ORIGINAL ARTICLE

Metabolomic analysis of amino acid and fat metabolism in rats with L-tryptophan supplementation

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Abstract Tryptophan (TRP) is an important precursor for several neurotransmitters and metabolic regulators, which play a vital role in regulating nutrient metabolism. The purpose of this study was to investigate the effects of tryptophan supplementation on the biochemical profiles, intestinal structure, liver structure and serum metabolome in rats. Rats received daily intragastric administration of either tryptophan at doses of 200 mg/kg body weight per day or saline (control group) for 7 days. TRP supplementation had a tendency to decrease the body weight of rats (P > 0.05). The levels of urea and CHO in serum were decreased in the TRP-supplemented group rats compared with control group rats (P < 0.05). TRP supplementation increased the villus height and the ratio of villus height to crypt depth in the jejunum compared to control group rats (P < 0.05).

Metabolic effects of tryptophan supplementation include: (1) increases in the serum concentrations of lysine, glycine, alanine, glutamate, glutamine, citrulline, methionine, tyrosine, 1-methylhistidine, and albumin, and decreases in the concentrations of serum branched-chain amino acid (isoleucine, valine and leucine); (2) decreases in the serum concentrations of formate and nitrogenous products (trimethylamine, TMAO, methylamine and dimethylamine), and in the contraction of trimethylamine in feces; (3) decreases in serum levels of lipids, low density lipoprotein, very low density lipoprotein, together with the elevated ratio of acetoacetate to β-hydroxybutyrate. The results indicate that tryptophan supplementation reduced the catabolism of dietary amino acids and promoted protein synthesis in rats, promoted the oxidation of fatty acid and reduced fat deposition in the body of rats.

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Abbreviations

TRP Tryptophan

PC Principal components

PCA Principal component analysis NMR Nuclear magnetic resonance

Introduction

Tryptophan (TRP) is not only one of the limiting dietary indispensable amino acids in protein metabolism, but also an important precursor for melatonin, serotonin, *N*-acetylserotonin and anthranilic acid (Biggio et al. 1974; Kim et al. 2007; Wu 2007). It was shown that the plasma levels of melatonin, serotonin, *N*-acetylserotonin and anthranilic acid were



increased when tryptophan was intragastrically administered (Esteban et al. 2004; Platten et al. 2005; Sánchez et al. 2008; Sugden et al. 1985). Previous studies have suggested that tryptophan and its metabolites can affect both innate and acquired immunity systems (Esteban et al. 2004; Perianayagam et al. 2005; Platten et al. 2005; Shi et al. 2004). Melatonin formed from tryptophan in gastrointestinal tract could be considered as a protective agent because of its recognized biological effects, including antioxidant, anti-inflammatory properties (Kolli et al. 2013a, b; Sewerynek et al. 1996). Tryptophan exerts this effect by scavenging free radicals with melatonin, by stimulating mucosal prostaglandin release and increasing the gastric blood flow (Brzozowski et al. 1997; Bülbüller et al. 2003). In addition, tryptophan plays an important role in regulating nutrient metabolism (Li et al. 2007; Moehn et al. 2012; Yao et al. 2010). Dietary tryptophan supplementation significantly increased in hepatic protein synthesis in vivo (Sidransky et al. 1968), and resulted in significant decreases in hepatic lipids and triglyceride (Adamstone and Spector 1950; Akiba et al. 1992). However, there is lack of data concerning the effect of dietary tryptophan supplementation on amino acid metabolism.

Metabonomics has been identified as a powerful topdown systems biological tool to assess functionalities of nutrients and foods via the simultaneous measurement of multiple metabolites in complex organisms. It can aid the understanding of how metabolic balances may be disturbed by nutritional interventions (Noguchi et al. 2003; Rezzi et al. 2007). Nuclear magnetic resonance (NMR) spectroscopy is one of the major techniques used in metabonomic studies (Wang et al. 2009a). On the basis of NMR analysis, He et al. (2009) demonstrated that dietary arginine supplementation decreases fat deposition, enhances protein synthesis in skeletal muscle, and modulates intestinal microbial metabolism in growing pigs. Liu et al. (2011) found that chronic cysteamine supplementation results in perturbation of energy metabolism in rats using an NMR technique. An NMR-based metabonomic approach was applied to evaluate the effects of intervention with a high-fat, highcholesterol diet in Syrian golden hamsters (Jiang et al. 2013). In these previous studies, metabonomics was shown to be very useful for exploring the complex relationship between nutritional intervention and metabolism in order to clarify the role of dietary components in maintaining health and the development of disease (He et al. 2011a).

