycine were

comparable between WT and KO mice fed a HF-CTRL diet (Fig. 4C). Dietary SAAR lowered

liver glucose in WT, but not liver PSAT1 KO mice (Fig. 4C). Liver serine and glycine were higher

in WT mice fed a HF-SAAR diet compared to WT mice on a HF-CTRL diet (Fig. 4C); however,

the increase in liver serine and glycine by SAAR was blunted in liver PSAT1 KO mice (Fig. 4C).

Consistent with these metabolite levels, a HF-SAAR diet prompted a rise in the ^{13}C-labeling of

liver serine and glycine in WT mice intravenously infused with [U-^{13}C]glucose (Fig. 4D). Loss of

liver PSAT1 attenuated the increased in serine and glycine ^{13}C-labeling by SAAR (Fig. 4D). These

data imply that the improved glucose tolerance by dietary SAAR is associated with enhanced

partitioning of circulating glucose to liver serine synthesis.

3.4. Serine sourced from glucose following SAAR is preferentially fated to glutathione

Serine is a precursor for cysteine synthesis via transsulfuration and donates a one-carbon

units to support methionine regeneration within the methionine cycle [41]. Given this, one could

speculate that the elevated diversion of glucose to serine is an adaptive response to prevent

limitations in SAA availability that may arise from dietary SAAR. To further test this hypothesis,

liver proteins, metabolite concentrations, and metabolite labeling from [U-^{13}C]glucose and [U-

^{13}C]serine administration were determined (Fig. 5). Regardless of diet, loss of hepatic PSAT1 did

not impact proteins involved in transsulfuration or cysteine catabolism (Fig. 5A and 5B). Dietary

SAAR increased cystathionine γ-lyase (CSE; involved in cysteine production), decreased cysteine

dioxygenase 1 (CDO1; involved in cysteine catabolism to taurine), and elevated GSH synthesis

enzymes, glutamate-cysteine ligase catalytic subunit (GCLC) and glutathione synthetase (GSS),

in both genotypes (Fig. 5A and 5B). SAAs and related metabolites were comparable between WT

and liver PSAT1 KO mice fed a HF-CTRL diet (Fig. 5C). The HF-SAAR diet decreased liver

cysteine, taurine, GSH, and oxidized glutathione (GSSG) in both genotypes compared to their

counterparts fed the HF-CTRL diet (Fig. 5C). Consistent with metabolite levels, ^{13}C-labeling of

liver SAA and related metabolites following a 30-minute [U-^{13}C]glucose infusion was similar

between WT and Liver PSAT1 KO mice on a HF-CTRL diet (Fig. 5D). HF-SAAR feeding

increased ^{13}C-labeling from glucose in liver methionine in both WT and liver PSAT1 KO mice

(Fig. 5D). Fractional enrichment in liver cysteine was not detectable due to the low cysteine pool

in mice fed a HF-SAAR diet; however, downstream fates of cysteine were measured. The [U-

^{13}C]glucose infusion showed lower ^{13}C-taurine, and increased ^{13}C-GSH and ^{13}C-GSSG in the

livers of both WT and KO mice fed the HF-SAAR diet relative to the HF-CTRL mice (Fig. 5D),

with the SAAR-mediated increase in GSH and GSSG ^{13}C-labeling from [U-^{13}C]glucose being

blunted in liver PSAT1 KO mice compared to their WT littermates (Fig. 5D). To more directly

assess the impact of dietary SAAR on serine fate, [U-^{13}C]serine was administered to WT mice fed

a HF-CTRL or a HF-SAAR diet for 6 weeks (Fig. 5E). ^{13}C-labeling was increased in liver

methionine, taurine, GSH, and GSSG in the HF-SAAR mice compared to the HF-CTRL (Fig. 5E).

The rise in ^{13}C-labeling was particularly pronounced for GSH (~12-fold) and GSSG (~37-fold)

(Fig. 5E). Together, these results suggest that serine synthesized *de novo* from glucose is important

for supporting GSH provision during SAAR.

3.5. SAAR reduces glyoxalase cycle intermediates and associated protein PTMs

To further explore the potential connectivity between serine synthesis and GSH

availability, we assessed markers of glyoxalase cycle metabolism (Fig. 6A). GSH can be used to

generate LGSH in the glyoxalase cycle and recent work identified LGSH-derived lysine

lactoylation inhibits PHGDH [42]. Liver glyoxalase cycle enzymes, glyoxalase 1 (GLO1) and

hydroxyacylglutathione hydrolase (GLO2), were comparable between genotypes on both diets

(Fig. 6B). However, SAAR decreased liver GLO1 protein (Fig. 6B). Consistent with data from our

untargeted metabolomic approaches (Fig. 5C), targeted quantification showed lower liver GSH in

WT and KO mice fed a HF-SAAR diet compared to the HF-CTRL diet (Fig. 6C). Dietary SAAR

also decreased liver LGSH and HTA in both genotypes (Fig 6C). Liver lactate was lower in liver

PSAT1 KO mice relative to WT mice fed HF-CTRL (Fig. 6C). SAAR decreased liver lactate in

WT, but not liver PSAT1 KO mice (Fig. 6C). PTMs derived from glyoxalase cycle metabolites

were broadly suppressed by SAAR. Specifically, lysine lactoylation was decreased in HF-SAAR

WT mice compared to WT HF-CTRL (Fig. 6D). In contrast, lysine lactoylation was comparable

between liver PSAT1 KO mice fed the HF-CTRL and -SAAR diets (Fig. 6D). Methylglyoxal

(MGO)-derived modifications, MG-H1 and CEA, were significantly lower in HF-SAAR- versus

HF-CTRL-fed mice regardless of genotype (Fig. 6D). Global lysine acetylation was not changed

by diet or genotype (Fig. 6D). Overall, SAAR reduces glyoxalase-cycle intermediates and the

protein modifications they support.

