

The putative role of ACAA2 in ovine milk traits




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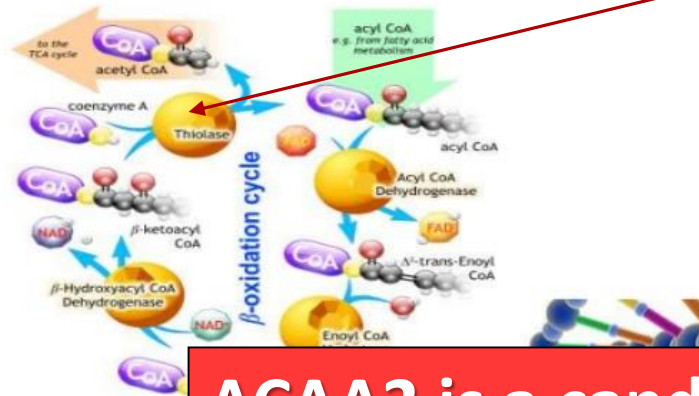
Summary

In the next 15 minutes

- Working hypothesis
 - Association of *ACAA2* polymorphism with
 - milk traits
 - in a closed nucleus
 - in an extended population
- } Chios sheep
- 
- with FA profile
 - Functional *ACAA2* study
 - Conclusions
-

ACAA2: Acetyl-CoA acyl transferase 2

FATTY ACID OXIDATION

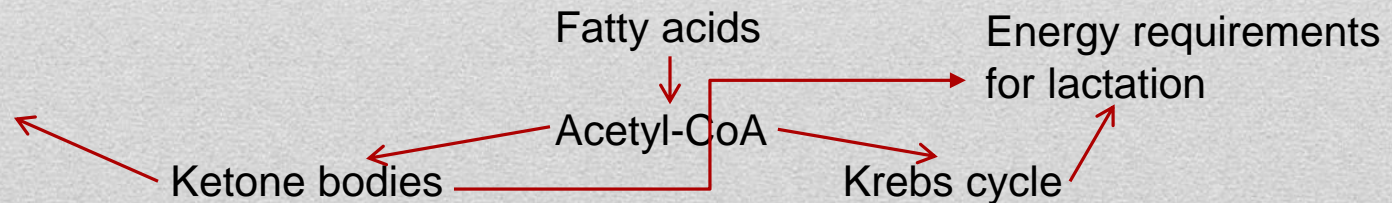


ACAA2 catalyses the last step of mitochondrial fatty acid oxidation

ACAA2 is a candidate gene for milk traits due to function

Biochemistry for Medics
www.namrata.co

Substrates for mammary FA synthesis



Working hypothesis

ACAA2

QTL for milk, fat and protein yield on ovine chromosome 23

QTL located around the middle of the region within markers MCM136 and URB031

ACAA2 is a candidate gene due to chromosomal location

Ovine chromosome OAR23

Content between Markers MCM136 and URB031 (according to virtual sheep genome v2)