In the present study, the global metabolic profile of serum samples after dietary tryptophan supplementation in rats was screened by a ¹H NMR-based metabolomic approach. Our objective was to provide insight into the effects of tryptophan supplementation on internal metabolic processes. Metabolic profiles of tryptophan supplementation in rats can improve the current understanding of the relationship between metabolites and tryptophan

Table 1 The composition and nutrient of experiment diet

Ingredients	Content (%)	Chemical composition	Content
Wheat	14.0	Digestible energy (Mcal/kg)	3.4
Corn	43.0	Dry matter (%)	90.0
Soybean meal	24.0	Crude protein (%)	21.0
Full fat soybean extruded	8.0	Crude fat (%)	4.5
Soybean oil	1.4	Calcium (%)	1.0
Whey powder	3.0	Total phosphate (%)	0.7
Fish meal	3.2	Sodium (%)	0.3
Limestone	1.3	Met + Cys (%)	0.78
Dicalcium phosphate	1.1	Lys (%)	1.35
Vitamin-mineral premix ^a	1.0	Thr (%)	0.88

The nutrient levels of the diets were based on China General Quality Standards for Animal Feed (GB14924.1-2001)

^a The vitamin–mineral premix provided (per kilogram feed): vitamin A, 14,000 IU; vitamin D_3 , 1,500 IU; vitamin E, 5 mg; vitamin K, 5 mg; thiamine, 13 mg; riboflavin, 12 mg; pyridoxine, 12 mg; vitamin B_{12} , 0.022 mg; niacin, 60 mg; pantothenic acid, 24 mg; biotin, 0.2 mg; folic acid, 6 mg; choline chloride, 350 mg; Fe (as iron sulfate), 120 mg; Cu (as copper oxide), 10 mg; Mn (as manganous oxide), 75 mg; Zn (as zinc oxide), 30 mg; I (as ethylenediamine dihydroiodide), 0.5 mg; and Se (as sodium selenite), 0.2 mg

supplementation and establish fundamental data for future experimental study on tryptophan. Growth performance, serum biochemical profiles, small intestine index, liver index, and the contents of dimethylamine, and trimethylamine in rat feces were measured, as well as histological analysis of jejunum and liver tissue were performed to achieve our study objective.

Materials and methods

Rats, diets and experimental design

Experimental protocols used in this study were approved by the Nanchang University Animal Experiment Ethics Committee. The experimental rats were used in compliance with the Chinese guidelines for the Laboratory Animals Care (Ruan et al. 2007). In the experiments, 16 adult male Sprague–Dawley rats (weighting 220 ± 10 g) were obtained from SLAC laboratory Animal CO., Ltd (Changsha, China). Afterward, they were transferred to individual metabolic cages after acclimatization for 7 days and maintained on a light–dark cycle of 12 h light and 12 h dark. Free access to standard rodent diet (Table 1) (Ruan et al. 2014) and drinking water was provided. The temperature between 22 and 25 °C, and humidity (50 \pm 10 %) were maintained throughout the study (Ren et al. 2012, 2013).



Rats were randomly divided into two equal groups, two treatments were as follows: (a) control group, which received oral administration of physiological saline solution (0.9 % NaCl, at a dose of 2 mL) per day for 1 week; (b) TRP-supplemented group, which was given oral administration of L-TRP (dissolved in saline solution at doses of 200 mg/kg body weight) (Aladdin, China) per day for 1 week. The dosage selected for this study was based on previous reports (Brzozowski et al. 1997; Bülbüller et al. 2005).

Growth performance and sample collection

The body weight of each rat was recorded everyday during the 7 days of experimental period (Ren et al. 2014).

At the end of the experiments, all rats were fasted overnight to avoid a postprandial effect on serum metabolites after the last TRP administration (Xiao et al. 2013). And blood samples (~4 mL) were collected from postcava under anaesthesia (intraperitoneal injection of sodium pentobarbital). Small intestine and liver samples were quickly collected (Liu et al. 2012). The weight of small intestine and liver were recorded, and the length of the small intestine was measured. Serum were obtained by centrifugation at 4,000 rpm and 4 °C for 15 min and stored at -80 °C until ready for NMR spectroscopy analysis and other biochemical analyses (He et al. 2011b).

The feces of each rat was collected at 0–24 h after the last oral administration of L-TRP. The samples were stored at -80 °C until ready for the determination of the contents of dimethylamine and trimethylamine (Tan et al. 2011).

Conventional biochemical measurements

Serum biochemical metabolites included alkaline phosphatase (ALP), alanine aminotransferase (ALT), aspartate aminotransferase (AST), glucose (GLU), lactate dehydrogenase (LDH), total protein (TP), blood ammonia (AMM), creatine kinase (CK), serum creatinine (CRE), urea, cholesterol (CHO), triglyceride (TG), low density lipoprotein (LDL), high density lipoprotein (HDL), serum cholinesterase (CHE). All assays were performed using a CX-4 Auto-Blood Biochemical Analyzer (Beckman Inc., USA) according to the manufacturer's protocol (Nanjing Jiancheng Technology Co., Ltd, Nanjing, China).