3.6. SAAR diverts glucose toward asparagine synthesis

Given that loss of hepatic PSAT1 blunted, but did not completely abolish the improvement

in glucose tolerance by SAAR, we further examined how SAAR could be influencing glucose

metabolism in the liver. On a HF-CTRL diet, liver TCA cycle, anaplerotic, and cataplerotic

metabolites were mostly comparable between WT and KO mice (Fig. 7A and B). SAAR increased

pyruvate, decreased malate (WT mice only), and elevated aspartate (Fig. 7B). [U-^{13}C]glucose

tracing showed lower ^{13}C-pyruvate, increased ^{13}C-aspartate, and significantly elevated ^{13}C-

asparagine (~370-fold) labeling in WT and KO mice on the HF-SAAR diet compared to the HF-

CTRL diet (Fig. 7C). Interestingly, SAAR lowered the ^{13}C-labeling of liver succinate in WT mice

(Fig. 7C). This decreased ^{13}C-labeling of liver TCA cycle intermediates was more pronounced in

PSAT1 KO mice on a HF-SAAR diet as indicated by lower ^{13}C-citrate, ^{13}C-succinate, and ^{13}C-

malate (Fig. 7C). Next, we assessed three isotopologue ratios to provide indices of nutrient flux

[43-48]. Livers of WT mice fed the HF-SAAR diet had a higher citrate M+3-to-pyruvate M+3

ratio relative to WT mice fed a HF-CTRL and KO mice fed a HF-SAAR diet (Fig. 7D). This

suggests that TCA cycle anaplerosis via pyruvate carboxylase (PC) was stimulated by SAAR. The

aspartate M+3-to-succinate M+3 and aspartate M+3-to-citrate M+3 ratios were elevated in HF-

SAAR mice compared to their HF-CTRL counterparts (Fig. 7D). The increase in these two ratios

suggest a preferential partitioning of pyruvate to aspartate compared to flux through the TCA

cycle. Consistent with the metabolite and ^{13}C-isotope tracing data, liver asparagine synthetase

(ASNS) protein was ~25-fold higher in mice fed a HF-SAAR diet compared to those receiving the

HF-CTRL diet (Fig. 7E). Most TCA cycle proteins tested were not altered by diet or genotype

(Fig. 7E). The cataplerotic enzyme, mitochondrial glutamic-oxaloacetic transaminase (GOT2),

was increased in PSAT1 KO mice fed a HF-SAAR diet compared to both their WT littermates and

KO mice fed HF-CTRL (Fig. 7E). These results indicate that SAAR shifts the fate of glucose, via

the TCA cycle anaplerosis, towards liver asparagine synthesis.

3.7. SAAR prevents liver lipid accumulation independently of hepatic PSAT1

In addition to glucose control, we investigated the role of hepatic PSAT1 action in liver

lipid adaptations to dietary SAAR. After 6 weeks of diet, liver triglycerides were lower in WT

mice fed a HF-SAAR diet compared to WT mice on the HF-CTRL diet (Fig. 8A). This dietary

effect was not observed in liver PSAT1 KO mice (Fig. 8A). The expression of liver *de novo*

lipogenesis enzymes, ATP-citrate lyase (ACLY) and stearoyl-CoA desaturase 1 (SCD1), were

suppressed with HF-SAAR feeding in both genotypes (Fig. 8B and D). SAAR decreased FASN

protein in WT mice only (Fig. 8B and D). Given that hepatic triglyceride concentrations may also

be impacted by changes in lipid catabolism, we next examined mitochondrial respiratory proteins

as a marker of potential changes in mitochondrial oxidative metabolism in response to SAAR. As

we previously observed [21], SAAR increased liver mitochondrial respiratory proteins (Fig. 8C

and D). Specifically, complex I (NADH dehydrogenase (ubiquinone) iron-sulfur protein 4;

NDUFS4) and complex V (ATP synthase F1 subunit alpha; ATP5A) were higher in WT mice fed

HF-SAAR compared to WT mice fed the HF-CTRL diet. (Fig. 8C and D). Complex IV

(mitochondrial encoded cytochrome c oxidase subunit II; MTCO2) protein was elevated in PSAT1

KO mice on the HF-SAAR diet versus KO mice fed the HF-CTRL diet (Fig. 8C and D). An

additional mechanism through which SAAR may lower liver triglycerides is the formation of

acylglycines (Fig. 8E). Protein expression of liver glycine N-acyltransferase (GLYAT), which

catalyzes the conjugation of acyl-CoA to glycine, was similar between groups (Fig. 8F). However,

HF-SAAR raised the levels of short-chain acylglycines (acetylglycine, isobutyrylglycine, and

isovalerylglycine) in the liver (Fig. 8G).

To further test if hepatic PSAT1 action was required for SAAR to lower liver triglycerides,

mice were fed the HF-SAAR diet for 20 weeks. Both WT and KO mice fed the HF-SAAR diet

had lower body weight, fat mass, and liver triglycerides compared to mice on the HF-CTRL diet

(Fig. 8H-J). This suggest that hepatic PSAT1 is not needed, particularly with increasing duration,

for SAAR to promotes a decline in liver triglycerides.

4. DISCUSSION

Dietary SAAR prevents obesity, dysregulated glucose control, and liver steatosis [1].

Analysis of changes at the level of the transcriptome has identified that the liver is particularly

responsive to SAAR [1]. These changes include an increased expression of liver *de novo* serine

synthesis pathway enzyme, PSAT1, which is among the most reproducible responses to dietary

SAAR [2; 9; 10; 15-23]. Given the interconnectedness of *de novo* serine synthesis with glycolysis

and gluconeogenesis pathways, this study tested the hypothesis that hepatic PSAT1 is needed for

the liver glucose and lipid adaptations to SAAR. The pertinent findings of this study are: 1)

enhanced hepatic *de novo* serine synthesis is required for SAAR to improve glucose tolerance, 2)

concurrent with transcriptional activation, a serine synthesis-GSH-lysine lactoylation feedback

loop may underlie the increased hepatic serine synthesis in response to SAAR, and 3) hepatic

serine synthesis is not necessary for the SAAR-mediated decline in adiposity and liver

triglycerides.

4.1. Role of hepatic PSAT1 in glucose adaptations to SAAR

Consistent with previous studies using rodents [2-7], we found that dietary SAAR

enhances glucose tolerance. Untargeted metabolomics showed this whole-body glucose phenotype

was associated with increased liver serine. Exogenous serine supplementation can [49], but does

not always [50], improve glucose tolerance. Thus, the SAAR-mediated increase in serine may

actively promote glucose tolerance via one or more downstream functions [51]. Our ^{13}C-isotope

tracing experiments showed elevated partitioning of circulating glucose to hepatic serine following

SAAR. Moreover, loss of hepatic PSAT1 impaired glucose tolerance in mice fed the SAAR diet

and abolished the increase in liver serine sourced from circulating glucose without completely

preventing the rise in liver serine levels. These results suggest that a higher rate of hepatic glucose

disposal and the diversion of glucose to the synthesis of serine is, in part, responsible for the

SAAR-mediated adaptations in whole-body glucose control.

