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CIDE gene expression in adipose tissue, liver, and skeletal muscle from obese and lean pigs*

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Abstract: The expression of the cell death-inducing DNA fragmentation factor α-like effector (CIDE) family including *Cidea*, *Cideb*, and *Cidec* was significantly increased in mouse and human models of obesity. However, there was less information on these genes' expression in pigs. Here, we hypothesized that different fat accumulation between lean (Duroc×Landrace×Yorkshire gilts, DLY) and obese (Lantang) pigs was attributed to porcine CIDE-modulating lipid metabolism. Our data showed that *Cidea* and *Cidec* were expressed at a high level in adipose tissue, and at a relatively high level in skeletal muscle, whereas *Cideb* was mainly expressed in the liver in both breeds of pig. Lantang pigs had higher white adipose and skeletal muscle *Cidea* and *Cidec* mRNA abundance, and hepatic and muscle *Cideb* mRNA than DLY pigs. Lipid metabolism-related genes including sterol regulatory element binding protein 1c (*SREBP-1c*), hepatocyte nuclear factor-4α (*HNF-4α*), peroxisome proliferator-activated receptor γ coactivator-1α (*PGC-1α*), fatty acid synthase (*FASN*), diacylglycerol *O*-acyltransferase 1 (*DGAT1*), and *DGAT2* showed a higher expression level in adipose tissue from obese pigs than in that from lean pigs. Lantang pigs exhibited higher mRNA abundance for liver *SREBP-1c*, *HNF-4α*, and *PGC-1α,* and higher skeletal muscle *SREBP-1c*, *HNF-4α*, *PGC-1α*, and *DGAT2* expression, as compared with DLY pigs. However, the *perlipin2* mRNA levels in adipose tissues, liver, and skeletal muscle were significantly lower in obese pigs than in their lean counterparts. Furthermore, plasma non-esterified fatty acid (NEFA), glucose, and triacylglycerol (TAG) levels were greater in obese pigs than in lean pigs. Finally, data from correlation analysis further found that CIDE mRNA expression was positively correlated with back fat thickness (BFT), abdominal fat mass (AFM), and the levels of NEFA, TAG, and glucose in the two breeds. Collectively, these data revealed that the porcine CIDEs possibly modulated lipid metabolism and contributed to the development of fat deposition and obesity in Lantang pigs.

Key words: Cell death-inducing DNA fragmentation factor α-like effector (CIDE); Adipose tissue; Liver; Skeletal muscle; Fat deposition; Lantang pig; DLY pig
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1 Introduction

Excessive fat deposition affects animal health and production efficiency, and constitutes a health risk to human consumers. Thus, modulation of fat deposition in adipose tissues of pigs is good for both animals and customers (Jiang *et al*., 2007). Lantang pig is a native breed (obese-type) of South China, whose carcass contains more fat content than hybrid

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pigs (Lu *et al*., 2008; Chen *et al*., 2010). DLY is the cross breed of three lean-type pigs, Duroc, Landrace, and Yorkshire; the lean percentage of DLY reaches 63%–65% (Lan *et al*., 2004). Lantang and DLY pigs show an obvious difference in total adipose mass and therefore offer an attractive comparison for studying the mechanism of obesity.

Adipose tissue, liver, and skeletal muscles play important roles in body lipid metabolism in animals (Ahima and Flier, 2000; Hulver *et al*., 2003; Leonhardt and Langhans, 2004). In pigs, adipose tissue is the central organ for fat synthesis and deposition (O'Hea and Leveille, 1969). Bernlohr *et al*. (2002) demonstrated that fat accumulation in animals depends on levels of triacylglycerol (TAG) synthesis and storage and levels of lipid mobilization and fatty acid oxidation. Excess fatty acids and glucose are converted into TAG after food intake. TAG, a major energy storage form, is stored in lipid droplets, so that other intracellular organelles can avoid lipotoxicity caused by fatty acid (Girousse and Langin, 2012). The lipid droplet is an important subcellular organelle responsible for lipid storage, and the sizes of unilocular lipid droplets reveal the lipid storage capacity and have a positive association with the development of obesity (Bell *et al*., 2008).

