Modulation of adipose tissue gene expression and fatty acid composition by dietary fat in pigs

Mohan, N.H[1*], B.C.Sarmah[2], M.K.Tamuli[1], A. Das[1], K.M.Bujarbaruah[2], S.Naskar[1] and D.Kalita[2]

[1]National Research Centre on Pig
Indian Council of Agricultural Research
Guwahati, Assam, India.
[2] Assam Agricultural University
Guwahati, India

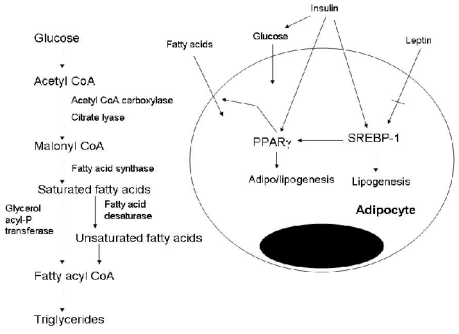
*mohannh.icar@nic.in

Session 22; Abstract no 3443

Introduction

- Fatty acid synthesis regulated by hormones as well as dietary fat
- Fatty acid synthase (FAS) and stearoyl-coenzyme desaturase (SCD) form key enzymes determine fatty acid composition
- Desaturation forms the first regulatory step in formation of long chain of unsaturated fatty acids
- Lipogenesis-highly responsive to changes in the diet (Madsen *et al.*, 1992) .

Fatty acid synthesis in adipocyte



Objectives

- **To study the effect of dietary fat on adipose tissue gene expression**
- **To study the effect of dietary fat on serum lipid profile**
- **To study the effect of dietary fat on subcutaneous adipose tissue fatty acid composition**

Materials and methods

- Eighteen crossbred (Hampshire x Assam local) male grower pigs (n=6)
- Fed with isocaloric ration containing either sunflower oil or coconut oil.
- Oil contributed 10% of the total feed energy.
- The control group on standard farm ration.
- The experimental feeding continued for two months.

Materials and methods (*contd.*)

- **Blood was collected and body weight was measured at ten day intervals to assess the following serum parameters**
  - **Glucose**
  - **Cholesterol**
  - **Total triglycerides**
  - **High density lipoprotein, low density lipoprotein, very low density lipoprotein**

Materials and methods (*contd.*)

- At the beginning and end of the study the subcutaneous adipose tissue to study gene expressions following RNA isolation, reverse transcription and real time polymerase chain reaction using gene specific primers.
- Enzymes (fatty acid synthase, Stearoyl CoA desaturase)
- Transcription factors (SREBP-1c, CEBP α, PPARγ)
- A part of adipose tissue collected at the time of slaughter analyzed for fatty acid composition using a gas chromatograph.

Materials and methods (*contd.*)

- Forty cycles of amplifications with the following thermal cycling conditions: initial denaturation-94°C for 6 minutes, cycling- 94°C for 40sec, 59°C for 60sec and 72°C for 40 sec and final extension for 6 minutes at 72°C except for SCD, where annealing temperature was kept at 56°C.
- The relative quantification of target genes expression were calculated using 2-$\Delta\Delta$Ct method (Livak and Schmittgen, 2001).
- All gene expression values normalized to 18S and control values taken arbitrarily as 100

Materials and methods (*contd.*)

- Serum lipid profile, glucose analysis using standard kits
- Fatty acid composition was determine using GC using and comparing with known fatty acid methyl ester standards

Statistical analysis

- The data was analyzed using Graphpad prism software and quantification software supplied along with PCR machine. All data are presented as means ±SEM.

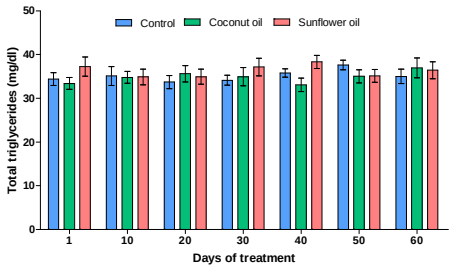
Results

Average daily gain (kg) of pigs fed with oil (Mean ± SE)