PSAT1 overexpression in mice enhances both glucose and insulin tolerance [26]. In the

experiments presented here, we found that the heightened insulin tolerance following SAAR was

not impacted by the loss of hepatic PSAT1. Prior work has reported that the enhanced insulin

action in response to PSAT1 overexpression is mediated by decreased expression of tribbles

homolog 3 (TRB3), which is a pseudokinase that inhibits insulin signaling by binding to Akt and

impairing its activation by phosphorylation [26]. Our studies showed the phosphorylation of liver

Akt was elevated similarly in both WT and liver PSAT1 KO mice. Together, these data suggest

the elevated liver PSAT1 increases glucose tolerance independent of insulin action. However,

future work should assess the role of liver PSAT1 on liver insulin action during hyperinsulinemic-

euglycemic clamps combined with isotope tracers. These conditions would allow for assessing

liver-specific insulin sensitivity under euglycemic conditions so that the impact of SAAR on

extrahepatic glucose flux and concentrations do not mask alterations at the liver.

4.2. Potential mechanisms promoting increased hepatic de novo serine synthesis from glucose

Work by independent groups indicate that SAAs negatively regulate serine synthesis.

Cysteine suppresses the expression of PHGDH by decreasing mRNA stability [52]. In addition to

post-transcriptional regulation, mechanisms at the level of transcription may also contribute to the

enhanced serine synthesis by SAAR. Deletion of the transcription factor, nuclear factor erythroid

2-related factor 2 (NRF2), in the livers of mice blunted but did not abolish the increase in PSAT1

mRNA [16]. These mechanisms of action are consistent with the elevated liver PHGDH and

PSAT1 mRNA and protein in response to SAAR. Serine is a precursor for cysteine, which is

generated via transsulfuration wherein the sulfur from methionine is transferred to serine [41]. It

may be that increased cysteine impedes the synthesis of its precursor, serine, to control SAA levels.

Conversely, when cysteine is low, serine synthesis is stimulated to promote SAA availability.

Ultimately, these findings suggest that SAAR-mediated increase in glucose tolerance is the result

of liver responses to maintain SAA homeostasis via serine synthesis.

A prominent fate of methionine and cysteine, particularly under conditions of low SAA

levels, is the synthesis of GSH [53-56]. Aligning with prior studies [23], we observed liver GSH

was decreased by SAAR. However, our [U-^{13}C]glucose and [U-^{13}C]serine isotope tracing

experiments showed that ^{13}C-labeling of liver GSH and GSSG was elevated in mice fed the SAAR

diet. While the [U-^{13}C]serine tracing showed SAAR increased labeling of other fates of cysteine

such as taurine, loss of hepatic PSAT1 uniquely attenuated the increased liver ^{13}C-GSH and ^{13}C-

GSSG from [U-^{13}C]glucose. These results indicate that serine synthesized *de novo* from glucose

is important to support GSH provision (via cysteine) during SAAR.

Beyond its antioxidant properties, GSH is a metabolite within the glyoxalase cycle. This

highly conserved metabolic cycle comprised of two enzymes, GLO1 and GLO2, uses GSH to

catabolize MGO to lactate through the intermediate, LGSH [57]. LGSH is an acyl-donor in a non-

enzymatic reaction with free lysine residues, yielding the PTM, lysine lactoylation [35; 58]. This

is notable because PHGDH and PSAT1 are heavily lactoylated and LGSH inhibits PHGDH

activity [35; 42]. Our results showed that SAAR lowered liver LGSH and lysine lactoylation.

Together, our data and the work of others suggest that SAAR may increase serine synthesis by

preventing the inhibition of PHGDH and/or PSAT1 by LGSH-derived lysine lactoylation.

Consistent with GSH regulating serine synthesis via post-translational mechanisms, the

pharmacologic inhibition of GSH synthesis using buthionine sulfoximine increased liver serine

without altering NRF2 or PHGDH expression [22]. While it remains to be fully tested, SAAR may

promote glucose tolerance through a hepatic serine synthesis-GSH-lysine lactoylation feedback

loop in which low SAA decreases liver GSH, lowers lysine lactoylation, and thereby prevents

inhibition of *de novo* serine synthesis from glucose.

4.3. SAAR shifts the fate of glucose towards liver asparagine

In addition to *de novo* serine synthesis, this study demonstrates that SAAR stimulates

glucose partitioning towards asparagine synthesis. Liver asparagine concentration was similar

between mice fed the HF-CTRL and SAAR diets. However, ^{13}C-labeling of liver asparagine from

[U-^{13}C]glucose increased markedly by ~370-fold in SAAR-fed mice. We also assessed indices of

nutrient flux [43-48]. Isotopologue ratios from our [U-^{13}C]glucose tracing experiments are

consistent with SAAR increasing TCA cycle anaplerosis through PC (i.e., the generation of OAA

from pyruvate) and the resulting OAA being preferentially directed to asparagine rather than flux

through the TCA cycle. In agreement with this, Xin et al.[59] show that SAAR increases liver

TCA cycle anaplerosis as evidenced by higher enrichment of TCA cycle metabolites following the

administration of [U-^{13}C]glucose and [U-^{13}C,^{15}N]glutamine. Herein, we show the SAAR-induced

shift in glucose and TCA cycle intermediates to asparagine was associated with a ~25-fold increase

in liver ASNS, which generates asparagine from aspartate. SAAR did not alter the expression of

other anaplerotic and cataplerotic enzymes (i.e., PC, MDH2, PCCA, and GOT2) linked to

asparagine synthesis. Interestingly, these aforementioned enzymes have been reported to be

modified by lysine lactoylation [35]. Thus, further research is warranted to determine if the SAAR-

driven reduction in lactoylation prevents the inhibition of these enzymes and favors the diversion

of glucose to asparagine. Future studies should also test whether the stimulation glucose

partitioning to asparagine is an additional means through which SAAR increases glucose tolerance.

522   The shift in glucose fate to asparagine during SAAR could be an additional means of

enhancing serine availability. Intracellular asparagine exchanges with extracellular serine to

promote serine uptake [60]. Liver PSAT1 KO mice receiving a HF-SAAR diet showed higher liver

serine levels compared to KO mice fed a HF-CTRL diet. This was accompanied by a trend towards

greater ^{13}C-labeling of liver serine [U-^{13}C]glucose in KO mice fed a HF-SAAR diet compared to

KO mice fed a HF-CTRL diet. To further explore if the liver was acquiring this serine from

extrahepatic sources, we administered [U-^{13}C]serine to mice. Liver ^{13}C-serine labeling was similar

between mice fed a HF-CTRL and HF-SAAR diet. Given that the liver serine pool size is larger

in mice fed a HF-SAAR diet, a greater amount of exogenous ^{13}C-serine would need to be taken up

by the liver to achieve a similar proportion of ^{13}C-serine labeling in livers of mice fed a HF-SAAR

diet. Thus, our data aligns with the hypothesis that SAAR increases asparagine synthesis from

glucose to promote liver serine uptake.

