

Tissue mRNA expression of branched-chain amino acid catabolism enzyme in early lactating dairy cows

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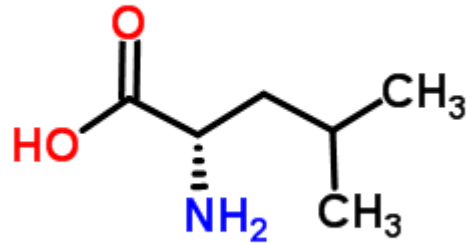
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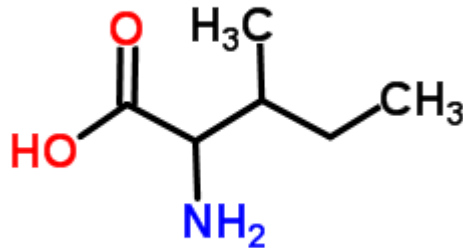
⁵Institute of Animal Nutrition, Friedrich-Loeffler-Institute, Braunschweig, Germany

Introduction

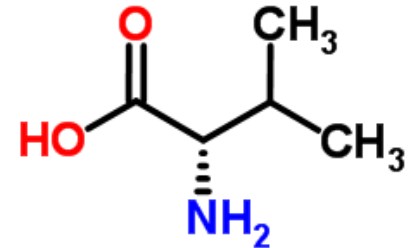
Branched-chain amino acids (**BCAA**)



Leucine



Isoleucine



Valine

Introduction

The **BCAA** are involved in numerous metabolic processes:

- as substrates for protein synthesis
- as energy substrates
- precursors for the synthesis of alanine and glutamine
- as a modulator of muscle protein synthesis via the insulin-signaling pathway and/or via insulin-independent manners (Macotela et al., 2011)