Position	Acc No	Description	Notes
SHEEP MARKER URB031 (GAG21649714) (AK0204) (c) (read)			
1	CA02162175	PREDICTED: Bos taurus similar to one cut domain, family member 2 (ONECUT2), mRNA	transcription factor activity
2	CA02162182	Bos taurus 578 alpha-(acyl)-lysine-omega alpha 2,8-acyltransferase 3 (STRB3), mRNA	protein amino acid glycosylation - sialyltransferase activity
3	CA02162189	Bos taurus similar to adenosine triphosphatase (ATP), mRNA	cell adhesion homeostasis
4	CA02162195	Bos taurus transcription factor 1 (TF1), mRNA	
SHEEP MARKER MCM136			
5	CA02162199	Bos taurus transcription factor 7-like 2 (T-cell specific, HMG-box) (TF7L2), mRNA	transcription regulator activity
6	CA02162207	PREDICTED: Bos taurus similar to coiled-coil domain containing 98, transcript variant 1 (CCO98), mRNA	
7	CA02162214	Bos taurus PAR2B, member PAR2B, mRNA	small GTPase mediated signal transduction
8	CA02162221	PREDICTED: Bos taurus hypothetical protein LOC101910303 (LOC101910303), mRNA	
9	CA02162228	PREDICTED: Bos taurus hypothetical LOC0241475 (LOC0241475), mRNA	
10	CA02162235	PREDICTED: Bos taurus similar to Uncharacterized protein C10b04 (LOC204151), mRNA	
11	CA02162242	PREDICTED: Bos taurus similar to START domain containing protein 5 (STAR5), mRNA	
12	CA02162249	Bos taurus polymerase (DNA directed), like POU1, mRNA	transporter activity / DNA repair
13	CA02162256	PREDICTED: Bos taurus similar to methyl-GDP-binding domain protein 2 (LOC023633), mRNA	
14	CA02162263	PREDICTED: Bos taurus similar to deleted in colorectal carcinoma (DCC), mRNA	
SHEEP MARKER KSL428			
15	CA02162270	PREDICTED: Bos taurus misc. RNA (LOC020119), miscRNA	
16	CA02162277	Non-coding protein	
17	CA02162284	PREDICTED: Bos taurus meta-3-hydroxy C-C elongase (MEKO3), partial mRNA	zinc ion binding / protein binding
18	CA02162291	Bos taurus SMD1 family member 4 (SMD4), mRNA	Multifunctional
19	CA02162298	Bos taurus e6c homolog 1 (E. coli) (ELAC1), mRNA	RNA processing / zinc ion binding / hydrolase activity
20	CA02162305	Bos taurus mtic enzyme 2, NAD(+)-dependent, mitochondrial (MTC2), nuclear gene encoding mitochondrial protein, mRNA	
21	CA02162312	PREDICTED: Bos taurus coiled-coil domain containing 11 (CCO11), mRNA	
22	CA02162319	Bos taurus mtm2-Q3 binding domain protein 1 (M2P), mRNA	zinc ion binding
23	CA02162326	Bos taurus CXC family 1 (P3D domain) (CXC1), mRNA	regulation of transcription, DNA-dependent / zinc ion binding
SHEEP MARKER GMP			
24	CA02162333	Bos taurus sphin1 and KT associated 1 (SKA1), Mtna	
25	CA02162340	PREDICTED: Bos taurus similar to Coiled-coil domain-containing protein 11 (LOC101705), mRNA	
26	CA02162347	PREDICTED: Bos taurus similar to myo I region heavy chain (LOC078653), mRNA	
27	CA02162354	PREDICTED: Bos taurus similar to Epsin 16 (LOC053478), mRNA	ATP binding / protein binding / actin filament binding
28	CA02162361	PREDICTED: Bos taurus similar to Acyl-Coenzyme A synthetase 2 (mitochondrial) (Acyl-CoS2), mRNA	ATP binding / protein binding / acyltransferase activity
29	CA02162368	Bos taurus acyl-Coenzyme A synthetase 2 (ACAA2), nuclear gene encoding mitochondrial protein, mRNA	acyltransferase activity
