Reduced beta-hydroxybutyrate body disposal after ketogenic diet feeding in mice.

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# ABSTRACT

# INTRODUCTION

The ketogenic diet has gained significant popularity in recent years, driven by several factors that appeal to individuals seeking weight loss, improved health outcomes, and even enhanced performance. One obvious concern with an increasing prevalence of individuals on a ketogenic diet is phenotypic variation, encompassing a broad spectrum of responses in weight loss, metabolic adaptation, blood glucose regulation, energy levels, cognitive function, and long-term adherence. Recognizing and understanding these variations would inevitably help individuals and healthcare practitioners tailor their dietary approach, monitor their progress, and optimize outcomes on a ketogenic diet.

Ketone body synthesis, or ketogenesis, primarily occurs in hepatocytes and to a lesser extent in astrocytes or kidney cells [1] The major utilization of ketone bodies happens in the heart, skeletal muscles, and brain [1–3]. The reduction in dietary carbohydrates leads to a decrease in insulin and an increase in glucagon in plasma, promoting hepatic glycogenolysis, gluconeogenesis, and adipose tissue lipolysis. After 4–7 days of carbohydrate restriction, glycogenolysis is exhausted, leading to increased ketogenesis, elevated levels of free fatty acids (FFA), and ketone bodies (KBs) [4,5].   
  
The enzyme BDH1 facilitates the reversible conversion of acetoacetate (AcAc) to beta-hydroxybutyrate (BHB). Positioned as the final enzyme in hepatic ketogenesis and the initial enzyme in ketolysis, BDH1 plays a pivotal role in these metabolic pathways. To date, there have been no reported cases of hereditary BDH1 deficiency in humans. Under normal dietary conditions, systemic BDH1 deficiency appears well tolerated. However, during fasting periods, its deficiency becomes apparent, marked by a significant increase in the AcAc/3HB ratio and the development of hepatic steatosis [6]. 3-hydroxymethylglutaryl-CoA synthase 2 (HMGCS2) serves as the rate-limiting enzyme in ketogenesis. Its function involves catalyzing the conversion of acetyl-CoA and acetoacetyl-CoA, derived from β-oxidation, into β-hydroxy β-methylglutaryl-CoA (HMG-CoA) and free Coenzyme A (CoA). Mice lacking *Hmgcs2* postnatally exhibited a deficiency in ketogenesis and subsequently developed fatty liver disease spontaneously [7]. However, early weaning proved effective in alleviating hepatosteatosis in postnatal *Hmgcs2* knockout mice. In adult mice, insufficient ketogenic activity heightened susceptibility to diet-induced fatty liver disease. Conversely, overexpression of Hmgcs2 ameliorated high-fat diet-induced fatty liver disease in adult mice [7]. In peripheral tissues, KBs, primarily in the form of BHB, re-enter the cell through MCT1-mediated transport. *SLC16A1*, encoding the monocarboxylate transporter 1 (MCT1), is involved in the transport of mono-carboxylates, such as lactate, pyruvate, and ketone bodies, across cell membranes [8]. BHBs then undergo re-oxidation to AcAc via BDH1, leading to subsequent reactions that generate two molecules of Ac-CoA. These Ac-CoA molecules are generally integrated into the TCA cycle through citrate synthase, facilitating terminal oxidation and ATP production. In skeletal muscle, this process contributes to powering muscular work [9–11]. Succinyl-CoA:3-oxoacid CoA transferase (OXCT1 or SCOT) plays a central role in ketolysis in extra-hepatic tissues, with hepatocytes exhibiting low abundance of OXCT, explaining their lack of ketolytic activity OXCT1 activity is highest in the heart and kidneys, followed by skeletal muscle and the brain [12]. However, due to skeletal muscle constituting approximately 40% of body mass in adult humans, this organ contributes the largest fraction to total KB catabolism at rest [9,13,14]. Although skeletal muscle exhibits a high capacity for KBs, their low circulating concentrations under normal conditions result in a contribution to energy provision in muscle of less than 5% in the post-absorptive state, with FFAs being the primary energy source under standard conditions [9]

For this study, we hypothesized that mice adapted to a ketogenic diet would demonstrate enhanced ketone body disposal. We aimed to test this in both inbred A/J and Diversity Outbred (DO) mice fed a ketogenic diet, comparing their baseline KTT to their post-diet ketone tolerance. We also predicted that variation in ketone disposal may affect cholesterol homeostasis due to the inter-relationship of these metabolic pathways.