The BCAA catabolic pathway



BCKD complex

BCKDHA gene

BCKDHB gene

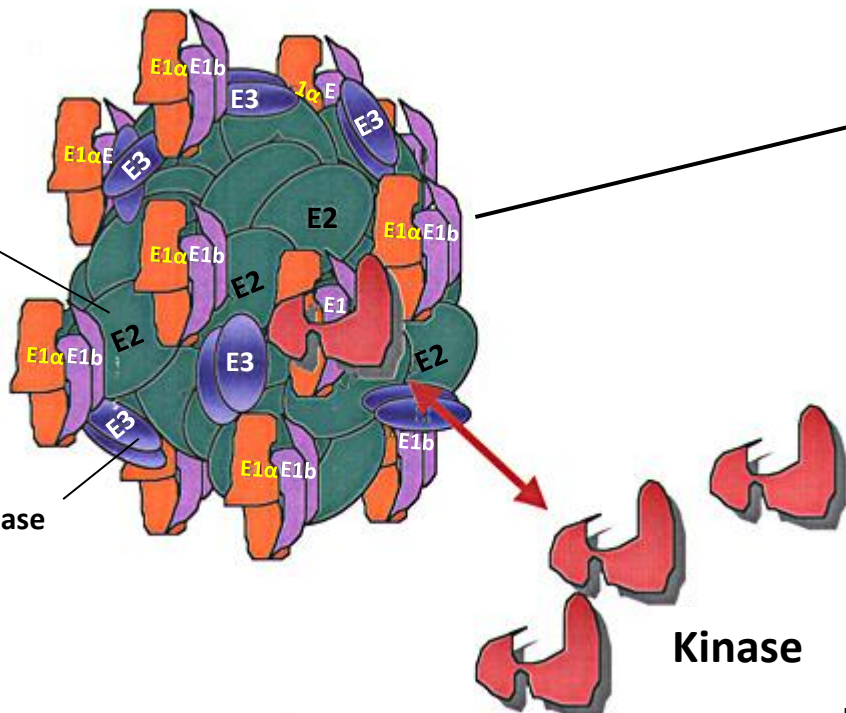
Dihydrolipoyl transacylase

Dihydrolipoamide dehydrogenase

E1 α E1b

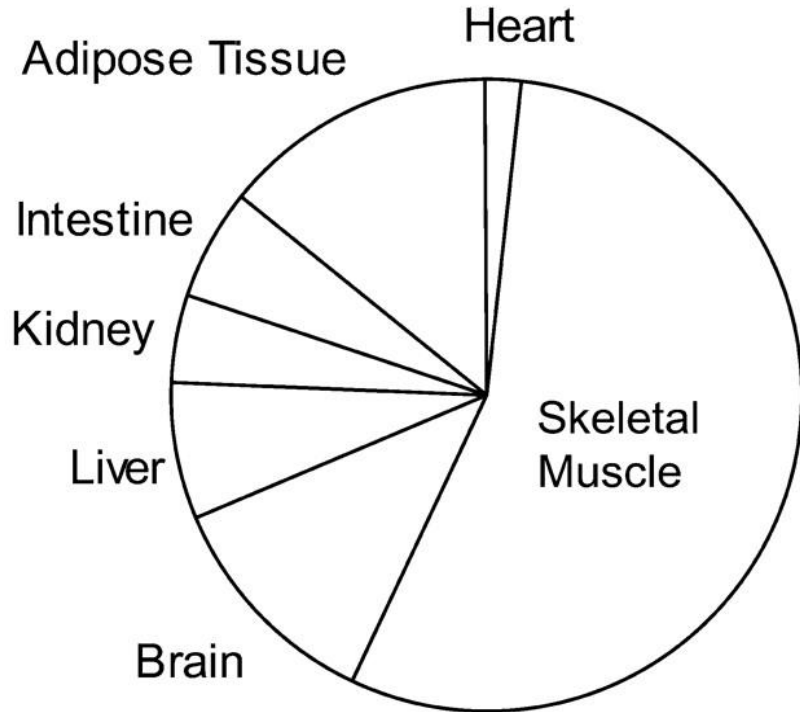
Branched-chain alpha-keto acid decarboxylase

Kinase

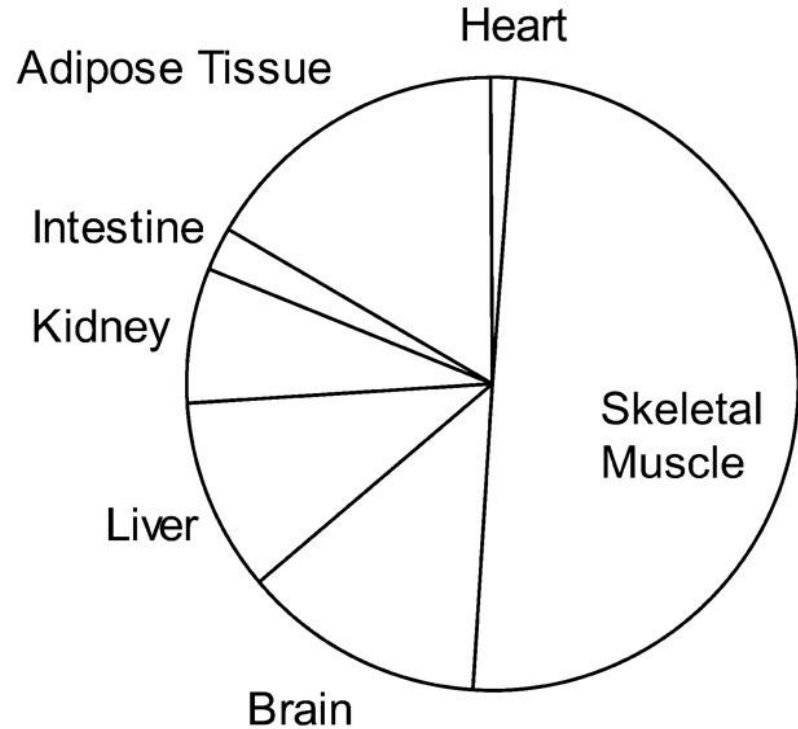


Tissue distribution of BCAT and BCKDH in human tissues (BW = 70 kg)

BCAT



BCKDH



Aim of the study

To test the potential involvement of adipose tissue in BCAA metabolism in dairy cows during early lactation, through assaying mRNA expression of BCKDHA and BCKDHB in visceral and subcutaneous adipose tissue.