30	CA02162375	PREDICTED: Bos taurus similar to endothelial lipase (LPLP), mRNA	
31	CA02162382	PREDICTED: Bos taurus similar to dynactin (DYN), mRNA (NO relative function)	
32	CA02162389	PREDICTED: Bos taurus similar to dynactin (DYN), mRNA (NO relative function)	
33	CA02162396	PREDICTED: Bos taurus similar to Mothes against DFF homolog 1 (DMD1) (MATH1) (MATH2), mRNA (No relative function)	
34	CA02162403	PREDICTED: Bos taurus similar to Mothes against DFF homolog 1 (DMD1) (MATH1) (MATH2), mRNA (No relative function)	
35	CA02162410	PREDICTED: Bos taurus similar to zinc finger and STR domain-containing 17, ZF17C3, mRNA	zinc ion binding / protein binding / nuclear acid binding
36	CA02162417	PREDICTED: Bos taurus similar to zinc finger and STR domain-containing 17, ZF17C3, mRNA	
37	CA02162424	Bos taurus SMD1 family member 2 (SMD2), mRNA	Multifunctional
38	CA02162431	PREDICTED: Bos taurus similar to Lysyloligohydrolase compressin 1 (L3O1) (compressin 1) (LOC033770), mRNA	
39	CA02162438	Bos taurus histone deacetylase-like hydrolase domain containing 1 (H4CD1), mRNA	hydrolase activity / metabolic process
40	CA02162445	PREDICTED: Bos taurus similar to protein tyrosine kinase 4-like 2 (PTK4L2), mRNA	nucleoside-hydrolase activity / ATP binding
41	CA02162452	PREDICTED: Bos taurus misc. RNA (LOC023554), miscRNA	
42	CA02162459	PREDICTED: Bos taurus similar to protein inhibitor of activated STAT 7, transcript variant 1 (PIAS7), mRNA	zinc ion binding / nucleic acid binding
43	CA02162466	PREDICTED: Bos taurus sialyltransferase 8 (alpha-2, 6-sialyltransferase) 8 (SIA7E8), mRNA	sialyltransferase activity / protein amino acid glycosylation
44	CA02162473	PREDICTED: Bos taurus similar to leucopressin homology domain 1 (LOC023525), mRNA	
45	CA02162480	PREDICTED: Bos taurus similar to C20orf105 protein (LOC023526), partial mRNA	
46	CA02162487	PREDICTED: Bos taurus similar to ring finger protein 165 (RNF165), mRNA	zinc ion binding / protein binding
47	CA02162494	Bos taurus hypothetical protein LOC051069 (LOC051069), mRNA	
48	CA02162501	Bos taurus coiled-coil domain containing 5 (spindle associated) (CCO5), mRNA	Cell cycle / mitosis / cell division / spindle
49	CA02162508	Bos taurus ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1 (ATP5A1), nuclear gene encoding mitochondrial protein, mRNA	Multifunctional
50	CA02162515	Bos taurus protein phosphatase 1 (PPP1C), mRNA	
51	CA02162522	PREDICTED: Bos taurus similar to discoidal protein 51a (LOC023528), mRNA	structural constituent of discosome
52	CA02162529	PREDICTED: Bos taurus misc. RNA (LOC023529), miscRNA	
53	CA02162536	PREDICTED: Bos taurus similar to sulfuric acid binding-like factor 15 (SGLC15), mRNA	
54	CA02162543	Bos taurus solute carrier family 14 (solute transporter), member 1 (SLC14A1) (SLC14A1), mRNA	solute transmembrane transporter activity
55	CA02162550	PREDICTED: Bos taurus solute carrier family 14 (solute transporter), member 2 (SLC14A2), mRNA	solute transmembrane transporter activity
SHEEP MARKER URB031 (GAG21649714) (AK0204) (c) (read)			