# METHODS

## Animal Husbandry and Rodent Diets

Mice were maintained in in ventilated cages at 70F at 40-60% humidity in a room with a 12-hour light/dark cycle (ZT0=6:00AM). Mice were provided *ad libitum* access to food and water unless otherwise noted. Muscle-specific *Tsc1* knockouts were generated by crossing FVB-Tg(*Ckmm*-Cre)5Khn/J transgenic mice (RRID: IMSR\_JAX:006405) with floxed *Tsc1*tm1Djk/J mice (RRID:IMSR\_JAX:005680). Mice heterozygous for the floxed allele and/or the cre allele were crossed to generate littermates of knockout mice (Tsc1fl/fl, Ckmm-CreTg/+) and wild type mice (Tsc1+/+, *Ckmm*-Cre+/+) as previously described [15]. A/J mice (RRID:IMSR\_JAX:000646) were purchased at 8 weeks of age from The Jackson Laboratories and at 10 weeks of age were fed control or ketogenic diets for four weeks. Diversity outbred mice (43rd generation, non-siblings RRID: IMSR\_JAX:009376) were purchased from the Jackson Laboratories and placed on ketogenic diet at 12 weeks of age for four weeks. Mice were maintained on a normal chow diet (Lab Diet 5L0D; 5% of calories from fat, 24% from protein, 36% carbohydrate) unless otherwise specified. For ketogenic diet interventions mice were placed on either a ketogenic diet (Research Diets D17053002, 85% fat, 15% protein, 0% carbohydrates) or a matched synthetic control diet (Research Diets D1053001 10% fat, 15% protein, 75% carbohydrates). Both diets were in meal, not pellet format and were provided in custom jars with holes to provide access. All procedures were approved by the University of Michigan Institutional Animal Use and Care Committee.

## BHB Tolerance Tests

Fed mice were intraperitoneally injected with 1 mg/kg (A/J mouse studies) or 1.5 mg/kg (muscle *Tsc1* knockout and diversity outbred studies) of beta-hydroxybutyrate dissolved in PBS at approximately ZT8. Prior to the injection, and then every 15 afterwards, a tail blood draw was collected and analyzed using a Precision Xtra Ketone Body Assay. To summarize these data we calculated area under the curve and baseline-adjusted area under the curve where we subtracted the contribution of the pre-injection ketone body levels to circulating amounts.

## mRNA Analysis

Quantitative real-time PCR was performed by extracting RNA from muscle lysates using PureLink mRNA kits (Thermo Scientific cat # 12183-018A) and synthesizing cDNA using a high capacity first strand cDNA synthesis kit (Thermo Scientific cat # 4368813). cDNA was amplified using SYBR Green (Thermo-Fisher 4367659) and the primers noted in Table 1 using a QuantStudio 5. Relative expression was determined us the Ct method. For RNAseq, data was re-analysed from GSE84312 [15].

## Cholesterol Analyses

Total cholesterol concentration was determined colorimetrically from serum blood samples, using the Infinity Cholesterol Reagent kit (Thermo Scientific cat # TR13421). Following the manufacturer's instructions, 100 uL of cholesterol reagent and 2uL serum were added to a clear 96-well plate, and incubated for 15 minutes at room temperature. Absorbance values were calculated via a standard curve. Each sample was measured in duplicate. The plate was then read on a XYZ model plate reader using SoftMaxPro 5.3 at 490 nm.

## Statistical Analyses

All statistical analyses were performed using R version 4.2.2 [16] (RRID:SCR\_001905). We set statistical significance for this study at 0.05. For pairwise testing, we first tested for normality via Shapiro Wilk tests, and then equal variance using Levene’s test. On this basis either Mann-Whitney, Welch’s or Student’s *t* tests were performed as noted in the text and figure legends. For longitudinal data, including BHB tolerance tests we constructed mixed linear models using the lme4 package (version 3.1; [17]). The repeated measure (random intercept) was the animal, and Chi-squared tests were performed comparing models with and without diet terms. For experiments with both rodent sexes, we first tested for modification by sex using the interaction terms from a 2x2 ANOVA, and if significant reported this effect while also stratifying by sex and reporting those results.