Changes of lipid homeostasis by over-expression or deletion of specific genes often result in obesity. Genetically modified animal models have highlighted that expression of several adipogenic and lipogenic genes, including fatty acid synthase (*FASN*), diacylglycerol *O*-acyltransferase (*DGAT*), sterol regulatory element binding protein 1c (*SREBP-1c*), and peroxisome proliferator-activated receptor γ coactivator-1α (*PGC-1α*), played important roles in fatty acid synthesis, TAG synthesis, and lipid storage (Liu *et al*., 2008; Malaguarnera *et al*., 2009). Over the past decade, it has been reported that the cell death-inducing DNA fragmentation factor α-like effector (CIDE) family plays an important role in lipid and fat metabolism (Zhou *et al*., 2003; Gong *et al*., 2009; Yonezawa *et al*., 2011). Previous studies have reported that animals with a deficiency in *Cidea*, *Cideb*, or *Cidec* exhibited a typical lean phenotype with high energy expenditure, high levels of plasma TAG and non-esterified fatty acid (NEFA) reduction (Zhou *et al*., 2003; Li *et al*., 2007; Nishino *et al*., 2008), and altered genes' expression in various metabolic and signaling networks (Li *et al*., 2010). These studies suggest that the CIDE family plays an important role in TAG synthesis, lipid storage, and the development of obesity (Gong *et al*., 2009). However, all the studies on CIDEs have been carried out in mice and humans; there was far less information on the expression of these genes in pigs.

In the present study, we evaluated mRNA abundance of the adipose, liver, and skeletal muscle tissues for CIDEs and several lipid metabolism genes in both genetically obese and lean pigs. Our aim was to explain the relationship between porcine CIDE gene expression and lipid accumulation. We think that this basic molecular information might be useful for further investigation of the functions of CIDEs in pig models.

2 Materials and methods

2.1 Animals and sample collection

Eight castrated male Duroc×Landrace×Yorkshire pigs of similar liveweight ((20.21±0.57) kg) as well as eight Lantang pigs, also castrated males of similar liveweight ((16.12±0.63) kg), were used in this study. All pigs were raised in the pig farm of the animal facilities of the Institute of Animal Science in the Guangdong Academy of Agricultural Sciences, China and were provided feed and watered ad libitum. The diets for the two breeds were made up of different proportions of ingredients because the growth rates of the two breeds were different (Tables 1 and 2). The trials were terminated when the pigs of DLY and Lantang reached 100 and 70 kg body weight, respectively. An ultrasonic instrument (Renco, USA) was used to determine back fat thickness (BFT) at the 1st, 10th, and last ribs before slaughter. Blood sample was obtained from the anterior vena cava using vacuum tubes (using ethylenediaminetetra-acetic acid (EDTA) as anticoagulant) and centrifuged for 5 min at 3000*g* at 4 °C, and the plasma was separated and stored at −20 °C following slaughter. The left-side carcass was dissected into abdominal fat following the procedure of Walstra and Merkus (1995). Subcutaneous adipose tissue (subcutaneous back fat) and liver and skeletal muscle (longissimus muscle) samples were immediately removed and frozen in liquid nitrogen, and stored at −80 °C.

Table 1 Composition of experimental diets fed to DLY and Lantang pigs

Group	Corn (%)	Soybean meal (%)	Wheat bran (%)	Fish meal (%)	Rice bran (%)	Zeolite powder (%)	Methionine (%)	Calcium hydrophosphate (%)	Salt (%)	Premix* (%)	Total (%)
DLY	67.38	23	4	0	0	0.96	0	0.6	0.06	4	100
Lantang	56.00	18	15	1	5	0.90	0.1	0	0	4	100

* Premix provided the following nutrients per kilogram of diet: vitamin A 1300 IU, vitamin D_3 150 IU, vitamin E 11 mg, vitamin K_3 0.5 mg, thiamin 1 mg, riboflavin 2 mg, pyridoxine 1 mg, vitamin B_{12} 6 μg, niacin 7.5 mg, pantothenic acid 7 mg, biotin 0.05 mg, folacin 0.3 mg, choline chloride 300 mg, Fe 50 mg, Zn 50 mg, Mn 2 mg, Cu 3.5 mg, and I 0.14 mg

Table 2 Nutrient contents of experimental diets fed to DLY and Lantang pigs

Group	Digestive energy (MJ/kg)	Crude protein (%)	Available phosphorus (%)	Lys (%)	Met+cysteine (%)
DLY	13.38	16.0	0.25	0.76	0.58
Lantang	12.04	15.1	0.17	0.72	0.63