4.4. Role of hepatic PSAT1 in lipid adaptations to SAAR

Our findings agree with prior studies reporting that SAAR lowers adiposity and liver

triglycerides [2; 5; 9; 18; 21; 59]. In the current study, the decline in liver triglycerides following

SAAR was associated with decreased *de novo* lipogenesis enzymes (ACLY, FASN, and SCD-1).

There was a modest increase in mitochondrial respiratory chain proteins (complexes I, IV, and V)

in response to SAAR. These results are consistent with our prior work showing dietary SAAR

increases the expression of select mitochondrial proteins without enhancing mitochondrial

respiration [21]. While terminal oxidation may not be enhanced by SAAR [21], other means of

lipid disposal could contribute to lower triglycerides. Studies using ^{14}C-palmitate in liver

homogenates have determined that SAAR increases liver β-oxidation [61]. We identified short-

chain acylglycines (acetylglycine, isobutyrylglycine, and isovalerylglycine) were increased. These

acylglycines are generated in the mitochondria by conjugating acyl-CoAs to glycine in a reaction

mediated by GLYAT [62]. Thus, the SAAR-mediated rise in glycine may facilitate acylglycine

synthesis and, consequently, promote the disposal of fatty acids during SAAR. Importantly, SAAR

elicited the molecular responses in lipid metabolism and lowered liver triglycerides similarly in

WT and PSAT1 KO mice. Overall, the prevailing signature under SAAR is a coordinated decrease

in *de novo* lipogenesis and stimulation of acyl-CoA disposal that is independent of PSAT1 action.

In summary, hepatic PSAT1 is necessary for adaptations to SAAR involving serine

synthesis that allow improvements in glucose tolerance to be fully realized. In contrast, PSAT1 is

dispensable for the adaptations in lipid accretion and disposal pathways that contribute to the

SAAR-mediated decline in liver lipids. Thus, the serine synthesis pathway is critical to the glucose,

but not lipid, adaptations to SAAR. These studies provide a mechanistic foundation for how SAAR

impacts the liver to prevent dysregulated glucose control.

ACKNOWLEDGEMENTS

The authors acknowledge the technical assistance provided by Ruth Pfeiffer. Figure schematics

were created using BioRender.com.

CRediT AUTHORSHIP CONTRIBUTION STATEMENT

A.F.O.: Writing – original draft, Visualization, Validation, Methodology, Investigation, Formal

analysis, Data curation, Conceptualization, and Project administration C.V., F.I.R., K.M.A.,

A.M.P., and A.B.N.: Investigation, and Writing - Review & Editing; P.A.C., and J.J.G.:

Methodology, Resources, and Writing - Review & Editing; S.C.H.: Resources, and Writing -

Review & Editing; C.C.H.: Writing – review & editing, Visualization, Validation, Supervision,

Resources, Methodology, Investigation, Funding acquisition, Dara curation, Conceptualization,

and Project administration.

FUNDING SOURCES

The National Institutes of Health Grants DK136772 (C.C.H.), DK091538 (P.A.C.), AG069781

(P.A.C.), DK133196 (J.J.G.) supported this research. A.F.O. was supported by the National

Institutes of Health Ruth L. Kirschstein National Research Service Award T32 DK007293.

DECLARATION OF COMPETING INTEREST

The authors declare that they have no known competing financial interests or personal

relationships that could have appeared to influence the work reported in this paper.

581
582

REFERENCES
[1]   Fang, H., Stone, K.P., Wanders, D., Forney, L.A., Gettys, T.W., 2022. The Origins,
Evolution, and Future of Dietary Methionine Restriction. Annu Rev Nutr 42:201-226.
[2]   Forney, L.A., Wanders, D., Stone, K.P., Pierse, A., Gettys, T.W., 2017. Concentration-
dependent linkage of dietary methionine restriction to the components of its metabolic
phenotype. Obesity (Silver Spring) 25(4):730-738.
[3]   Malloy, V.L., Krajcik, R.A., Bailey, S.J., Hristopoulos, G., Plummer, J.D., Orentreich, N.,
2006. Methionine restriction decreases visceral fat mass and preserves insulin action in aging
male Fischer 344 rats independent of energy restriction. Aging Cell 5(4):305-314.
[4]   Thyne, K.M., Salmon, A.B., 2022. Metabolic benefits of methionine restriction in adult
mice do not require functional methionine sulfoxide reductase A (MsrA). Sci Rep 12(1):5073.
[5]   Lees, E.K., Banks, R., Cook, C., Hill, S., Morrice, N., Grant, L., et al., 2017. Direct
comparison of methionine restriction with leucine restriction on the metabolic health of
C57BL/6J mice. Sci Rep 7(1):9977.
[6]   Lees, E.K., Krol, E., Grant, L., Shearer, K., Wyse, C., Moncur, E., et al., 2014.
Methionine restriction restores a younger metabolic phenotype in adult mice with alterations in
fibroblast growth factor 21. Aging Cell 13(5):817-827.
[7]   Ables, G.P., Perrone, C.E., Orentreich, D., Orentreich, N., 2012. Methionine-restricted
C57BL/6J mice are resistant to diet-induced obesity and insulin resistance but have low bone
density. PLoS One 7(12):e51357.
[8]   Wanders, D., Burk, D.H., Cortez, C.C., Van, N.T., Stone, K.P., Baker, M., et al., 2015.
UCP1 is an essential mediator of the effects of methionine restriction on energy balance but not
insulin sensitivity. FASEB J 29(6):2603-2615.
[9]   Wanders, D., Forney, L.A., Stone, K.P., Burk, D.H., Pierse, A., Gettys, T.W., 2017.
FGF21 Mediates the Thermogenic and Insulin-Sensitizing Effects of Dietary Methionine
Restriction but Not Its Effects on Hepatic Lipid Metabolism. Diabetes 66(4):858-867.
[10]   Wanders, D., Stone, K.P., Forney, L.A., Cortez, C.C., Dille, K.N., Simon, J., et al., 2016.
Role of GCN2-Independent Signaling Through a Noncanonical PERK/NRF2 Pathway in the
Physiological Responses to Dietary Methionine Restriction. Diabetes 65(6):1499-1510.

[11]   Stone, K.P., Wanders, D., Orgeron, M., Cortez, C.C., Gettys, T.W., 2014. Mechanisms of increased in vivo insulin sensitivity by dietary methionine restriction in mice. Diabetes 63(11):3721-3733.