~12Mb
~10cM

ACAA2

Working hypothesis

(whole genome QTL identification study in sheep; Gutierrez-Gill, 2009)

PROJECT TITLE: USE OF MOLECULAR AND QUANTITATIVE GENETICS FOR THE IMPROVEMENT OF CHIOS SHEEP



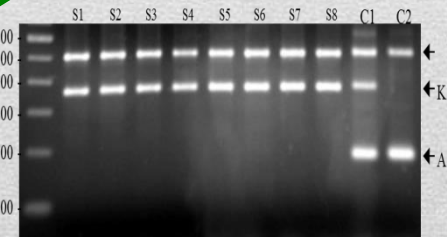
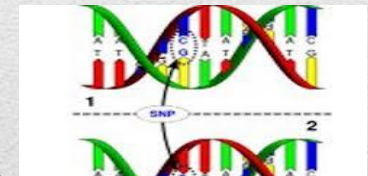
Pedigree and records of traits for 43 years (1968-2012)



Data obtained during the project (blood for SNP identification and genotyping, milk for chemical analysis)



Correlation!



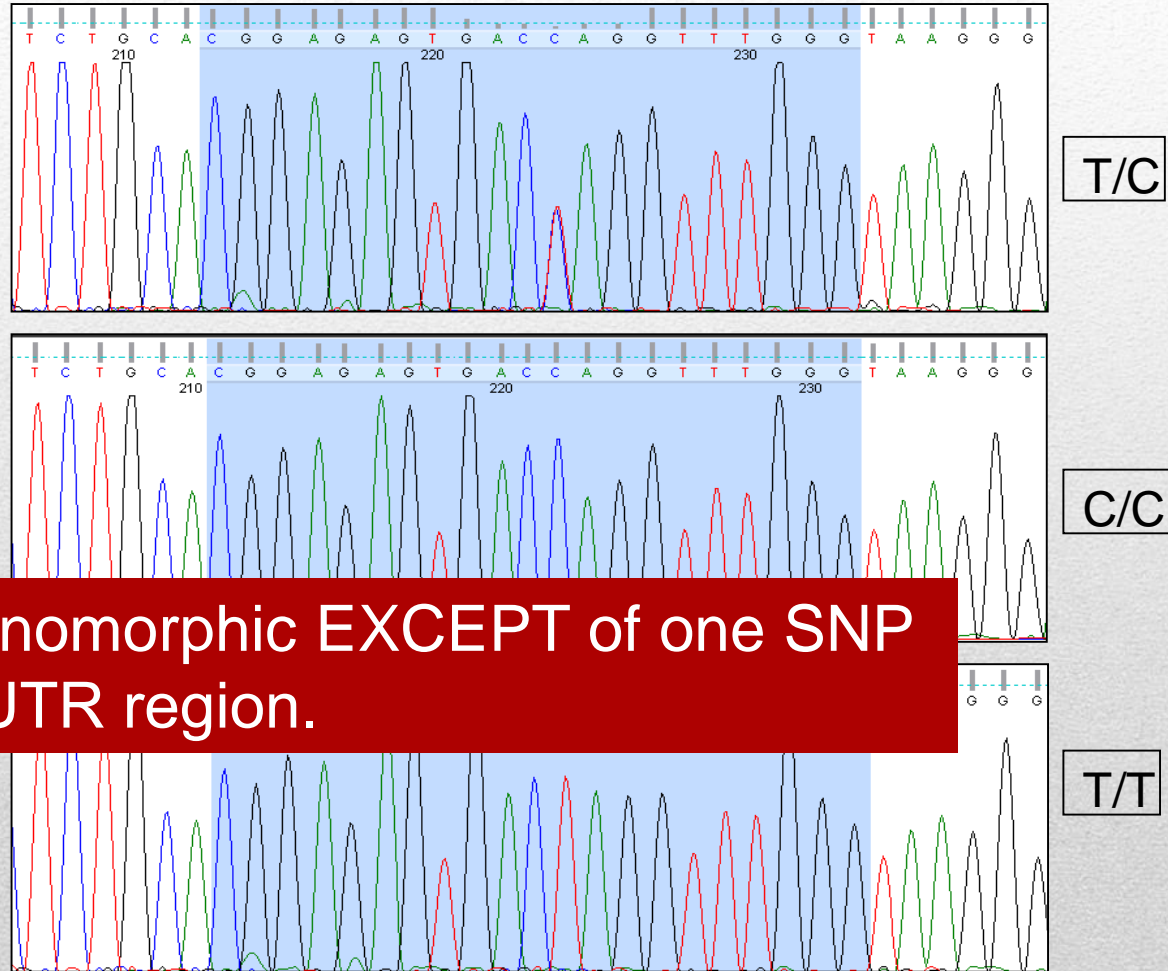
Agricultural Research Institute nucleus flock



Work flow of the project

ACAA2

Sequence based SNP identification



All exons were monomorphic EXCEPT of one SNP identified in the 3'UTR region.