2.2 Real-time quantitative PCR analysis

Real-time quantitative polymerase chain reaction (PCR) was done as we described previously (Tian *et al.*, 2016). Briefly total RNA was isolated from subcutaneous adipose and liver tissue samples using TRIzol reagent (Invitrogen Co., Carlsbad, CA, USA) according to the manufacturer's instructions. All complementary DNAs (cDNAs) were synthesized from 1 μg of total RNA using a reverse transcription kit (TaKaRa, Tokyo, Japan) according to the manufacturer's recommendations. Then the synthesized cDNA was diluted (1:10, v/v) and real-time quantitative PCR amplification was performed with SYBR green I (TaKaRa, Tokyo, Japan) and specific primers for pig messenger RNA (mRNA) sequences (Table 3). Conditions for real-time PCR were an initial denaturation at 95 °C for 180 s, followed by 40 cycles at 95 °C for 15 s and 58 °C for 30 s, with a final elongation at 72 °C for 30 s. Each sample for each gene was amplified three times, in three independent wells, in order to have technical replicates. To normalize expression data, we used multiple internal control genes as described by Vandesompele *et al.* (2002). The expression stability was evaluated by the *M* value and pairwise variations of geNorm (Version 3.5; PrimerDesign Ltd., Southampton, Hampshire, UK). We found that *β-actin* had a lower *M* value than glyceraldehyde-3-phosphate dehydrogenase (*GAPDH*), both below 1.5. Thus, *β-actin* was ranked as the most stably expressed gene. Furthermore, the pairwise variations of *β-actin* and *GAPDH* from subcutaneous adipose and liver tissue samples of Lantang and DLY pigs were below the threshold (0.150) that required the inclusion of an additional normalization gene. Therefore, *β-actin* and *GAPDH* could be used for normalization. In the present study, the expression of the target genes relative to the *β-actin* was analyzed by the $2^{-\Delta\Delta Ct}$ method. ΔCt=Ct (target gene)−Ct (*β-actin*) and ΔΔCt=ΔCt (Lantang pigs)−ΔCt (DLY pigs), where Ct is cycle threshold.

2.3 Analysis of biochemical variables in plasma

Plasma concentrations of high density lipoprotein (HDL), low density lipoprotein (LDL), glucose, cholesterol, NEFA, and TAG were measured using commercial kits purchased from the Nanjing Jiancheng Institute of Bioengineering, China.

2.4 Statistical analysis

Data were presented as mean±standard error of the mean (SEM). Analysis was performed using GraphPad Prism Version 5 (GraphPad Software Inc., San Diego, CA, USA). Significance was predominantly established using a two-tailed Student's *t*-test. $P<0.05$ was considered a statistically significant difference. Correlation analysis between CIDE mRNA expression levels and apparent index (BFT, abdominal fat mass (AFM), NEFA, TAG, and glucose) was calculated using the Pearson's correlation coefficient of the IBM SPSS Statistics 22 software (IBM Corp., Armonk, NY, USA). $P<0.05$ and $P<0.01$ were considered as significant and highly significant correlations, respectively.

Table 3 Primer sequences used in this study

Gene	Sequence (5'→3')	Product size (bp)	GenBank accession
Cidea	Forward: CACCGTGGTAGATACAGAGG Reverse: GGACAGGAACCGCAACA	292	NM_001112696.1
Cideb	Forward: TGGGGACTCTGATGCTGAA Reverse: CCCGTAGAATGTGGCTTTG	284	NM_001112688.1
Cidec	Forward: CGGTGCCTACTCCCTTTCCT Reverse: TGGGTCTTTGCCCTTGGT	184	NM_001112689.1
Perilipin2	Forward: GCTGGCGACATCTACTCA Reverse: AAGTCCACAACAGAACCCTA	250	NM_214200.2
DGAT1	Forward: AGGACGGACACGACGAT Reverse: GAACGCAGTCACAGCAAA	287	NM_214051.1
DGAT2	Forward: TCCTGTCTTTCCTCGTGC Reverse: ACCTTTCTTGGGCGTGT	131	NM_001160080.1
HNF-4α	Forward: ATCGCCACCATCGTCAA Reverse: CCTCACCCTTTCCACTACCA	200	NM_001044571.1
SREBP-1c	Forward: AAGCGGACGGCTCACAA Reverse: GCAAGACGGCGGATTTATT	121	NM_214157.1
PGC-1α	Forward: TCACCACCCAAATCCTTAT Reverse: ATTCTTCCCTCTTCAGCCT	295	NM_213963.2
FASN	Forward: CCTGGGAAGAGTGTAAGCA Reverse: GGAACTCGGACATAGCG	108	NM_001099930.1
β-actin	Forward: CATCGTCCACCGCAAAT Reverse: TGTCACCTTCACCGTTCC	210	NC_010445