[12]   Plaisance, E.P., Greenway, F.L., Boudreau, A., Hill, K.L., Johnson, W.D., Krajcik, R.A., et al., 2011. Dietary methionine restriction increases fat oxidation in obese adults with metabolic syndrome. J Clin Endocrinol Metab 96(5):E836-840.

[13]   Olsen, T., Stolt, E., Ovrebo, B., Elshorbagy, A., Tore, E.C., Lee-Odegard, S., et al., 2024. Dietary sulfur amino acid restriction in humans with overweight and obesity: a translational randomized controlled trial. J Transl Med 22(1):40.

[14]   Richie, J.P., Jr., Sinha, R., Dong, Z., Nichenametla, S.N., Ables, G.P., Ciccarella, A., et al., 2023. Dietary Methionine and Total Sulfur Amino Acid Restriction in Healthy Adults. J Nutr Health Aging 27(2):111-123.

[15]   Fang, H., Stone, K.P., Ghosh, S., Forney, L.A., Gettys, T.W., 2021. The Role of Reduced Methionine in Mediating the Metabolic Responses to Protein Restriction Using Different Sources of Protein. Nutrients 13(8).

[16]   Fang, H., Stone, K.P., Ghosh, S., Forney, L.A., Sims, L.C., Vincik, L., et al., 2021. Hepatic Nfe2l2 Is Not an Essential Mediator of the Metabolic Phenotype Produced by Dietary Methionine Restriction. Nutrients 13(6).

[17]   Fang, H., Stone, K.P., Forney, L.A., Sims, L.C., Gutierrez, G.C., Ghosh, S., et al., 2021. Implementation of dietary methionine restriction using casein after selective, oxidative deletion of methionine. iScience 24(5):102470.

[18]   Stone, K.P., Ghosh, S., Kovalik, J.P., Orgeron, M., Wanders, D., Sims, L.C., et al., 2021. The acute transcriptional responses to dietary methionine restriction are triggered by inhibition of ternary complex formation and linked to Erk1/2, mTOR, and ATF4. Sci Rep 11(1):3765.

[19]   Forney, L.A., Fang, H., Sims, L.C., Stone, K.P., Vincik, L.Y., Vick, A.M., et al., 2020. Dietary Methionine Restriction Signals to the Brain Through Fibroblast Growth Factor 21 to Regulate Energy Balance and Remodeling of Adipose Tissue. Obesity (Silver Spring) 28(10):1912-1921.

[20]   Ghosh, S., Forney, L.A., Wanders, D., Stone, K.P., Gettys, T.W., 2017. An integrative analysis of tissue-specific transcriptomic and metabolomic responses to short-term dietary methionine restriction in mice. PLoS One 12(5):e0177513.

[21]   Rome, F.I., Hughey, C.C., 2022. Disrupted liver oxidative metabolism in glycine N-methyltransferase-deficient mice is mitigated by dietary methionine restriction. Mol Metab 58:101452.

[22]   Ommi, N.B., Mattocks, D.A.L., Kalecky, K., Bottiglieri, T., Nichenametla, S.N., 2025. Pharmacological recapitulation of the lean phenotype induced by the lifespan-extending sulfur amino acid-restricted diet. Aging (Albany NY) 17(4):960-981.

[23]   Nichenametla, S.N., Mattocks, D.A.L., Cooke, D., Midya, V., Malloy, V.L., Mansilla, W., et al., 2022. Cysteine restriction-specific effects of sulfur amino acid restriction on lipid metabolism. Aging Cell 21(12):e13739.

[24]   Kalhan, S.C., Hanson, R.W., 2012. Resurgence of serine: an often neglected but indispensable amino Acid. J Biol Chem 287(24):19786-19791.

[25]   Hamano, M., Esaki, K., Moriyasu, K., Yasuda, T., Mohri, S., Tashiro, K., et al., 2021. Hepatocyte-Specific Phgdh-Deficient Mice Culminate in Mild Obesity, Insulin Resistance, and Enhanced Vulnerability to Protein Starvation. Nutrients 13(10).

[26]   Yu, J., Xiao, F., Guo, Y., Deng, J., Liu, B., Zhang, Q., et al., 2015. Hepatic Phosphoserine Aminotransferase 1 Regulates Insulin Sensitivity in Mice via Tribbles Homolog 3. Diabetes 64(5):1591-1602.

[27]   Sim, W.C., Lee, W., Sim, H., Lee, K.Y., Jung, S.H., Choi, Y.J., et al., 2020. Downregulation of PHGDH expression and hepatic serine level contribute to the development of fatty liver disease. Metabolism 102:154000.

[28]   Raines, L.N., Zhao, H., Wang, Y., Chen, H.-Y., Gallart-Ayala, H., Hsueh, P.-C., et al., 2022. PERK is a critical metabolic hub for immunosuppressive function in macrophages. Nature immunology 23(3):431-445.

[29]   Rome, F.I., Shobert, G.L., Voigt, W.C., Stagg, D.B., Puchalska, P., Burgess, S.C., et al., 2023. Loss of hepatic phosphoenolpyruvate carboxykinase 1 dysregulates metabolic responses to acute exercise but enhances adaptations to exercise training in mice. Am J Physiol Endocrinol Metab 324(1):E9-E23.

[30]   Chan, T.M., Exton, J.H., 1976. A rapid method for the determination of glycogen content and radioactivity in small quantities of tissue or isolated hepatocytes. Analytical biochemistry 71(1):96-105.

[31]   Puchalska, P., Crawford, P.A., 2019. Application of stable isotope labels for metabolomics in studies in fatty liver disease. Metabolomics: Methods and Protocols. Springer, p. 259-272.

[32]   Nelson, A.B., Reese, L.E., Rono, E., Queathem, E.D., Qiu, Y., McCluskey, B.M., et al., 2025. Deciphering Colorectal Cancer–Hepatocyte Interactions: A Multiomics Platform for Interrogation of Metabolic Crosstalk in the Liver–Tumor Microenvironment. International journal of molecular sciences 26(5):1976.

[33]   Queathem, E.D., Moazzami, Z., Stagg, D.B., Nelson, A.B., Fulghum, K., Hayir, A., et al., 2025. Ketogenesis supports hepatic polyunsaturated fatty acid homeostasis via fatty acid elongation. Science Advances 11(5):eads0535.

[34]   Koelmel, J.P., Kroeger, N.M., Gill, E.L., Ulmer, C.Z., Bowden, J.A., Patterson, R.E., et al., 2017. Expanding lipidome coverage using LC-MS/MS data-dependent acquisition with automated exclusion list generation. Journal of the American Society for Mass Spectrometry 28(5):908-917.