Materials and Methods



Primiparous German
Holstein cows (n = 25)

Control (CTR)
(n = 10)

100 g/d rumen-protected **fat preparation** (Silafat®);
CLAs were substituted by stearic acid

Treatment (CLA)
(n = 10)

100 g/d rumen-protected **CLA preparation** (Lutrell®).
Contained **12%** each of **c-9, t-11** and **t-10, c-12**

Days in milk

1

42

105

No. of animals
slaughtered

5

CTR = 5
CLA = 5

CTR = 5
CLA = 5

Sample collection

Skeletal Muscle

M. semitendinosus

Visceral adipose tissue

Mesenterial

Omental

Retroperitoneal

Subcutaneous adipose tissue

Sternum

Tail head

Withers

Materials and Methods

Gene Expression Analysis

- ❑ Using real-time RT-PCR in an Mx3000P cycler (Stratagene, Amsterdam, the Netherlands)
- ❑ Accordance with MIQE guidelines (Bustin et al., 2009)
- ❑ Data normalization: using the most stable reference genes (qBASEplus, Biogazelle, Ghent, Belgium)

Target Genes

BCKDHA
BCKDHB

Reference Genes

Muscle

LRP10
EMD
POLR2A
EIF3K

Fat depots

EIF3K
LRP10
POLR2A
EMD
MARVELD1
HPCAL1

Materials and Methods

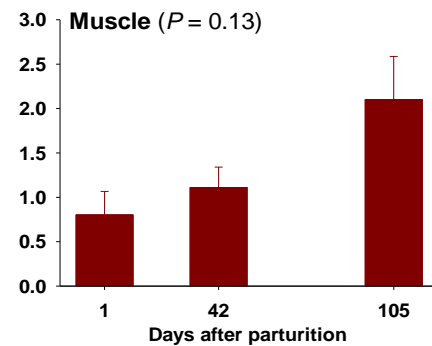
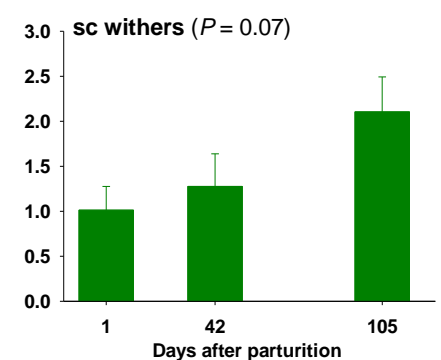
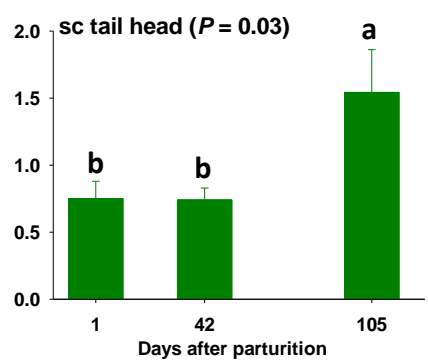
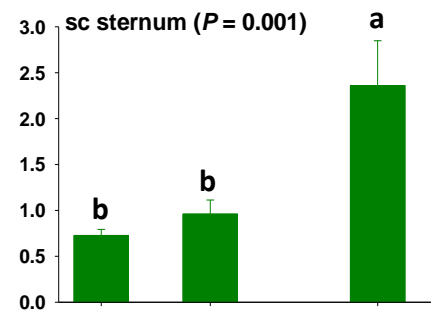
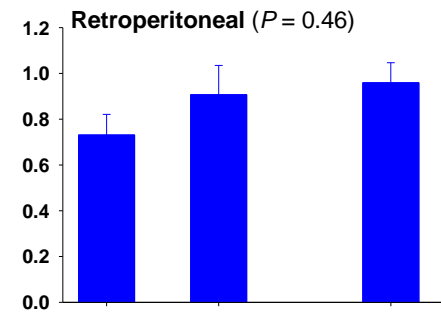
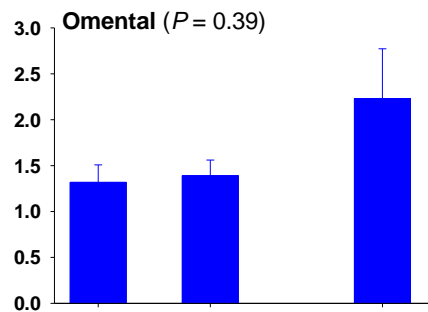
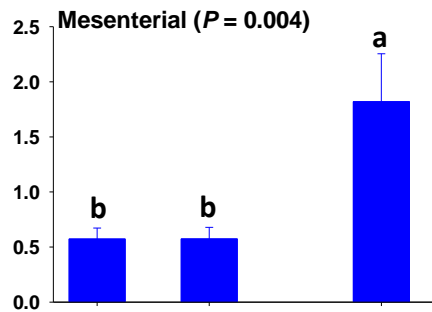
Statistical Analysis