3 Results

3.1 Animal performance

As shown in Table 4, Lantang pigs exhibited significantly greater BFT and AFM than DLY pigs.

3.2 Expression of CIDEs in adipose, liver, and skeletal muscle tissues

As shown in Fig. 1, porcine *Cidea* and *Cidec* mRNAs were highly expressed in white adipose tissue. Both were expressed at a relatively high level in skeletal muscle. However, *Cidea* was not expressed in liver, and *Cidec* mRNA was expressed at a much lower level in liver. *Cideb* mRNA was mainly expressed in porcine liver tissue, at a lower level in adipose tissue, and was not detected in skeletal muscle. Moreover, obese pigs (Lantang) had a significantly higher *Cidea* and *Cidec* mRNA levels in adipose and skeletal muscle tissues, and a higher *Cideb* in adipose and liver than lean breeds (DLY).

3.3 Expression levels of genes responsible for lipid metabolism

The mRNA levels of *PGC-1a* and *SREBP-1c* in adipose tissue from Lantang pigs increased 3.67-fold ($P<0.01$) and 10-fold ($P<0.001$), respectively, in comparison with DLY pigs. mRNA abundances for *HNF-4α*, *FASN*, *DGAT1*, and *DGAT2* mRNAs were significantly higher in adipose tissue from the Lantang breed than in that from DLY pigs. We observed that Lantang pigs exhibited higher *PGC-1a*, *SREBP-1c*, and *HNF-4α* mRNA expression in liver tissue than the DLY breed ($P<0.05$, $P<0.01$, and $P<0.05$, respectively). *FASN*, *DGAT1*, and *DGAT2* mRNA expression tended to be greater in liver tissue from obese pigs than in that from lean pigs, although at a non-significant level by the Student's *t*-test. In skeletal muscle, the amounts of *PGC-1a*, *SREBP-1c*, and *DGAT2* mRNAs in Lantang pigs were higher than those in DLY pigs. However, the mRNA levels of *perlipin2* in adipose, liver, and skeletal muscle from obese pigs were significantly decreased, as compared with their lean counterparts (Fig. 2).

3.4 Assessment of biochemical variables in different swine breeds

No difference in the level of HDL, LDL, or cholesterol was observed between Lantang and DLY breeds (Figs. 3d–3f). However, plasma NEFA and TAG as well as glucose levels in Lantang pigs were significantly higher than those in DLY breeds (Figs. 3a–3c).

3.5 Relationship between CIDE mRNA expression and BFT, AFM, NEFA, TAG, and glucose

The results of correlation analysis between CIDE mRNA expression and BFT, AFM, NEFA, TAG, and glucose are presented in Table 5. *Cidea* mRNA expression in adipose is positively correlated with BFT, AFM, TAG, and glucose ($P<0.01$) in the two breeds of pig. *Cidea* mRNA expression in skeletal muscle had a positively significant correlation with BFT, AFM, and NEFA ($P<0.05$). The correlations of *Cidec* mRNA expression level in adipose but not in liver or skeletal muscle, and BFT, AFM, NEFA, TAG, and glucose were positive and highly significant ($P<0.01$) in the two breeds. Expression of *Cideb* mRNA in both adipose and liver tissues correlated positively with BFT, AFM, NEFA, TAG, and glucose in two porcine breeds ($P<0.01$).