Small intestine index and histological analysis

Small intestine index (%) was calculated as: (small intestine weight/body weight) \times 100 (Castro et al. 1975).

The small intestines were cut and separated using the following protocol: the first 10-cm segment being duodenum; the last 20-cm segment being ileum; the rest of the small intestine segment being jejunum. A portion of mid-jejunum (~3 cm) was collected for subsequent analysis of morphology (Chen et al. 2003). Intestinal tissue sections from jejunum were washed with cold phosphate buffered saline, fixed by immersion in 10 % neutral-buffered formalin. Samples were embedded in paraffin, sectioned at a 5 μm thickness and stained with hematoxylin and eosin as described by Nabuurs et al. (1993). The height of the villi and the depth of the crypts were evaluated using Image-Pro Plus 6.0 image processing and analysis system. For each sample, 10 fields were measured and the mean value was calculated. The method was according to the description of van Beers-Schreurs et al. (1998). The histological analysis was performed by an investigator who was unaware of the origin of tissue sections.

Liver index and histological analysis

Liver index (%) was calculated as: (liver weight/body weight) \times 100 (Mahaffey et al. 1981).

Histological analysis and hematoxylin–eosin staining were performed as previously reported (Zou et al. 1998). Liver tissue was fixed in 10 % neutral-buffered formalin, and then processed into paraffin section by routine procedure. The sections of 5 μm thickness were cut and affixed to glass slides, deparaffinized, and stained with hematoxylin and eosin.

Determination of dimethylamine and trimethylamine production

Each feces sample (2 g) was homogenized in 8 mL of 7.5 % cold trichloroacetic acid (TCA) using a homogenizer and the homogenate was centrifuged at 4,000 rpm and 4 °C for 15 min. The residue was re-extracted twice with 4 mL of 5 % TCA and treated as above. All supernatants were combined and it was made up to 50 mL with deionized water. The contents of dimethylamine and trimethylamine in rat feces were determined by spectrophotometer 722E (Shanghai Spectrum, China). The methods were according to the description of Benjakul et al. (2004).

¹H NMR spectroscopy of plasma samples

For 1H NMR spectroscopy experiments, serum samples were prepared by mixing 350 μL of serum with 350 μL of saline (0.9 % NaCl was dissolved in D_2O) in a microcontainer. D_2O for field frequence lock purposes. The resulting solution was centrifuged at 13,000 rpm for 10 min to remove precipitates. A 550 μL aliquot of the supernatant was transferred into 5-mm NMR tubes. 1H NMR measurements of serum were acquired on a Bruker Avance DRX-600 spectrometer (Bruker Biospin, Rheinstetten, Germany) at a temperature of 298 K, operating at a proton frequency of 295.0 MHz, using a cryogenic high-resolution probe. The measurement



of ¹H NMR spectra for each serum sample, a Carr–Purcell–Meiboom–Gill (CPMG) spin-echo pulse sequence was used to emphasize resonances from low molecular-weight metabolites (Liu et al. 2011; Wang et al. 2008; He et al. 2009, 2011c). A total of 64 transients were collected into 32,000 data points using a spectral width of 8,417.5 Hz, a relaxation delay of 3.0 s, and an acquisition time of 3.9 s.

Multivariate analysis and data processing

All NMR spectra from serum samples were Fourier-transformed, phase adjusted and baseline corrected using MNova-6.1.1 (MestreLab, Santiago de Compostela, Spain). The chemical shift was compared to the reference of the lactate doublet at δ1.33 (Ruan et al. 2013). Each spectrum was segmented into contiguous segments having an equal width (0.01 ppm) and integrated over the region from $\delta 8.5$ to 0.8. The region 84.66-5.20 was removed to avoid the influence of the water signal. The integral of each region was determined. Resultant data sets were then imported into SIMCA-P 12.0 (Umetrics, Sweden) for multivariate statistical analysis. In order to discern the presence of inherent similarities of spectral profiles, an unsupervised PR method, principal component analysis (PCA), was applied to all data sets from serum samples (Wei et al. 2008). The resulting data of PCA were visualized by the PC score plots and loading plots. Each point in the score plots represents an individual spectrum of a sample, and each point in the loading plots represents a single NMR spectral region or chemical shifts. Therefore, the loading plots indicate the spectral variables of metabolites that most strongly influence patterns in the score plots. Similarities and differences between samples can be observed in the scores plots, while spectral regions responsible for the differences can be viewed in the corresponding loading plots (Liu et al. 2011).