Preliminary statistical evaluation: no CLA effect on the tested variables

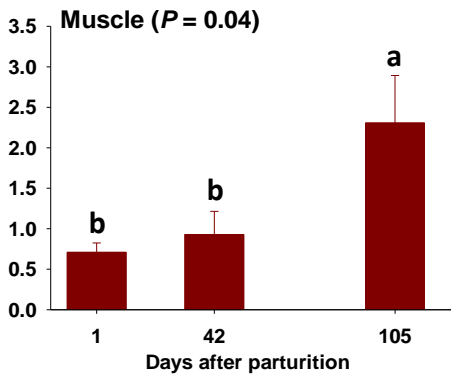
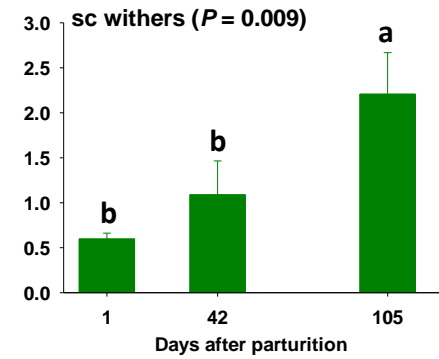
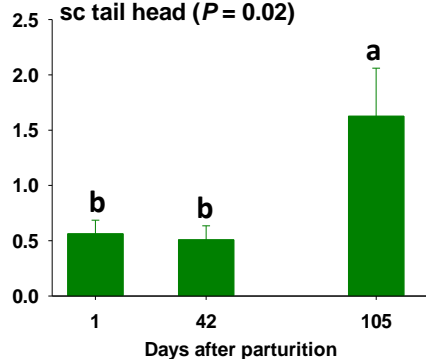
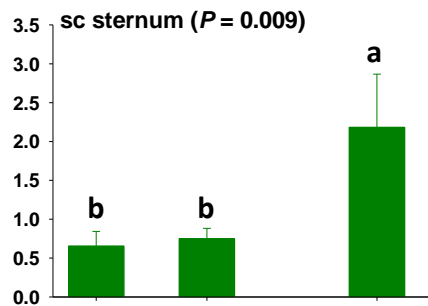
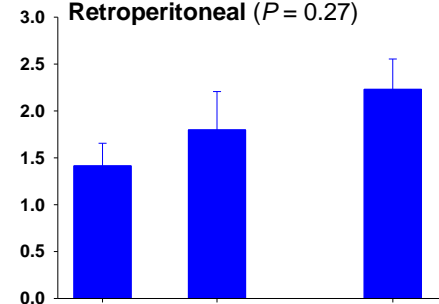
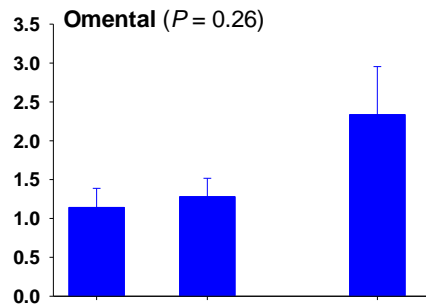
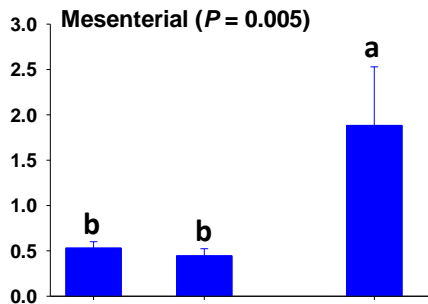
- The PROC MIXED procedure of SAS (9.3) using repeated measures:
 - Fixed effect: Time (sampling day)
 - Random effect: Cow
- The threshold of significance: $P < 0.05$; Trends: $0.05 < P < 0.10$.
- Data are presented as means \pm SEM.