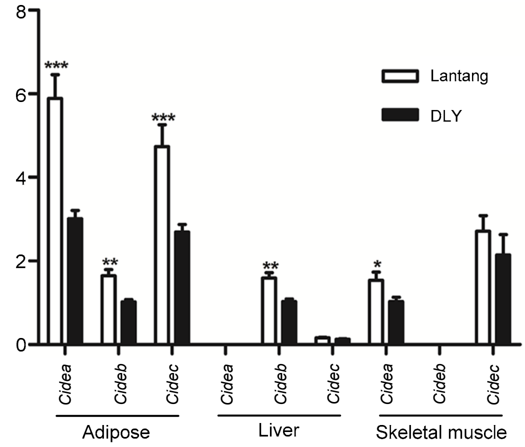

Fig. 1 CIDE gene expression patterns
Relative mRNA levels of *Cidea*, *Cideb*, and *Cidec* in adipose tissue, liver, and skeletal muscle of Langtang and DLY pigs. Data were expressed as mean±SEM, with n=8. * $P<0.05$, ** $P<0.01$, *** $P<0.001$ vs. DLY pigs

Table 4 Growth performance of DLY and Lantang pigs

Group	Initial body weight (kg)	Final body weight (kg)	Average back fat thickness (cm)	Abdominal fat mass (kg)
DLY	20.21±0.57	101.60±2.40	2.10±0.24	0.61±0.06
Lantang	16.12±0.63	68.90±1.83	4.05±0.03*	1.57±0.06*

Data are expressed as mean±SEM, with n=8. * $P<0.05$ vs. DLY pigs

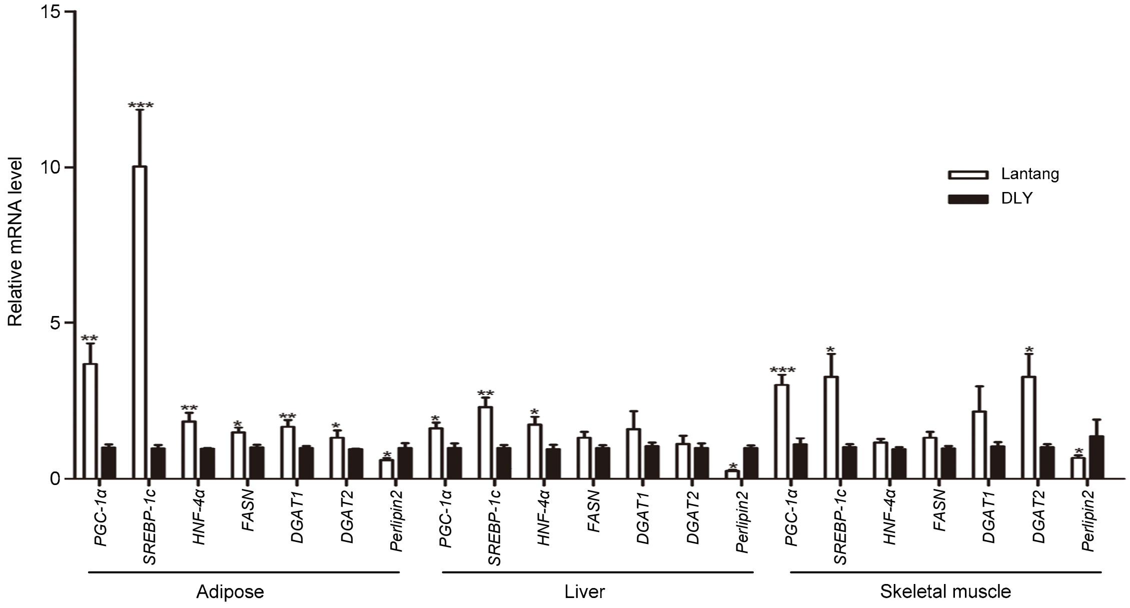

Fig. 2 Relative mRNA levels of *SREBP-1c*, *HNF-4α*, *PGC-1α*, *FASN*, *DGAT1*, *DGAT2*, and *perlipin2* in adipose tissue, liver, and skeletal muscle from Lantang and DLY pigs
Data were expressed as mean±SEM, with n=8. * $P<0.05$, ** $P<0.01$, *** $P<0.001$ vs. DLY pigs