Statistical analysis

All experimental results were statistically analyzed using the software of SPSS 16.0 (SPSS Inc., Chicago, USA), and data were presented as mean \pm standard error (SE). The independent samples t test was conducted to examine significant differences between the two groups (Gao et al. 2013). Values of P < 0.05 were regarded as significant statistical significance.

Results

The effects of TRP supplementation on body weight in rats

The effect of TRP supplementation on the body weight of rats was shown in Fig. 1. At the beginning of the study, the body weight of rats in the TRP-supplemented group was the same as in the control group. At the end of the experiments,

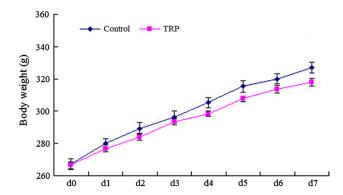


Fig. 1 The effects of TRP supplementation on the body weight in rats. Data from each group (n=8) were averaged and presented as mean \pm SE. The rats were treated with TRP (at doses of 200 mg/kg body weight) for 7 days, and control group rats received an isovolumetric amount of physiological saline solution in the same manner. The body weight of each rat was recorded everyday during the 7 days of experimental period

Table 2 The effects of TRP supplementation on serum biochemical profiles in rats

Parameters	Control group	TRP-supplemented group	P values
ALP (U/L)	263.20 ± 6.54	243.60 ± 9.90	0.14
ALT (U/L)	22.50 ± 1.04	23.40 ± 1.25	0.61
AST (U/L)	88.25 ± 3.86	84.00 ± 4.45	0.51
GLU (mmol/L)	7.74 ± 0.41	8.98 ± 0.43	0.06
LDH (U/L)	499.50 ± 43.56	455.60 ± 53.22	0.56
TP (g/L)	53.64 ± 0.96	55.24 ± 1.41	0.41
AMM (µmol/L)	34.83 ± 1.21	31.64 ± 2.84	0.30
CK (U/L)	573.60 ± 43.83	512.80 ± 61.95	0.45
CRE (µmol/L)	37.72 ± 2.28	39.10 ± 4.31	0.76
Urea (mmol/L)	6.85 ± 0.10	5.97 ± 0.34	0.03
CHO (mmol/L)	1.52 ± 0.05	1.31 ± 0.08	0.04
TG (mmol/L)	0.85 ± 0.05	0.75 ± 0.04	0.20
LDL (mmol/L)	0.16 ± 0.01	0.15 ± 0.01	0.17
HDL (mmol/L)	1.09 ± 0.02	1.08 ± 0.04	0.76
CHE (U/L)	154.40 ± 7.78	151.00 ± 6.04	0.74

Data from each group (n=8) were averaged and presented as mean $\pm\,{\rm SE}$

 ${\it P}$ values less than 0.05 were regarded as significant statistical significance

TRP supplementation had a tendency to decrease the body weight of rats, but there was no statistically significant difference between the two groups (P > 0.05).

The effects of TRP supplementation on conventional biochemical indices in serum

Serum biochemical indices in control and TRP-supplemented group rats were shown in Table 2. The serum level



of GLU was greater, and the level of LDL was lower in the TRP-supplemented group rats than in the control group rats (P > 0.05). These data were consistent with those on the relative signal integrals using ¹H-NMR-based metabonomics method (Table 4). In addition, the serum level of urea and CHO were decreased in the TRP-supplemented group rats compared with control group rats (P < 0.05).

Small intestine index and histological analysis

Representative figures for the jejunum stained with hematoxylin and eosin taken from the control and TRP-supplemented group rats are shown in Fig. 2a, b. There are no significant difference for small intestine length and index between control and TRP group (P > 0.05) (Fig. 2c, d). The villus height (Fig. 2e) and the ratio of villus height to crypt depth (Fig. 2g) in the jejunum were higher in the TRP-supplemented group rats than in control group rats (P < 0.05).

Liver index and histological analysis

The effects of TRP supplementation on liver index and morphology in rats were depicted in Fig. 3. TRP supplementation had no significant effects on liver weight, liver index (P > 0.05) and morphology in TRP-supplemented group rats compared with control group rats.

The effects of TRP supplementation on the contents of dimethylamine and trimethylamine in rat feces

The effects of TRP supplementation on the contents of dimethylamine and trimethylamine in rat feces were showed in Table 3. Compared with control group, TRP-supplemented group showed a significant decrease in the content of trimethylamine in rat feces (P < 0.05). TRP supplementation had a tendency to decrease the content of dimethylamine in rat feces, but there was no statistically significant difference between the two groups (P > 0.05).