[35]   Gaffney, D.O., Jennings, E.Q., Anderson, C.C., Marentette, J.O., Shi, T., Schou Oxvig, A.M., et al., 2020. Non-enzymatic Lysine Lactoylation of Glycolytic Enzymes. Cell Chem Biol 27(2):206-213 e206.

[36]   Galligan, J.J., Wepy, J.A., Streeter, M.D., Kingsley, P.J., Mitchener, M.M., Wauchope, O.R., et al., 2018. Methylglyoxal-derived posttranslational arginine modifications are abundant histone marks. Proc Natl Acad Sci U S A 115(37):9228-9233.

[37]   Galligan, J.J., Kingsley, P.J., Wauchope, O.R., Mitchener, M.M., Camarillo, J.M., Wepy, J.A., et al., 2017. Quantitative Analysis and Discovery of Lysine and Arginine Modifications. Anal Chem 89(2):1299-1306.

[38]   Mehran, A.E., Templeman, N.M., Brigidi, G.S., Lim, G.E., Chu, K.Y., Hu, X., et al., 2012. Hyperinsulinemia drives diet-induced obesity independently of brain insulin production. Cell Metab 16(6):723-737.

[39]   Thomas, D.D., Corkey, B.E., Istfan, N.W., Apovian, C.M., 2019. Hyperinsulinemia: An Early Indicator of Metabolic Dysfunction. J Endocr Soc 3(9):1727-1747.

[40]   Wiebe, N., Ye, F., Crumley, E.T., Bello, A., Stenvinkel, P., Tonelli, M., 2021. Temporal Associations Among Body Mass Index, Fasting Insulin, and Systemic Inflammation: A Systematic Review and Meta-analysis. JAMA Network Open 4(3):e211263-e211263.

[41]   Werge, M.P., McCann, A., Galsgaard, E.D., Holst, D., Bugge, A., Albrechtsen, N.J.W., et al., 2021. The Role of the Transsulfuration Pathway in Non-Alcoholic Fatty Liver Disease. J Clin Med 10(5).

[42]   Trujillo, M.N., Jennings, E.Q., Farrera, D.O., Kitamura, N., Anderson, C.C., Gehrke, S., et al., 2025. Glyoxalase 2 Coordinates de Novo Serine Metabolism. Chembiochem 26(7):e202401086.

[43]   Buescher, J.M., Antoniewicz, M.R., Boros, L.G., Burgess, S.C., Brunengraber, H., Clish, C.B., et al., 2015. A roadmap for interpreting 13C metabolite labeling patterns from cells. Current opinion in biotechnology 34:189-201.

[44]   Christen, S., Lorendeau, D., Schmieder, R., Broekaert, D., Metzger, K., Veys, K., et al., 2016. Breast cancer-derived lung metastases show increased pyruvate carboxylase-dependent anaplerosis. Cell reports 17(3):837-848.

[45]   Bruntz, R.C., Lane, A.N., Higashi, R.M., Fan, T.W.-M., 2017. Exploring cancer metabolism using stable isotope-resolved metabolomics (SIRM). Journal of Biological Chemistry 292(28):11601-11609.

[46]   Johnston, K., Pachnis, P., Tasdogan, A., Faubert, B., Zacharias, L.G., Vu, H.S., et al., 2021. Isotope tracing reveals glycolysis and oxidative metabolism in childhood tumors of multiple histologies. Med 2(4):395-410. e394.

[47]   Lau, A.N., Li, Z., Danai, L.V., Westermark, A.M., Darnell, A.M., Ferreira, R., et al., 2020. Dissecting cell-type-specific metabolism in pancreatic ductal adenocarcinoma. Elife 9:e56782.

[48]   Pachnis, P., Wu, Z., Faubert, B., Tasdogan, A., Gu, W., Shelton, S., et al., 2022. In vivo isotope tracing reveals a requirement for the electron transport chain in glucose and glutamine metabolism by tumors. Science Advances 8(35):eabn9550.

[49]   Holm, L.J., Haupt-Jorgensen, M., Larsen, J., Giacobini, J.D., Bilgin, M., Buschard, K., 2018. L-serine supplementation lowers diabetes incidence and improves blood glucose homeostasis in NOD mice. PLoS ONE 13(3):e0194414.

[50]   Lopez-Gonzales, E., Lehmann, L., Ruiz-Ojeda, F.J., Hernandez-Bautista, R., Altun, I., Onogi, Y., et al., 2022. L-Serine Supplementation Blunts Fasting-Induced Weight Regain by Increasing Brown Fat Thermogenesis. Nutrients 14(9).

[51]   Handzlik, M.K., Metallo, C.M., 2023. Sources and Sinks of Serine in Nutrition, Health, and Disease. Annu Rev Nutr 43:123-151.

[52]   Achouri, Y., Robbi, M., Van Schaftingen, E., 1999. Role of cysteine in the dietary control of the expression of 3-phosphoglycerate dehydrogenase in rat liver. Biochem J 344 Pt 1:15-21.

[53]   Garcia, R.A., Stipanuk, M.H., 1992. The splanchnic organs, liver and kidney have unique roles in the metabolism of sulfur amino acids and their metabolites in rats. J Nutr 122(8):1693-1701.

[54]   Stipanuk, M.H., Coloso, R.M., Garcia, R.A., Banks, M.F., 1992. Cysteine concentration regulates cysteine metabolism to glutathione, sulfate and taurine in rat hepatocytes. J Nutr 122(3):420-427.

[55]   Coloso, R.M., Hirschberger, L.L., Stipanuk, M.H., 1991. Uptake and metabolism of L-2-oxo-[35S]thiazolidine-4-carboxylate by rat cells is slower than that of L-[35S]cysteine or L-[35S]methionine. J Nutr 121(9):1341-1348.

[56]   Bagley, P.J., Stipanuk, M.H., 1995. Rats fed a low protein diet supplemented with sulfur
amino acids have increased cysteine dioxygenase activity and increased taurine production in
hepatocytes. J Nutr 125(4):933-940.
[57]   Farrera, D.O., Galligan, J.J., 2022. The Human Glyoxalase Gene Family in Health and
Disease. Chem Res Toxicol.
[58]   Trujillo, M.N., Jennings, E.Q., Hoffman, E.A., Zhang, H., Phoebe, A.M., Mastin, G.E., et
al., 2024. Lactoylglutathione promotes inflammatory signaling in macrophages through histone
lactoylation. Mol Metab:101888.
[59]   Xin, C., Cai, M., Jia, Q., Huang, R., Li, R., Wang, J., et al., 2025. Dietary sulfur amino
acid restriction improves metabolic health by reducing fat mass. Life Metab 4(3):loaf009.
[60]   Krall, A.S., Xu, S., Graeber, T.G., Braas, D., Christofk, H.R., 2016. Asparagine promotes
cancer cell proliferation through use as an amino acid exchange factor. Nat Commun 7:11457.
[61]   Hasek, B.E., Boudreau, A., Shin, J., Feng, D., Hulver, M., Van, N.T., et al., 2013.
Remodeling the integration of lipid metabolism between liver and adipose tissue by dietary
methionine restriction in rats. Diabetes 62(10):3362-3372.
[62]   Badenhorst, C.P.S., van der Sluis, R., Erasmus, E., Van Dijk, A.A., 2013. Glycine
conjugation: importance in metabolism, the role of glycine N-acyltransferase, and factors that
influence interindividual variation. Expert opinion on drug metabolism & toxicology 9(9):1139-
1153.