Results

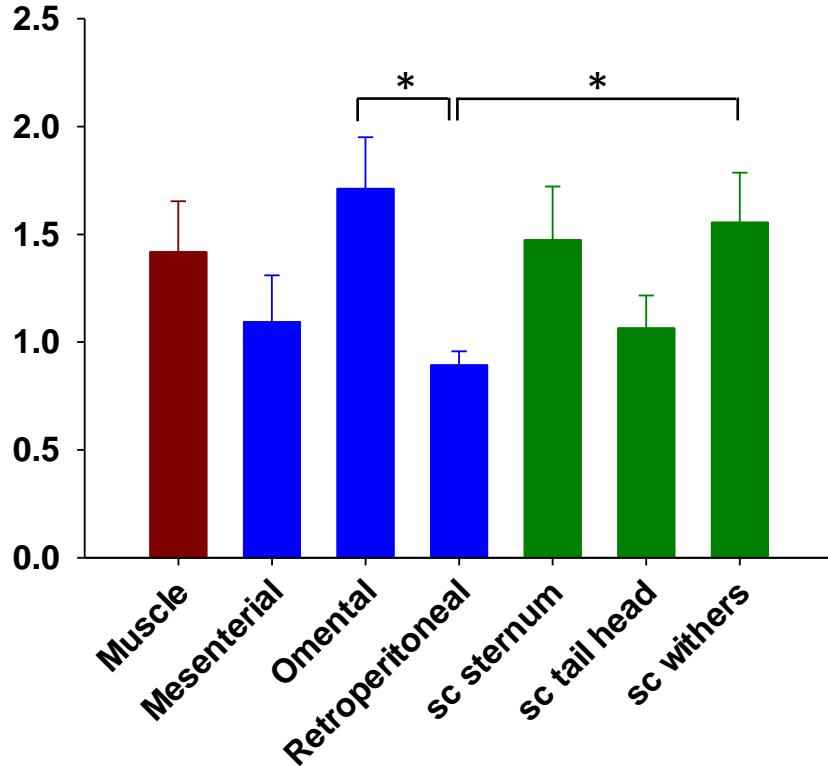
BCKDHA mRNA abundance (AU)



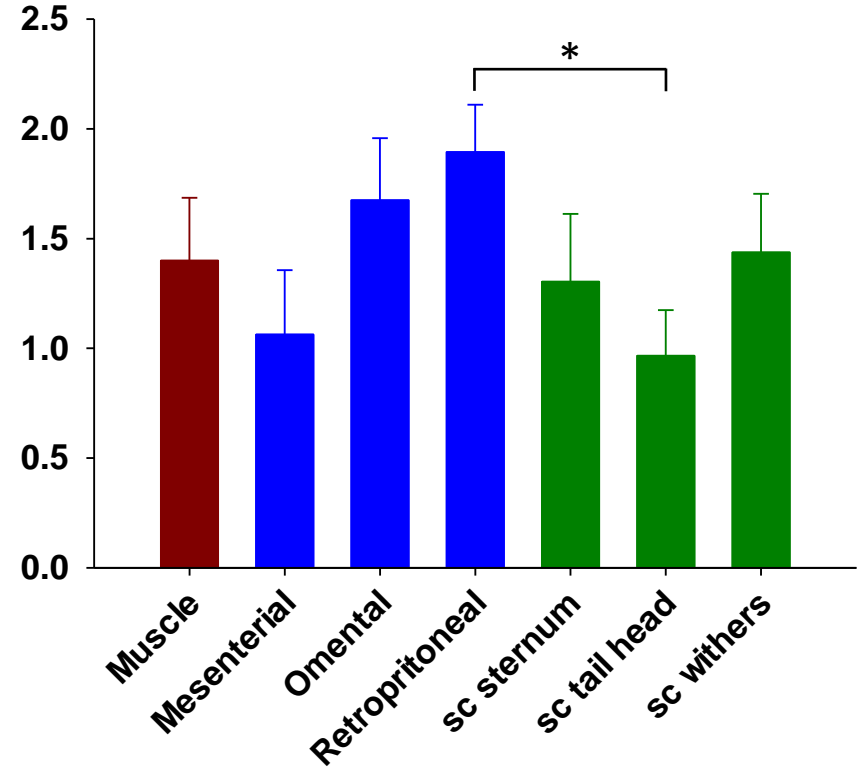
BCKDHB mRNA abundance (AU)



BCKDHA mRNA abundance (AU)



BCKDHB mRNA abundance (AU)



Conclusion

- ❑ The BCKDHA and BCKDHB mRNA expression were detectable in different fat depots in a comparable abundance with that of muscle.
- ❑ The reduced abundance of **BCKDHA/B** mRNA on days 1 and 42 compared to day 105, may suggest an attenuation of BCAA oxidation in the studied tissues shortly after parturition. This would favor sparing of BCAA for milk protein synthesis and protein synthesis in other organs.
- ❑ Further studies that include protein expression and activity of this enzyme may provide additional clues to the involvement of adipose tissue in whole body BCAA metabolism in dairy cows.

Thank you for your attention