# RESULTS

## mTORC1 Activity Increases the Expression of Ketolysis Genes

In evaluating factors that affect skeletal muscle expression, we noted that skeletal muscle *Tsc1* knockout mcie had elevations in several ketolytic genes. These mice, due to the deletion of the negative regulator TSC1 have elevated mTORC1 signaling [15,18,19]. We evaluated expression of the putative BHB transporter (*Slc16a1*; upregulated 4.0 fold, padj=1.56 x 10-10). Among the ketone body catabolic enzymes, *Bdh1* (2.1 fold, padj=0.011) and *Oxct1* (1.5 fold, padj=1.5 x 10-5 were elevated. *Acat1* was unchanged in these muscles. These data support the hypothesis that there is transcriptional upregulation of ketolytic genes in muscles with elevated mTORC1 activity.

## Activation of mTORC1 promotes Ketone Disposal

To test whether activation of mTORC1 in muscle tissue alters disposal of ketone bodies, we performed a BHB tolerance test in *Tsc1* knockout mice. The *Ckmm*-Cre induced ablation of *Tsc1* causes activation of mTORC1 in muscle tissues. As shown in Figure 3A, both male and female knockout mice cleared the injected beta-hydroxybutyrate much more rapidly than their wild-type littermates. Using mixed-linear models and using sex as a covariate, and the animal as a random intercept, we found a significant reduction in BHB levels after the challenge (p=0.004). Similarly, when calculating the area under the curve from 0 to 60 minutes, there was a reduction in the knockouts, after adjusting for sex (25%; p=0.016). When stratifying by sex, knockouts had 41% lower AUC in males and 11% lower in females though this modification by did not reach statistical significance (p=0.20). Some [20], but not all [21,22] studies evaluating the effect of ketogenic diets on muscle mTORC1 function have suggested activation of this signaling pathway, so we evaluated how ketogenic diet feeding alters ketone disposal.

## KD Feeding Does not Improve BHB Disposal in A/J Mice

We hypothesized that prolonged exposure to elevated ketone body levels would result in physiological adaptations, resulting in improved disposal of ketone bodies. To test this hypothesis in male wild-type A/J mice we fed 10-week-old A/J mice a control or a ketogenic diet for three weeks and then performed a BHB tolerance test. As expected, baseline ketone body levels were elevated from 0.43 mg/dL to 0.75 mg/dL in this assay (p=0.017). Upon injection we were surprised to observe that ketone body levels remain elevated more-so in the ketogenic diet-fed mice than the control mice (Figure 2A), even after subtracting for baseline differences (Figure 2B-C). These data suggest that ketone disposal is not improved after three weeks of a ketogenic relative to a control diet, and may actually be somewhat worsened in A/J mice (p=0.274 via linear mixed models).

To understand this surprising lack of adaptation, we performed mRNA quantification of quadriceps from these A/J mice evaluating the expression of key transporters and enzymes involved in ketolysis. As shown in Figure 2D, most ketolytic gene expression was reduced. Among the MCT1 family transporters that conduct ketone bodies into cells, *Slc16a1* transcripts were modestly reduced in muscles from A/J mice fed ketogenic diets (17% reduced, pdiet from a 2x2 ANOVA =0.064). *Bdh1* encodes beta hydroxybutyrate dehydrogenase, the interconversion step between beta-hydroxybutyrate and acetoacetate. We found that this gene is downregulated in A/J muscles by 42% (pdiet from a 2x2 ANOVA =0.009). *Oxct1* encodes succinyl-CoA:3-ketoacid CoA transferase (also known as SCOT). This transcript was downregulated in both male and female mice by 52% (pdiet from a 2x2 ANOVA=8.4 x 10-9). While there was no significant sex x diet interaction in these analyses, we thought it was notable that male mice had higher expression of each of these genes than female mouse muscle lysates, with 15-30% increases (psex from a 2x2 ANOVA=4.7 x 10-3 for *Slc16a1*, 8.9 x 10-3 for *Bdh1* and 0.055 for *Oxct1*). This may suggest enhanced ketone body catabolism in male versus female mice, but this was not explored further. We think the key finding here is that the transcriptional downregulation of genes involved in ketone body disposal in muscle is consistent with reduced disposal of injected BHB. This brings up an interesting question though, if ketone bodies are at steady state in serum, but disposal is reduced, that would imply that production may also be reduced. To test this we also looked at three ketogenic enzymes in the livers of these mice, and indeed found downregulation of hepatic *Hmgcl, Hmgcs2,* and *Bdh1* in the livers of male mice, though only *Bdh1* was downregulated in female mouse livers (Supplementary Figure 1, psex x diet <0.01 for both *Hmgcl* and *Hmgcs1*).