FIGURE CAPTIONS

Figure 1. Sulfur amino acid restriction (SAAR) prevents obesity and improves systemic
glucose control in C57BL/6J mice. A. A schematic representation of the study design. C57BL/6J
male mice were fed a low-fat control (LF-CTRL), high-fat control (HF-CTRL), or HF-SAAR diet
for 6 weeks starting at 6 weeks of age. **B.** Body weight time course (g), body weight change over
the 6 weeks on diet (g), fat mass (% of body weight), and lean mass (% of body weight). **C.** Liver
triglycerides ($mg \cdot g^{-1}$) and liver weight (g). **D.** Liver glycogen ($mg \cdot g^{-1}$). **E.** Blood glucose ($mg \cdot dL^{-1}$). **F.** Glucose excursion and area under the curve (AUC) during a glucose tolerance
test. **G.** Glucose excursion and AUC during an insulin tolerance test. **H.** Plasma insulin ($pmol \cdot L^{-1}$). n=3-17. *p<0.05, **p<0.01, ***p<0.001, ****p<0.0001.

776
777
Figure 2. Sulfur amino acid restriction (SAAR) increases liver glucose partitioning to *de novo*
***serine synthesis in C57BL/6J mice. A.** A schematic representation of the select reactions involved
in *de novo* serine synthesis and SAA synthesis and catabolism. **B.** Liver methionine, cysteine, and
taurine (arbitrary units) in C57BL/6J male mice fed a low-fat control (LF-CTRL), high-fat control
(HF-CTRL), or HF-SAAR diet for 6 weeks starting at 6 weeks of age. **C.** Liver phosphoglycerate
dehydrogenase (PHGDH) and phosphoserine aminotransferase 1 (PSAT1) as determined by
immunoblotting and representative immunoblots in mice fed a LF-CTRL, HF-CTRL, and HF-
SAAR diet. **D.** Liver PSAT1 as determined by immunoblotting and representative immunoblots in
mice fed a LF-CTRL and HF-CTRL diet only. **E.** Liver serine and glycine (arbitrary units). **F.** A
schematic representation of the study design. C57BL/6J mice were fed a LF-CTRL (0.88% kcal
from methionine, 510072, Dyets Inc., Bethlehem, PA) or low-fat SAAR (LF-SAAR; 0.18% kcal
from methionine, 510071, Dyets Inc., Bethlehem, PA) for 6 weeks starting at 6 weeks of age. See

Supplementary Table 3 for diet details. A 30-minute intravenous infusion of [U-^{13}C]glucose in the
conscious, unrestrained mouse was completed at 12 weeks of age. **G.** Arterial blood glucose
(mg·dL^{-1}). **H.** Fractional enrichment (% total pool) of liver glucose, serine and glycine from [U-
^{13}C]glucose. n=6-10. $^{\#}$p<0.05 by *t*-test, *p<0.05, **p<0.01, ***p<0.001, ****p<0.0001 by
ANOVA.
795
796
Figure 3. Liver PSAT1 is required for systemic glucose adaptations to sulfur amino acid
restriction (SAAR). A. A schematic representation of the study design. Liver-specific PSAT1
knockout (KO) mice and wild type (WT) littermates were fed a high-fat control (HF-CTRL) or
HF-SAAR diet for 6 weeks. **B.** Body weight time course (g) and body weight change over 6 weeks
on diet (g). **C.** Fat mass and lean mass (% of body weight). **D.** Glucose excursion curves and area
under the curve (AUC) for glucose tolerance tests. **E.** Glucose excursion curves and AUC for
insulin tolerance tests. **F.** Plasma insulin (pmol·L^{-1}) before (0 min) and 15 minutes after an insulin
injection. **G.** Liver phosphor-Akt (p-Akt)-to-Akt ratio as determined by immunoblotting and
representative immunoblots. **H.** Liver glycogen (mg·g^{-1}). **I.** Liver phospho-glycogen synthase (p-
GS)-to-GS ratio and phospho-glycogen phosphorylase (p-PYGL)-to-PYGL ratio as determined by
immunoblotting and representative immunoblots. n=5-18. *p<0.05, **p<0.01, ***p<0.001,
****p<0.0001.
809
810
Figure 4. Sulfur amino acid restriction (SAAR) increases liver *de novo* serine synthesis from
glucose. A. A schematic representation of select metabolites and enzymes involved in *de novo*
serine synthesis from glucose. **B.** Liver phosphoglycerate dehydrogenase (PHGDH),
phosphoserine aminotransferase 1 (PSAT1), and serine hydroxymethyltransferase 2 (SHMT2) as
determined by immunoblotting and representative immunoblots in wild type (WT) and liver-
specific PSAT1 knockout (KO) mice fed a high-fat control (HF-CTRL) or HF-SAAR diet for 6
weeks. **C.** Liver glucose, serine, and glycine (arbitrary units) in 7-hour fasted mice. **D.** Fractional
enrichment (% of total pool) of liver glucose, serine, and glycine following a 30-minute
intravenous infusion of [U-^{13}C]glucose. n=7-9. *p<0.05, **p<0.01, ***p<0.001, ****p<0.0001.
820
821
Figure 5. Sulfur amino acid restriction (SAAR) increases partitioning of glucose-sourced
serine to liver glutathione. A. A schematic representation of the select reactions involved in *de*
novo serine synthesis and SAA synthesis and catabolism. **B.** Liver cystathionine β-synthase (CBS),
cystathionine γ-lyase (CSE), cysteine dioxygenase 1 (CDO1), glutamate-cysteine ligase catalytic
subunit (GCLC), and glutathione synthetase (GSS) as determined by immunoblotting and
representative immunoblots in wild type (WT) and liver-specific PSAT1 knockout (KO) mice fed
a high-fat control (HF-CTRL) or HF-SAAR diet for 6 weeks. **C.** Liver methionine, cysteine,
taurine, reduced glutathione (GSH), and oxidized glutathione (GSSG; arbitrary units) in 7-hour
fasted mice. **D.** Fractional enrichment (% of total pool) of liver methionine, taurine, GSH, and
GSSG following a 30-minute intravenous infusion of [U-^{13}C]glucose. **E.** Fractional enrichment
(% of total pool) of liver serine, methionine, taurine, GSH, and GSSG at 15 minutes following an
i.p. injection of [U-^{13}C]serine. n=6-9. *p<0.05, **p<0.01, ***p<0.001, ****p<0.0001.
834