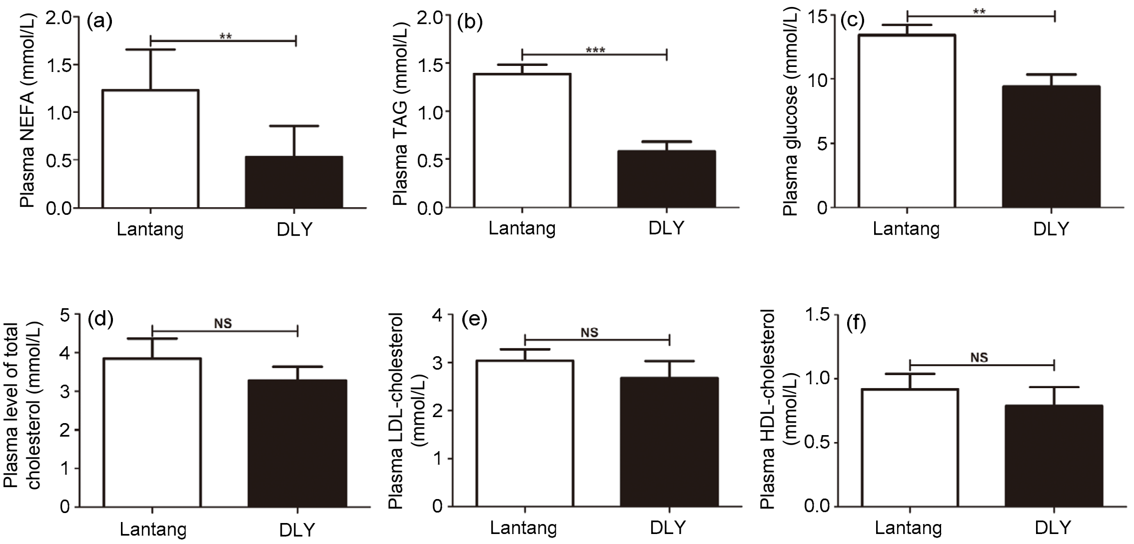

Fig. 3 Plasma levels of NEFA (a), TAG (b), glucose (c), total cholesterol (d), LDL-cholesterol (e), and HDL-cholesterol (f) in Lantang and DLY pigs

The results show higher plasma levels of NEFA, TAG, and glucose in Lantang pigs than in DLY pigs. Data were expressed as mean±SEM, with n=8. * P<0.05, ** P<0.01, *** P<0.001. NS: not statistical significant; NEFA: non-esterified fatty acid; TAG: triacylglycerol; LDL: low density lipoproteins; HDL: high density lipoproteins

Table 5 Correlation analysis between CIDE mRNA expression and BFT, AFM, NEFA, TAG, and glucose in adipose, liver, and skeletal muscle

Parameter	*Cidea* mRNA expression		*Cideb* mRNA expression		*Cidec* mRNA expression		
	Adipose	Muscle	Adipose	Liver	Adipose	Liver	Muscle
BFT	0.788**	0.580*	0.707**	0.751**	0.743**	0.120	0.214
AFM	0.818**	0.570*	0.668**	0.614**	0.668**	0.246	0.170
NEFA	0.460	0.514*	0.636**	0.549**	0.618**	−0.265	0.383
TAG	0.685**	0.488	0.665**	0.659**	0.675**	0.123	0.237
Glucose	0.652**	0.385	0.810**	0.583**	0.582**	0.103	0.067

BFT: back fat thickness; AFM: abdominal fat mass; NEFA: non-esterified fatty acid; TAG: triacylglycerol. * P<0.05, ** P<0.01

4 Discussion

In the present study, we have observed several interesting findings regarding obese Lantang pigs exhibiting higher CIDE gene expression than lean DLY pigs. Some expressions of lipid metabolism genes-related CIDEs also were up-regulated or down-regulated in Lantang pigs, as compared with DLY pigs, and the correlation analysis data found that porcine CIDE mRNA abundances were positively associated with BFT, AFM, NEFA, TAG, and glucose in the two breeds. These observations were considered novel as there were no reports, to our knowledge, comprehensively evaluating the difference of porcine adipose, liver, or skeletal muscle CIDE mRNA expression between obese and lean pigs, or elucidating the relationship between the roles of CIDEs and fat accumulation.