## Evaluation of Diversity Outbred Mice Demonstrates Substantial Variation in BHB Disposal

To evaluate if A/J mice were atypical in their lack of adaptation to improved ketolysis, we performed BHB tolerance tests on diversity outbred mice before or after four weeks of a ketogenic diet. Diversity outbred (DO) mice are genetically unique, so represent the integrated genetic variability of the intercrossed eight founder strains [23]. As hypothesized by this level of genetic variability, DO mice had variable responses to BHB Tolerance Tests at both baseline and after four weeks of ketogenic diet (Figure 3A). In Figure 3B we describe the within-mouse effects of the diet, again showing substantial between-strain variability, likely due to genetic differences. There was more variability in the area under the curve post-diet than pre-diet (SDfollow-up/SDbaseline= 1.93; p<1 x 10-15 via Levene’s test) suggesting diet-induced variability. Consistent with our findings using inbred A/J mice the majority of DO mice had worsened ketone disposal after diet (35 mice), with a smaller number of mice having improved ketone disposal by our assay (10 mice), more than would be expected by chance (p=1.9 x 10-4 from a χ2 test). Taking the population together there was a significant decrease in ketone disposal (increase in baseline adjusted KTT) in these mice after four weeks of ketogenic diet (p=4.8 x 10-5 from a paired Wilcoxon test).

To better understand the physiological basis and repercussions of this variation we performed an exploratory analysis to identify potential correlations between baseline, follow-up and changes in ketone disposal and a variety of other outcomes (Figure 3C). While none of these associations met our threshold for statistical significance we three interesting potential relationships between i) baseline ketone disposal and baseline weight, ii) between follow up and changes in ketone disposal and weight gain on a ketogenic diet (STATS), and iii) baseline ketone disposal and changes in and follow up total cholesterol levels (STATS, Figure 3C-D). The relationships between ketone disposal and other physiological parameters warrant further investigation.

# DISCUSSION

Activation of mTORC1 in skeletal muscle appears to play a positive role in promoting the disposal of ketone bodies and regulating the expression of genes associated with ketolysis. It was tempting to speculate based on prior reports of mTORC1 activation in muscles after a ketogenic diet that this was a common adaptation to the LCHF state.  Surprisingly, however, our findings revealed that a 4-week feeding period of a ketogenic diet did not result in an enhancement of ketone body disposal in both inbred A/J mice and Diversity Outbred mice, but rather an impairment in disposal of a bolus of BHB.  Our results are somewhat at odds with those of [24], which showed upregulation of OXCT1 protein in LCHF fed C57BL/6J muscles (BDH1 and SLC16A1 were not tested). In our case we demonstrate downregulation of mRNA, so this could implicate translational regulation or strain differences with respect to OXCT1 but would not explain our observation of reduced ketone disposal (this was not reported in [24]). In terms of strain differences, we observed that the majority of DO mice experienced a decline in BHB disposal following the dietary intervention (35 mice), but there was a subset of mice that exhibited an improvement in BHB disposal as assessed by KTT (10 mice).

Given the biochemical relationship between ketone body production, hepatic fatty acid oxidation, and cholesterol biogenesis it was not surprising to find a potential relationship between these adaptations and cholesterol levels in these mice. The reduction of ketone body disposal may be due to saturation kinetics in skeletal muscle. Prior research has demonstrated that for the KB concentration-oxidation relationship, there is likely a saturating point between 1 and 2 mm, as evidenced by studies involving fasting of various durations [9] or step-wise βHB infusion [25].