Figure 6. Sulfur amino acid restriction (SAAR) lowers glyoxalase cycle metabolites and associated post-translational modifications (PTMs). A. A schematic of select reactions, metabolites, and PTMs related to the glyoxalase cycle. **B.** Liver glyoxalase 1 (GLO1) and hydroxyacylglutathione hydrolase (GLO2) as determined by immunoblotting and representative immunoblots in wild type (WT) and liver-specific PSAT1 knockout (KO) mice fed a high-fat control (HF-CTRL) or HF-SAAR diet for 6 weeks. **C.** Liver glutathione (GSH; arbitrary units), hemithioacetal (HTA; arbitrary units), lactoylglutathione (arbitrary units), and lactate (arbitrary units). **D.** Global PTMs (pmol·nmol Leu^{-1}): lactoyllysine, methylglyoxal-derived hydroimidazolone 1 (MG-H1), carboxyethylarginine (CEA), and acetyllysine. n=6-9. *p<0.05, **p<0.01, ****p<0.0001.

Figure 7. Sulfur amino acid restriction (SAAR) increases glucose partitioning toward asparagine synthesis. A. A schematic representation of select reactions and metabolites linking tricarboxylic acid (TCA)-cycle intermediates to asparagine synthesis. **B.** Liver TCA cycle, anaplerotic and cataplerotic metabolites (arbitrary units) in wild type (WT) and liver-specific PSAT1 knockout (KO) mice fed a high-fat control (HF-CTRL) or HF-SAAR diet for 6 weeks. **C.** Fractional enrichment (% of total pool) of liver TCA cycle, anaplerotic and cataplerotic metabolites following a 30-minute intravenous infusion of [U-^{13}C]glucose. **D.** Ratios of isotopologues used as indices of anaplerotic and cataplerotic flux. **E.** Liver asparagine synthase (ASNS), pyruvate carboxylase (PC), propionyl-CoA carboxylase subunit A (PCCA), malate dehydrogenase 2 (MDH2), and mitochondrial glutamic-oxaloacetic transaminase (GOT2) as determined by immunoblotting and representative immunoblots. n=6-9. *p<0.05, **p<0.01, ***p<0.001, ****p<0.0001.

Figure 8. Sulfur amino acid restriction (SAAR) reduces lipid accumulation independently of hepatic PSAT1. Panels A-G are measurements in in wild type (WT) and liver-specific PSAT1 knockout (KO) mice fed a high-fat control (HF-CTRL) or HF-SAAR diet for 6 weeks. Panels H-J are measurements in WT and KO mice fed the HF-CTRL and -SAAR diets for 20 weeks. **A.** Liver triglycerides (mg·g^{-1}). **B.** Liver *de novo* lipogenesis enzymes: ATP-citrate lyase (ACLY), acetyl-CoA carboxylase (ACC), fatty acid synthase (FASN), and stearoyl-CoA desaturase 1 (SCD1) as determined by immunoblotting (arbitrary units). **C.** Liver mitochondrial respiratory complexes I-V (CI-V) as determined by immunoblotting. **D.** Representative immunoblots for panels B, C, and F. **E.** A schematic representation of select metabolites and enzymes related to the synthesis of acylglycines. **F.** Liver glycine N-acyltransferase (GLYAT) as determined by immunoblotting. **G.** Liver acylglycines (arbitrary units): acetylglycine, isobutyrylglycine, isovalerylglycine, hexanoylglycine, and capryloylglycine. **H.** Body weight time course (g) and change in body weight (g) over 20 weeks on diet. **I.** Fat mass and lean mass (% body weight). **J.** Liver triglycerides (mg·g^{-1}). n=5-9 *p<0.05, **p<0.01, ***p<0.001, ****p<0.0001.

Supplementary Figure 1. Sulfur Amino Acid Restriction (SAAR) impacts systemic glucose control and hepatic glucose partitioning in C57BL/6J mice independent of insulin levels. A. A schematic representation of the study design. C57BL/6J male mice were fed a low-fat control

(LF-CTRL), high-fat control (HF-CTRL), or HF-SAAR diet for 6 weeks starting at 6 weeks of age. A subset of mice fed the HF-SAAR diet had a subcutaneous insulin pellet (HF-SAAR + Insulin) implanted at 7 weeks of age for sustained release of insulin until 12 weeks of age. **B.** Body weight time course (g), body weight change over the 6 weeks on diet (g), fat mass (% of body weight), and lean mass (% of body weight). **C.** Liver triglycerides ($mg \cdot g^{-1}$) and liver weight (g). **D.** Liver glycogen ($mg \cdot g^{-1}$). **E.** Blood glucose ($mg \cdot dL^{-1}$). **F.** Glucose excursion and area under the curve (AUC) during a glucose tolerance test. **G.** Glucose excursion and AUC during an insulin tolerance test. **H.** Plasma insulin ($pmol \cdot L^{-1}$). **I.** Liver methionine, homocysteine, cysteine, and taurine (arbitrary units). **J.** Liver phosphoglycerate dehydrogenase (PHGDH) and phosphoserine aminotransferase 1 (PSAT1) as determined by immunoblotting and representative immunoblots. **K.** Liver serine and glycine (arbitrary units). n=3-17. [#]$p<0.05$ by *t*-test. *$p<0.05$, **$p<0.01$, ***$p<0.001$, ****$p<0.0001$ by ANOVA.

Graphical Abstract. Schematic representation of liver glucose adaptations to SAAR

Figure 1. SAAR prevents obesity and improves systemic glucose control in C57BL/6J mice

Figure 2. SAAR increased glucose partitioning to de novo serine synthesis in C57BL/6J mice

Figure 3. Liver PSAT1 is required for systemic glucose adaptations to SAAR.

Figure 4. SAAR increases liver de novo serine synthesis from glucose

Figure 5. SAAR increases partitioning of glucose-sourced serine to glutathione

Figure 6. SAAR lowers liver glyoxalase cycle metabolites and associated post-translational modifications

Figure 7. SAAR increased glucose partitioning toward liver asparagine synthesis

Figure 8. SAAR reduces lipid accumulation independently of hepatic PSAT1