¹H NMR spectroscopic analysis of serum samples

Typical 600 MHz ¹H NMR spectra obtained from rats serum were shown in Fig. 4. From these spectra, a total of 41 metabolites were unambiguously assigned in the ¹H NMR spectra of serum samples. Their chemical shifts, peak multiplicity and the corresponding ¹H NMR signal multiplicities are displayed in Table 4. Assignment of metabolites was made by comparison with the basis of existing literature (Jiang et al. 2013; Liao et al. 2007; Nicholson and Wilson 1989; Zira et al. 2013).

To detect more subtle treatment-related metabolic differences, pattern recognition techniques were applied. PCA was performed on the ¹H NMR spectra of serum samples

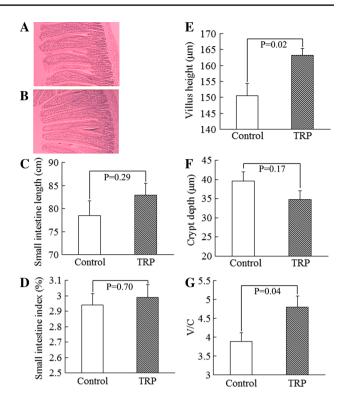


Fig. 2 The effects of TRP supplementation on small intestine length, small intestine index and the morphology of jejunum in rats. Histological features of jejunum sections stained with H&E, typical images (original magnification $\times 100$) were chosen from control group rats (a) and TRP-supplemented group rats (b); the effects of TRP supplementation on small intestine length (c) and small intestine index (d) in rats; the effects of TRP supplementation on villus height (e), crypt depth (f) and ratio of villous height to crypt depth (g) of jejunum in rats. Data from each group (n = 8) were averaged and presented as mean \pm SE

between control group and TRP-supplemented group. The PCA score plot of the ¹H NMR serum data was shown in Fig. 5a. This plot displayed the first two PCs and accounts for 73.1 % of the variation in the samples. And the corresponding loading plot is shown in Fig. 5b, which suggested that increased serum ¹H NMR peaks of acetoacetate and decreased peaks of isoleucine and trimethylamine are the major contributors to the separate clustering of the control group and TRP-supplemented group (Table 5).

Discussion

Tryptophan is the precursor of several neurotransmitters and metabolic regulators, which plays an important role in regulating nutrient metabolism (Moehn et al. 2012; Peters 1991). In the present study, ¹H nuclear magnetic resonance spectroscopy was used to demonstrate that the effect of tryptophan supplementation on the metabolome in serum of rats. The results from both PCA and system statistical metabolic



Fig. 3 The effects of TRP supplementation on liver index and the morphology of liver in rats. a Liver weight; b liver index; histological features of liver sections stained with H&E, typical images (original magnification $\times 200$) were chosen from the control group rats (c) and TRP-supplemented group rats (d). Data from each group (n=8) were averaged and presented as mean \pm SE

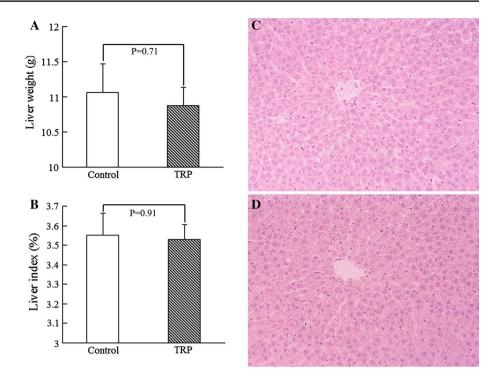


Table 3 The effects of TRP supplementation on the contents of dimethylamine and trimethylamine in rat feces

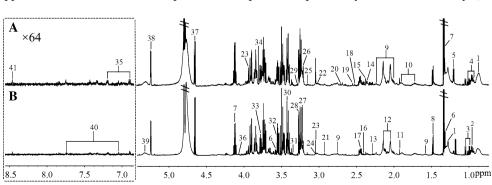
Parameters	Control group	TRP-supplemented group	P values
Dimethylamine (mg/kg)	60.78 ± 5.61	48.58 ± 5.11	0.14
Trimethylamine (mg/kg)	167.23 ± 7.38	141.97 ± 6.04	0.02

Data from each group (n=8) were averaged and presented as mean \pm SE

 ${\it P}$ values less than 0.05 were regarded as significant statistical significance

correlation analysis probed the global disturbances in the metabolic profiles, including metabolites involved in amino acid metabolism, intestinal bacteria-related metabolism and lipid metabolism reflected the molecular mechanisms of the response of rats to tryptophan supplementation.

