

Early molecular events of adipose tissue development during overfeeding and weight gain in humans

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OBESITY : a worldwide epidemic







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Obesity-related complications:

Type 2 diabetes Cardio-vascular diseases Cancers Sleep apnea Reduction of life expectancy

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How to study the development of adipose tissue during normal life in humans, using an experimentally feasible protocol and under ethical conditions?



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Overfeeding protocol with a lipid-enriched dietary supplement, providing about 760 Kcal/day in excess during 8 weeks (56 days) in healthy volunteers

combined with successive subcutaneous abdominal adipose tissue biopsies at D0, D14 and D56 for transcriptomics





Lipid overfeeding protocol

 Objective : to characterize the mechanisms of subcutaneous development during the early phase of weight gain induced by an overfeeding period with a lipid enriched-diet providing about 30% (760 kcal/d) of daily energy excess

- Duration : 8 weeks (56 days)
- Subjects : 44 volunteers (healthy men, 33 ± 1 years, BMI = 25 ± 1)

Asked to maintain their normal lifestyle and feeding behaviour and to add each day:



100 g (380 kcal) of cheese

40 g (230 kcal) of almonds







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Anthropometric and metabolic parameters

	D0	D14	D56
n	44	44	44
Age (years)	33 ± 1	-	-

Anthropometric parameters			
Body weight (kg)	79.1 ± 1.8	79 .9 ± 1.8***	81 .6 ± 1.8 ***
Weight gain (kg)	-	0.76 ± 0.14	2.51 ± 0.21
Waist circumference (cm)	89.3 ± 1.5	-	92 .4 ± 1.5 ***
Fat mass (%)	19.6 ± 0.8	-	20 .3 ± 0.8 ***

Metabolic parameters			
Fasting glucose (mM)	5.11 ± 0.06	5.10 ± 0.09	5.21 ± 0.08
Fasting insulin (mU/L)	10.1 ± 0.6	11 .6 ± 0.7***	10 .5 ± 0.6
НОМА	2.29 ± 0.16	2.63 ± 0.17 **	2.44 ± 0.15 *

*: p<0.05 **: p<0.01

***: p<0.001

Transcriptomic analysis in subcutaneous adipose tissue



AFFYMETRIX

HG U133 Plus 2.0 arrays (47,401 transcripts)

N = 13 subjects

Statistical analysis using Limma test

Probes with p-value < 0.05 and fold change > |1.25| at D14 and D56 were considered as differentially expressed during overfeeding

Biological functions and pathways identified using DAVID (Database for Annotations, Visualization and Integrated Discovery)



> 180 regulated genes between D0 and D14 (p-value<0.05/ FC>1.25)



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Pathway enrichment (DAVID)





> 486 regulated genes between D0 and D56 (p-value<0.05/ FC>1.25).







		Fold change Microarray		Fold change RT-qPCR	
Gene Symbol Entrez Gene	D14	D56	D14	D56	
Lipid metab	olism				
AACS	65985	1.4 ± 0.1	1.6 ± 0.3	1.7 ± 0.2	2.5 ± 0.4
ACLY	47	1.8 ± 0.3	2.2 ± 0.7	1.8 ± 0.3	2.6 ± 0.4
CETP	1071	1.3 ± 0.2	3.2 ± 0.7	1.7 ± 0.3*	2.7 ± 0.6
DGAT2	84649	2.0 ± 0.4	1.7 ± 0.2	2.8 ± 0.6	1.9 ± 0.2
LPIN1	23175	1.4 ± 0.2	1.1 ± 0.1	1.5 ± 0.4	1.4 ± 0.1
SCD	6319	1.2 ± 0.1	2.4 ± 0.7	$2.0 \pm 0.4 \star$	2.5 ± 0.3
SLC2A5	6518	2.2 ± 0.5	4.0 ± 1.9	1.2 ± 0.4 ×	2.4 ± 0.3
SREBF1	6720	1.5 ± 0.2	1.4 ± 0.1	2.0 ± 0.4	1.7 ± 0.2
VLDLR	7436	1.4 ± 0.2	1.2 ± 0.1	1.6 ± 0.3	1.5 ± 0.2
CIDEA	1149	0.9 ± 0.3	0.8 ± 0.1	0.8 ± 0.1	0.8 ± 0.1
Extracellula	r matrix				
COL6A3	1293	1.0 ± 0.1	1.3 ± 0.1	1.0 ± 0.1	1.3 ± 0.1
Angiogenes	is				
APLNR	187	1.0 ± 0.1	1.3 ± 0.1	0.9 ± 0.1	1.4 ± 0.1
ANGPTL4	51129	0.9 ± 0.1	0.8 ± 0.1	0.9 ± 0.2	0.9 ± 0.1 💈
EDN1	1906	0.8 ± 0.1	1.0 ± 0.1	0.7 ± 0.1	1.4 ± 0.2
Renin-angio	tensin syster	n			
ACE	1636	1.2 ± 0.1	1.5 ± 0.6	1.2 ± 0.1	1.4 ± 0.1
AGT	183	1.5 ± 0.2	1.4 ± 0.1	2.5 ± 0.5	2.2 ± 0.3
ENPEP	2028	1.1 ± 0.1	1.5 ± 0.1	1.2 ± 0.2	1.7 ± 0.2
MME	4311	14 + 01	14 + 01	14 + 02	15 + 02

Validation of microarray data using real-time PCR (24 subjects)

Data are presented as mean ± SE.

Underlined values indicate significant changes at D14 or D56 with respect to D0 (p < 0.05 with paired t-test for qPCR, p< 0.05 with Limma for microarray). * Indicates different result between microarray and RT-PCR







Validation of DGAT2 gene expression change by RT-qPCR and Western-blot





Increased angiogenesis and vascularization in human subcutaneous adipose tissue during overfeeding



Microvascular density : 21.2 ± 9.7 / mm2

32.1 ± 14.9 / mm2 (p<0.01, n = 12)





Remodeling of subcutaneous adipose tissue during overfeeding: Increased extracellular matrix and conjonctive tissue deposits







The Wnt signalling networks is a putative paracrine regulator of adipogenesis



J.K. Sethi and A. Vidal-Puig, Biochemical Journal 2010 427, 1-17

The canonical Wnt/ß-catenin signaling pathways must be inhibited to allow adipogenesis



Adapted from Takeda, I. et al. (2009) Nat. Rev. Rheumatol.



The expression of several inhibitors of the canonical pathway is up-regulated during overfeeding

Inhibition of the canonical Wnt/ ß-catenin pathways in human subcutaneous adipose tissue during overfeeding



Western-blot analysis, n= 8 * p < 0.05



Inflammation ?



No evidence for immune cells (macrophages) recruitment during lipid overfeeding













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