Treatment	Period of treatment (days)					
	10	20	30	40	50	60
Sunflower oil	0.28± 0.03	0.29± 0.05	0.32± 0.04	0.31± 0.02	0.34± 0.02	0.39± 0.03
Coconut oil	0.29± 0.03	0.31± 0.02	0.31± 0.03	0.34± 0.03	0.37± 0.03	0.40± 0.02
Control	0.26± 0.03	0.29± 0.02	0.29± 0.05	0.33± 0.03	0.36± 0.03	0.38± 0.02

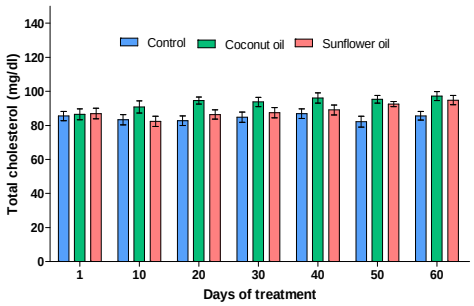
All values within same column does not differ significantly ($p<0.05$)

Change in serum total triglycerides following oil feeding



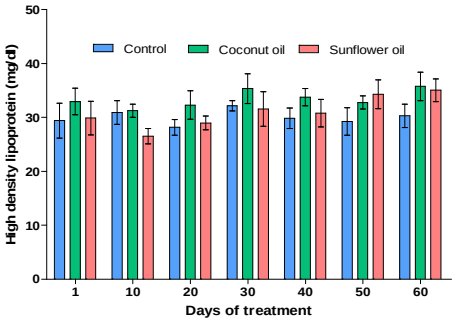
The values between groups did not differ significantly (P>0.05)

Change in serum total cholesterol following oil feeding



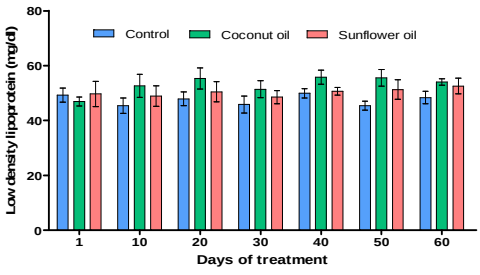
The values between groups did not differ significantly (P>0.05)

Change in serum total HDL following oil feeding



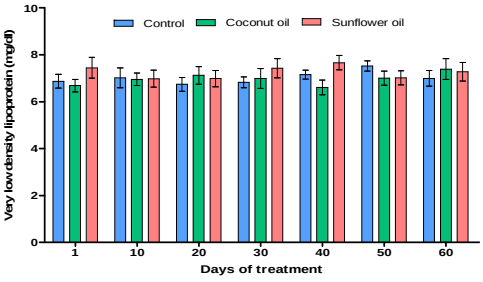
The values between groups did not differ significantly (P>0.05)

Change in serum LDL following oil feeding



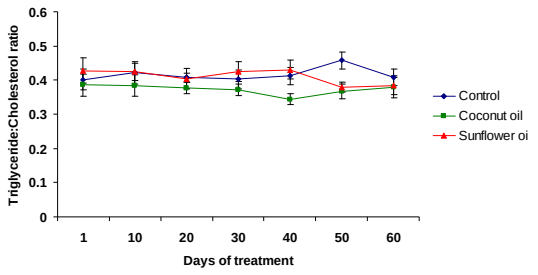
The values between groups did not differ significantly (P>0.05)

Change in serum VLDL



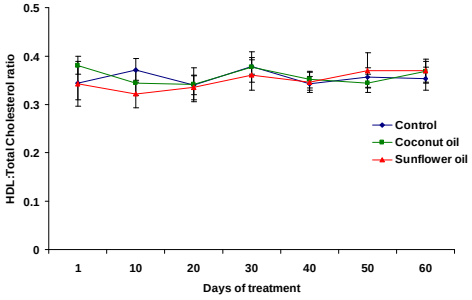
The values between groups did not differ significantly (P>0.05)

Serum TG: total cholesterol ratio



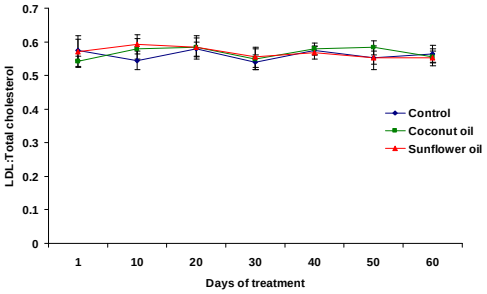
The values between groups did not differ significantly (P>0.05)