Fig. 4 Typical 600 MHz ¹H NMR spectra of serum taken from rats with the control group (a) and TRP-supplemented group (b)





A novel and unexpected finding from this study was that tryptophan supplementation affected amino acid metabolism, and promoted protein synthesis in the body. Tryptophan is one of the amino acids essential for protein synthesis (Jessen and Sheikh 1992). Previous research has shown that dietary tryptophan deficiency decreased muscle and liver protein synthesis rates (Cortamira et al. 1991), and tryptophan supplementation significantly increased in hepatic protein synthesis in vivo (Sidransky et al. 1968). Sidransky (2010) reported that dietary tryptophan deficiency reduced plasma protein concentration, and tryptophan deficiency resembled protein deficiency. In this study, we found that tryptophan supplementation led to increases in the levels of many amino acids, including lysine, glycine, alanine, glutamate, glutamine, citrulline, methionine, tyrosine, 1-methylhistidine and albumin, together with the increases in serum concentrations of TP through traditional clinical chemistry method, implying that tryptophan supplementation promoted protein synthesis in the body (Li

Table 4 Changes in relative concentrations of serum metabolites in TRP-supplemented rats on the basis of chemical shifts relative to lactate at \$1.33

Key	Metabolites	Moieties	$\delta^{1}H$ (ppm) and multiplicity	Tryptophan	P values
1	LDL/VLDL	CH ₃ ,CH ₂ CH ₂ C=	0.88(m), 1.28(m)	<u> </u>	0.25
2	Leucine	α CH, δ CH $_3$, δ CH $_3$	0.91(d), 0.96(d), 3.72(t)	\downarrow	0.33
3	Valine	$\alpha CH_3, \beta CH, \gamma CH_3$	0.99(d), 1.04(d)	\downarrow	0.15
4	Isoleucine	γCH_3 , δCH_3	0.94(t), 1.01(d)	\downarrow	0.01
5	β-Hydroxybutyrate	γCH_3	1.22(d)	\downarrow	0.17
6	Threonine	α CH, β CH, γ CH ₃	1.32(d), 4.25(m), 3.58(d)	_	0.51
7	Lactate	αСН,βСН ₃	1.33(d), 4.11(q)	↑	0.26
8	Alanine	αСН,βСН ₃	3.77(q), 1.48(d)	↑	0.32
9	Lipids	CH ₂ *CH ₂ CO,CH ₂ -C=C	1.58(m), 2.04(m)	↓	0.41
		CH ₂ -C=O,CH-O-CO	2.24(m), 2.75(m)	↓	0.07
10	Lysine	αCH,βCH ₂ ,γCH ₂ ,δCH ₂	3.77(t), 1.89(m), 1.73(m)	<u>†</u>	0.19
11	Acetate	CH ₂ -C=O	1.92(s)	,	0.28
12	Glycoprotein	CH ₃ -C=O	2.05(s), 2.08(m), 2.15(s)	_	0.75
13	Acetoacetate	CH ₃ ,CH ₂	2.29(s), 3.49(s)	↑	0.04
14	Glutamate	αCH, β CH ₂ , γ CH ₂	3.75(m), 2.08(m), 2.37(m)	, †	0.42
15	Pyruvate	CH ₃	2.37(s)	_	0.89
16	Succinate	α,βCH ₂	2.41(s)	_	0.57
17	Glutamine	α CH, β CH ₂ , γ CH ₂	3.68(t), 2.15(m), 2.45(m)	↑	0.43
18	Citrate	CH ₂	2.52(d), 2.70(d)	_	0.71
19	Methylamine	CH ₃	2.54(s)	\downarrow	0.37
20	Dimethylamine	CH ₃	2.71(s)	1	0.39
21	Trimethylamine	CH ₃	2.92(s)	.l.	0.04
22	Albumin	Lysyl-CH ₂	3.02(s)	*	0.21
23	Creatine	N-CH ₃ ,CH ₂	3.04(s), 3.93(s)	· ↑	0.26
24	Creatinine	CH ₃ ,CH ₂	3.05 (s), 4.05(s)	· ↑	0.47
25	Citrulline	α CH ₂ , γ CH ₂ , δ CH ₂	3.70(m), 1.58(m), 3.15(t)	· ↑	0.38
26	Choline	$N-(CH_3)_3,\alpha CH_2,\beta CH_2$	3.20(s), 4.05(t), 3.51(t)	_	0.69
27	GPC	N-(CH ₃) ₃ ,OCH ₂ ,NCH ₂	3.22(s), 4.32(t), 3.51(t)	_	0.56
28	TMAO	CH ₃	3.26(s)	↓	0.24
29	Betaine	CH ₃ ,CH ₂	3.28(s), 3.90(s)	1	0.19
30	Taurine	N-CH ₂ ,S-CH ₂	3.27(t), 3.43(t)	*	0.48
31	Proline	$\beta CH_2, \gamma CH_2, \delta CH_2$	2.02–2.33(m), 2.00(m), 3.35(t)	l I	0.35
32	Glycine	CH ₂	3.56(s)	*	0.22
33	Methionine	α CH, β CH ₂ , γ CH ₂ , δ CH ₃	3.78(m), 2.16(m), 2.6(dd), 2.14(s)	· ↑	0.29
34	Ornithine	$CH_2,\alpha CH$	3.80(s), 3.79(t)	_	0.87
35	Tyrosine	αCH,CH ₂	7.19(d), 6.89(d)	↑	0.43
36	Myo-Inositol	5-CH,4,6-CH,2-CH	3.30(t), 3.63(t), 4.06(t)	 -	0.43
37	β-Glucose	2-CH,1-CH	3.25(dd), 4.65(d)	_ ↑	0.07
38	α-Glucose	1-CH	5.24(d)	I ↑	0.07
39	Unsaturated lipids	=C-CH ₂ -C=,-CH=CH-	5.19(m), 5.31(m)	l I	0.09
40	1-Methylhistidine	4-CH,2-CH	7.05(s), 7.77(s)	∀	0.14
41	Formate	CH	8.45(s)	I I	0.43