Earlier studies have reported that *Cidea* was mainly expressed in the heart, and at a lower level in the brain, skeletal muscle, thymus, appendix, lymph nodes, and bone marrow, but neither in normal adult human nor mouse liver tissue (Inohara *et al.*, 1998; Zhou *et al.*, 2003). Our study found that porcine *Cidea* was highly expressed in white adipose and at a relatively high level in skeletal muscle tissue, but was not detected in liver, although Li *et al.* (2009) showed that porcine *Cidea* can be detected in the liver of

Tongcheng and Large White pigs. Danesch *et al.* (1992) demonstrated that *Cidec* was an adipocyte-specific marker gene. Consistently, we found that porcine *Cidec* gene mRNA was expressed at a high level in white adipose tissue, at a relatively high level in skeletal muscle, and at a lower level in liver. It has been reported that *Cideb* mRNA was expressed in many tissues with the highest levels in the liver (Inohara *et al.*, 1998). Our result agreed with the report that porcine *Cideb* was mainly expressed in the liver, but was not detected in skeletal muscle. The differential tissue distribution patterns of the three CIDE genes can imply that they may have different functions.

Previous studies reported that with CIDE deficiency mice showed a typical lean phenotype and a markedly lower adiposity index. Plasma TAG and NEFA levels, and the size of white adipocytes in CIDE-deficient mice were significantly reduced, compared with those in wild-type mice (Li *et al.*, 2007; Nishino *et al.*, 2008; Toh *et al.*, 2008; Gong *et al.*, 2009). In addition, it has been shown that over-expressed *Cidec* can increase lipid droplet size and enhance the accumulation of lipids (Keller *et al.*, 2008), whereas deletion of *Cidea* by RNA interference in human adipocyte stimulated lipolysis (Nordström *et al.*, 2005). In our results, we found that mRNA expressions of *Cidea* and *Cidec* in adipose tissue and skeletal muscle, and *Cideb* in adipose and liver from obese pigs were significantly higher than that from the lean breed. These data indicated that higher mRNA abundance for *Cidea* and *Cidec* in adipose tissue and skeletal muscle, and *Cideb* in liver from Lantang breeds, might play an important role in the development of fat deposition.

The molecular basis for CIDE-modulated lipid metabolism has been elucidated. CIDE deletion in mice resulted in significant reductions of the expression of *SREBP-1c* and its downstream target genes (*ACC1*, *FASN*, *Elovl6*, and *SCD1*) (Abu-Elheiga *et al.*, 2003; Li *et al.*, 2007), which were required for fatty acid synthesis (Shimomura *et al.*, 1999) and TAG synthesis (Horton *et al.*, 2002). Similarly, we found that CIDE-enriched Lantang pigs exhibited greater mRNA abundance for *SREBP-1c* and *FASN*. Therefore, it has been indicated that CIDEs could positively modulate the expression of *SREBP-1c* and its downstream target genes, and lead to increased TAG secretion and lipogenesis (Gong *et al.*, 2009). *PGC-1α* and *HNF-4α* mRNA expression, which were critical to de novo lipogenesis and gluconeogenesis (Herzig *et al.*, 2001) and controlling the expression of *Cidea* and *Cideb* (Hallberg *et al.*, 2008; Chen *et al.*, 2010; Yu *et al.*, 2013), were higher in adipose and liver tissue from obese pigs than in those from their lean counterparts. At the same time, skeletal muscle *PGC-1α* mRNA abundance from Lantang pigs was increased compared to the DLY pigs. In addition, adipose *DGAT1* and *DGAT2* mRNA expression, which play a central modulation role in animal fat deposition (Nishizuka, 1992), were higher in Lantang pigs that in DLY pigs. Skeletal muscle *DGAT2* mRNA abundance was also increased in DLY pigs. The present data uncovered that the mRNA levels of *perilipin2* in adipose, liver, and skeletal muscle tissue from CIDE-enriched Lantang pigs were lower than those from DLY pigs. Our result was consistent with the report by Singaravelu *et al.* (2013) who demonstrated that *Cideb* over-expression resulted in a significant down-regulation of perilipin2 protein levels. In addition, a study by Li *et al.* (2012) indicated that *Cideb* and *perilipin2* played opposite roles in modulating TAG accumulation, with *Cideb* as a positive regulator and *perilipin2* as a negative regulator of lipid droplet size in hepatocytes. Collectively, these results revealed that the CIDE gene family modulated fat deposition through controlling the expression of lipid metabolism-related genes.