Serum HDL: total cholesterol ratio



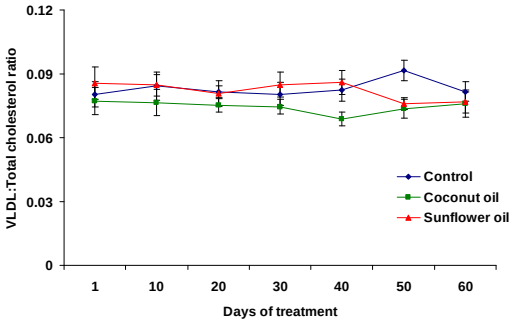
The values between groups did not differ significantly (P>0.05)

Serum LDL: total cholesterol ratio



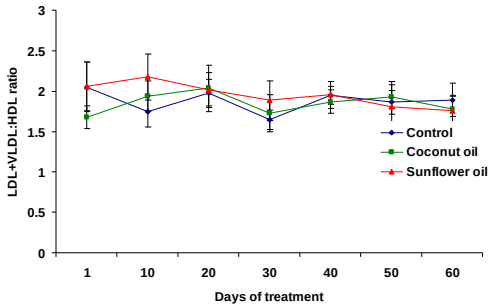
The values between groups did not differ significantly (P>0.05)

Serum VLDL: total cholesterol ratio



The values between groups did not differ significantly (P>0.05)

Serum VLDL+LDL: HDL ratio



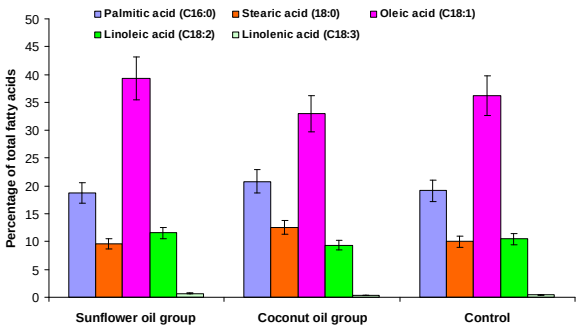
The values between groups did not differ significantly (P>0.05)

Subcutaneous adipose tissue gene expression

	FAS	SCD	SREBP-1c	PPAR ɣ	CEBP β
Coconut oil	0.84 ±0.08^{a*}	1.08 ±0.09^{a}	0.99 ±0.06^{a}	1.02 ±0.06^{a}	0.95 ±0.06^{a}
Sunflower oil	0.39 ±0.06^{b}	0.51 ±0.04^{b}	0.47 ±0.03^{b}	1.18 ±0.09^{b}	0.96 ±0.09^{a}
Control	1.03 ±0.14^{a}	1.02 ±0.05^{a}	1.05 ±0.08^{a}	1.01 ±0.08^{a}	1.09 ±0.08^{a}

*The values with same superscript within a column did not differ significantly (P<0.01)

Change in fatty acid composition



Change in FA profile following oil feeding (%)

Fatty acid	Sunflower oil group	Coconut oil group
C16:0	-1.88	8.52
C18:0	-4.86	24.48
C18:1	8.52	-9.07
C18:2	10.622	-10.62
C18:3	54.7619	-19.05

Conclusions

- Replacement of 10% feed energy by oil had no significant effect on body weight gain, serum glucose, cholesterol, triglycerides and cholesterol fractions, HDL, LDL and VLDL
- Feeding of coconut oil and sunflower oil caused a shift in subcutaneous adipose tissue fatty acid composition towards saturation and unsaturation respectively
- The feeding of sunflower oil decreased FAS, SCD, SREBP-1c and CEBP β gene expression but increased PPAR γ which suggests that sunflower/PUFA tend to decrease lipogenesis as well as adipogenesis.
- Feeding of coconut oil, does not change expression of lipogenic genes but decreased CEBP β expression, suggesting that saturated fat may decrease adipogenesis

Future suggestions

- Approaches for understanding regulation of genes by nutrients-nutrigenomics/functional genomics
- Identification of pathways of gene regulation by nutrients
- Molecular regulation of FAS and SCD has implication on manipulation of carcass composition of animals
- Understanding mechanisms in obesity, diabetes, insulin resistance, atherosclerosis etc.
- Role in cellular signaling