Prior research has shown that knockout of *Ppargc1a* results in modestly lowered expression of BDH1, OXCT1 and ACAT1 in skeletal muscle, brain and kidneys, along with decreased expression of MCT1 SLC16A1. This was concordant with impaired ketone body disposal by a similar assay [26]. The converse was also true with muscle transgenic overexpression of PGC1A resulting in iunduction of Bdh1, Oxct1, Slc16a1 and Acat1 and improved ketone body disposal [26]. It is possible that PGC1a/b is downstream of mTORC1 in muscle. In the muscle *Tsc1* knockout data we describe a 34% reduction in *Ppargc1a* mRNA, but a 1.5x increase in *Ppargc1b* mRNA. Of course the downstream PGC1a targets are more relevant, so we used Harmonizome to identify canonical Ppargc1a targets from ENCODE ChIPseq datasets and contrasted those with differentially expressed genes from muscle *Tsc1* knockout mice. Only 4/28 of these genes were differentially expressed in muscles, lower than what would be predicted by chance.

As it relates to other aspects of physiology in the carbohydrate reduced state, this was to our knowledge the first report of diversity outbred mice and ketone disposal analysis, and we evaluated if this was associated with other relevant traits. Our results of lowered ketone body disposal suggested a reduction in ketogenesis over this period, and given the biochemical overlap between cholesterol synthesis and ketone body synthesis pathways it is not surprising that impaired ketone disposal might be associated with elevated cholesterol, but more data is needed to be confident of this hypothesis.

There are several limitations to the present study.  While this study was done in a diverse set of mice, it is plausible that ketone disposal may differ in humans, as may their relationships with cholesterol and energy metabolism.  Our approach was to investigate the short-term disposal of a supraphysiological bolus of BHB which again may have different kinetics than elevated steady state levels of ketone bodies.  Based on our pilot study of 43 mice we estimate we would are only powered able to detect correlations or r>0.55 between two correlated but independent variables. Finally, we do not yet know the mechanism by which skeletal muscle *Tsc1* ablation or mTORC1 activation causes transcriptional changes in ketone body disposal. In our case our assay measured total body ketone disposal, so we do not know that ketone disposal is primarily or exclusively modified in skeletal muscle or also in other tissues.

These findings underscore the necessity for a more in-depth and comprehensive exploration into the factors influencing KB catabolism, including its potential associations with elevated cholesterol. Ketolysis may be influenced by a range of variables, including genetic predispositions, metabolic states, and environmental factors. Based on this research, further investigations are warranted to dissect the molecular pathways, signaling cascades, and genetic factors that contribute to the observed variations in ketone disposal, with the ultimate goal of refining our understanding of the interplay between mTORC1 activation and ketogenic dietary interventions. Such insights may pave the way for personalized therapeutic strategies that consider individual differences in responding to interventions aimed at modulating ketone metabolism.

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# Figure Legends

**Figure 1: Knockout of Muscle *Tsc1* enhances BHB disposal.** A) Ketolytic gene expression in muscle *Tsc1* knockout quadricepts. BHB Tolerance tests in male and female wild-type and muscle *Tsc1* knockout mice. Mice were injected with 1 g/kg BHB and followed for 1h (n=4-10/group). B) Absolute values stratified by sex. C) Area under the curve. Asterisks indicate p<0.05.

**Figure 2: Ketone body disposal is reduced in male A/J mice after ketogenic diet feeding.** BHB Tolerance tests in male A/J mice fed a control or ketogenic diet for three weeks. Mice were injected with 1.5 g/kg BHB and followed for 1h. A) Absolute values. B) Baseline subtracted values. C) Area under the curve for baseline subtracted values. D) qRT-PCR analysis of muscle quadriceps mRNA expression in male and female A/J mice. Asterisks indicate p<0.05 from Welch’s *t*-tests (n=3-8 in A-B and Student’s *t*-tests in D).

**Figure 3: Reduced ketone body disposal in diversity outbred mice after ketogenic diet feeding.**

# Supplementary Figures

**Supplementary Figure 1:** Downregulation of ketogenic gene mRNA levels after four weeks of ketogenic diet in A/J mice. Asterisks indicate pairwise p<0.05 by Student’s *t* test (n=7-8/group).