CIDE-sufficient Lantang pigs also exhibited higher plasma NEFA, TAG, and glucose levels than DLY pigs. Our results agreed with the reports that CIDE deficiency resulted in a reduction of plasma TAG and fatty acid levels (Zhou *et al.*, 2003; Li *et al.*, 2007; Toh *et al.*, 2008). We also found that Lantang pigs had greater BFT and AFM than DLY pigs (Lu *et al.*, 2008). Therefore, there may be a close association between CIDE mRNA expression and fat deposition. The further correlation analysis results uncovered an interesting finding that *Cidea* mRNA expression in adipose was positively correlated with BFT, AFM, TAG, and glucose, and in skeletal muscle was positively correlated with BFT, AFM, and NEFA in the two breeds of pigs. Adipose and liver *Cideb* mRNA abundance and BFT, AFM, TAG, NEFA, and glucose had a positively significant correlation in the two breeds. *Cidec* mRNA in adipose but not in liver or skeletal muscle was positively correlated with BFT, AFM, TAG, NEFA, and glucose in Lantang and DLY pigs. We made a correlation analysis between porcine CIDE mRNA and fat deposition-related factors. These results further suggested that CIDE genes contributed to fat deposition of the fatty Lantang pigs.

5 Conclusions

In conclusion, our data suggest that the porcine CIDEs possibly modulated lipid metabolism and contributed to the development of fat deposition and obesity.

Compliance with ethics guidelines

Yue-qin QIU, Xue-fen YANG, Xian-yong MA, Yun-xia XIONG, Zhi-mei TIAN, Qiu-li FAN, Li WANG, and Zong-yong JIANG declare that they have no conflict of interest.

All institutional and national guidelines for the care and use of laboratory animals were followed.

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中文概要

题　目：肥胖型和瘦肉型猪的脂肪、肝脏及骨骼肌组织中 CIDE 家族基因表达水平的比较研究

目　的：研究 CIDE 家族基因在肥胖型和瘦肉型猪的脂肪、肝脏及肌肉组织中的基因表达水平差异，并初步探 CIDE 家族基因与脂质代谢的关系。

创新点：首次在肥胖型与瘦肉型猪模型中解释 CIDE 家族基因可以调节脂质代谢，并有助于脂肪沉积及导致肥胖。

方　法：采用荧光定量聚合酶链式反应（qPCR）检测肥胖型蓝塘猪和瘦肉型杜长大猪的脂肪、肝脏和骨骼肌中 CIDE 家族基因、*SREBP-1c*、*PGC-1α*、*HNF-4α*、*FASN*、*DGAT1* 和 *DGAT2*、*perlipin 2* 等基因表达水平。采用血浆生化指标仪试剂盒检测两个品种猪血浆中甘油三酯、葡萄糖、游离脂肪酸及胆固醇的含量。

结　论：肥胖型蓝塘猪脂肪和背最长肌组织中的 *Cidea* 和 *Cidec*，及肝脏中 *Cidec* 的基因表达量明显高于瘦肉型杜长大猪。在脂肪组织中，脂质代谢相关的基因（包括 *SREBP-1c*、*PGC-1α*、*HNF-4α*、*FASN*、*DGAT1* 和 *DGAT2* 基因）表达量都是蓝塘猪高于杜长大猪。蓝塘猪肝脏中的 *SREBP-1c*、*HNF-4α* 和 *PGC-1α* 基因表达水平显著高于杜长大猪。蓝塘猪背最长肌组织的 *SREBP-1c*、*HNF-4α*、*PGC-1α* 和 *DGAT2* 基因表达量高于杜长大猪。然而，蓝塘猪的脂肪、肝脏及背最长肌三种组织中的 *perlipin 2* 的表达量显著低于杜长大猪。此外，蓝塘猪血浆中的甘油三酯、葡萄糖及游离脂肪酸浓度明显高于杜长大猪。通过相关性分析，我们发现肥胖型和瘦肉型猪不同组织中的 CIDE 家族基因表达水平与背部脂肪厚度、腹部脂肪重量、血浆中的甘油三酯、葡萄糖及游离脂肪酸浓度有明显的正向相关性。综上所述，CIDE 家族基因可以调节脂质代谢，并促进脂肪沉积及导致肥胖。

关键词：CIDE 家族基因；脂肪沉积；脂肪；肝脏；骨骼肌；蓝塘猪；杜长大猪