[&]quot; \downarrow " and " \uparrow " indicates the metabolite levels are lower or higher, respectively, compared with the control group; "-"indicates the metabolite levels are the same as the control group



s singlet, d doublet, t triplet, q quartet, m multiplet, dd doublet of doublets, GPC glycerophosphoryl choline, TMAO trimethylamine-N-oxide

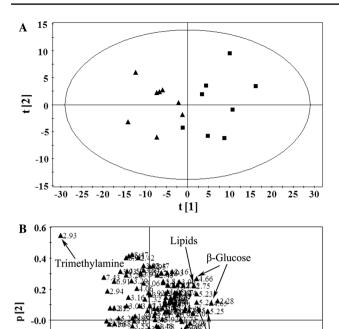


Fig. 5 PCA score plot (**a**) and loading plot (**b**) from ¹H NMR spectra of serum obtained from control group (*filled triangle*) and TRP-supplemented group (*filled square*) rats

0.10

p[1]

-0.00

-Glucose

0.20

Isoleucine

0.30

et al. 2009). The increased concentrations of these amino acids in serum may be explained by tryptophan supplementation increasing the absorption of amino acids. Tryptophan was transformed into serotonin in gut, and serotonin played an important role in promoting gastrointestinal motility (Brown 1995; Jin et al. 1999), and intestinal secretion (Siriwardena and Kellum 1993), which possibly led to an increase in the digestion of dietary protein and the absorption of amino acids from the lumen of the small intestine. In support of this notion, tryptophan supplementation led to an increase in villus height and the ratio of villus height to crypt depth, compared with the control group. The villus height, crypt depth and the ratio of villus height to crypt depth can be considered as a criterion that reflects the development and the absorption capacity of small intestine (Montagne et al. 2003; Pluske et al. 1996). Thus, an increase in villus height, villus/crypt ratio or a decrease in crypt depth means a promotion in the digestion of protein and absorption of amino acids (Hou et al. 2010). The branched-chain amino acid (isoleucine, valine and leucine) cannot be synthesized by animals, but are essential nutrients that must be obtained from foods (Harper et al. 1984). And that they are primarily metabolized in skeletal muscle

Table 5 Changes in relative concentrations of serum metabolites in TRP-supplemented rats compared to control group rats

Metabolites	NMR chemical shift (δ)	Change in direction	P values
LDL/VLDL	0.86(m)		0.25
β-Hydroxybutyrate	1.22(d)	\downarrow	0.17
Acetoacetate	2.29(s)	↑	0.04
Lipids	2.75(m)	\downarrow	0.07
Unsaturated lipids	5.31(m)	\downarrow	0.14
β-Glucose	4.65(d)	↑	0.07
α-Glucose	5.24(d)	↑	0.09
Lactate	1.33(d)	↑	0.26
Isoleucine	1.01(d)	\downarrow	0.01
Valine	1.04(d)	\downarrow	0.15
Albumin	3.02(s)	↑	0.21
Lysine	1.89(m)	↑	0.19
Glycine	3.56(s)	\uparrow	0.22
Trimethylamine	2.93(s)	\downarrow	0.04
TMAO	3.26(s)	\downarrow	0.24

"\" indicates a relative increase, and "\" indicates a relative decrease in the integral value for the region containing the identified metabolite

P values are significant at the <0.05 level

(Buse and Reid 1975; Shinnick and Harper 1976). Skeletal muscle takes up branched-chain amino acid from the arterial blood, synthesizes other amino acids and proteins (Ferrando et al. 1995; Wu 2007). In the present study, the decrease in serum concentrations of branched-chain amino acid in TRP-supplemented group suggested that tryptophan supplementation enhanced protein synthesis in skeletal muscle (Platell et al. 2000), and led to an increase of branched-chain amino acid absorption from serum.

Another novel and unexpected finding from this study is that tryptophan supplementation modulates intestinal microbial metabolism. The serum concentrations of nitrogenous products (trimethylamine, TMAO, methylamine and dimethylamine), formate, as well as short-chain fatty acids (acetate) were decreased in TRP-supplemented group rats. Trimethylamine, TMAO, methylamine and dimethylamine, acetate and formate are microbial metabolites of carbohydrates and amino acids (Dumas et al. 2006; Louis et al. 2007; Smith et al. 1994; Walker et al. 2005), and they are likely produced in the lumen of the small intestine and large intestine. The decrease in the serum levels of these metabolites may be explained by a reduced number and/or altered activity of intestinal microflora. In addition, tryptophan supplementation decreased the contents of trimethylamine and dimethylamine in rat feces. These results also support the view that tryptophan supplementation modulates intestinal microbial metabolism. Bülbüller et al. (2005) found that tryptophan supplementation (at doses of



-0.2

-0.4

-0.20

Acetoacetate

-0.10

200 mg/kg body weight) significantly reduced the ability of intestinal bacteria. A decrease in the number of intestinal bacteria may reduce the catabolism of dietary amino acids in the gut, therefore contributing to an increase in the entry of dietary amino acids into the portal venous blood (Wang et al. 2009b). In support of this notion, plasma concentrations of lysine, glycine, alanine, glutamate, glutamine, citrulline, methionine and tyrosine were higher in TRPsupplemented group than in control group rats. The ammonia generated from intestinal amino acids catabolism, and either enters the portal venous blood or is utilized locally for urea synthesis (Wu 1995). The presence of a functional urea cycle in enterocytes serves as the first line of defense against ammonia toxicity in mammals (Wu 2007). Therefore, the reduction of intestinal bacterial populations can beneficially decrease the production of ammonia and urea in serum due to the reduced catabolism of amino acids in gut. The result is consistent with the decrease in concentrations of serum ammonia and urea through traditional clinical chemistry method.

We found that tryptophan supplementation affected lipid metabolism, leading to reduced fat deposition in the body of TRP-supplemented group, compared with the control group. Both acetoacetate and β-hydroxybutyrate are products of fatty acid oxidation in liver (Gaou et al. 2001; Wojtczak 1968), and the ratio of acetoacetate to hydroxybutyrate is an indicator of cytosolic and mitochondrial redox states (Pérez et al. 2004; Yamamoto et al. 1980). In this study, tryptophan supplementation increased the level of acetoacetate and decreased the level of β -hydroxybutyrate in serum (Table 5), thus elevated the ratio of acetoacetate to β -hydroxybutyrate. The result suggested that tryptophan supplementation promoted the oxidation of fatty acid. So it would lead to a reduced availability of fatty acids for the synthesis of lipids, LDL and VLDL in the body. In support of this view, tryptophan supplementation decreased the serum concentrations of lipids, unsaturated lipids, LDL and VLDL in TRP-supplemented group rats compared to the control group rats. In addition, we found that the changes in serum conventional biochemical indices (the decreased levels of CHO, TG, and LDL) also supported the notion that tryptophan supplementation promoted lipid metabolism and reduced fat accumulation in the body. Previous studies have suggested that tryptophan-deficient diet led to heavy accumulation of fat in the liver, and increasing with the duration of the experiment, but tryptophan supplementation remarkably reduced the amount of fat in liver (Adamstone and Spector 1950). Akiba et al. (1992) also confirmed that dietary L-tryptophan supplementation resulted in significant decreases in hepatic lipids, in particular triglyceride. Özer et al. (2004, 2007) revealed that tryptophan supplementation (intraperitoneal injection, at doses of 100 mg/kg body weight, for 7 days) significantly decreased in the body weight of mice. This is in agreement with the result of our study that TRP supplementation also led to the decreased body weight in rats. The result also demonstrated that tryptophan supplementation reduced fat accumulation in the body.

In conclusion, the results of our study indicate that tryptophan supplementation affects the serum metabolome in rats. The changes in the serum levels of amino acids and related metabolites, nitrogenous products and short-chain fatty acids, lipids and related metabolites suggested that tryptophan supplementation enhanced protein accretion and reduced fat deposition and modulated intestinal microbial metabolism in the body of rats.

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Conflict of interest The authors declare that they have no conflict of interests.

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