SNP identification

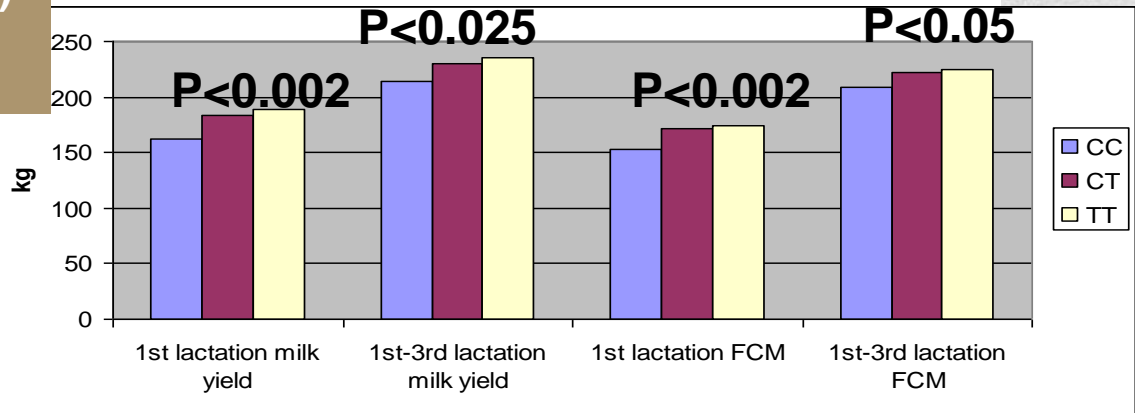
ACAA2 IS SIGNIFICANTLY ASSOCIATED WITH MILK YIELD AND FCM

- ❑ 318 genotyped ewes
- ❑ Offspring from 104 sires
- ❑ 717 records for
 - ❖ milk yield
 - ❖ fat corrected milk (FCM)
 - ❖ fat percentage

<i>ACAA2 genotype</i>			<i>Allelic frequency</i>	
CC	CT	TT	C-allele	T-allele

Hardy-Weinberg Prediction

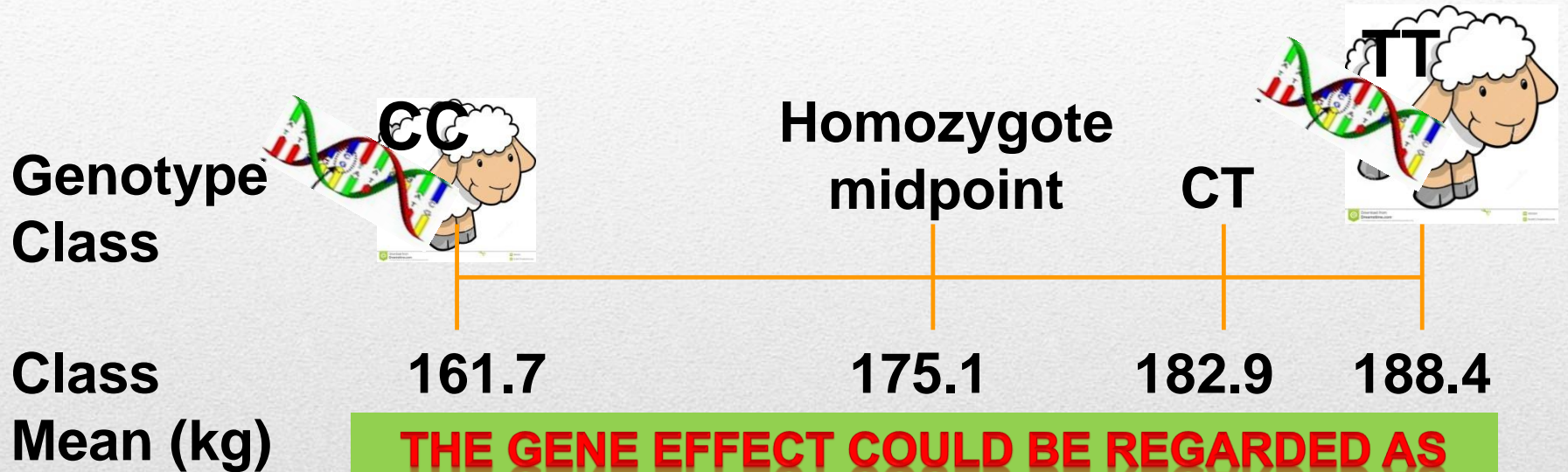
343



ACAA2 association with milk traits

ACAA2

Genotype means for first lactation milk yield



- Ewes with the T
- ewes with CC g
- Partial dominan

Orford M., Tzamaloukas O., Hadjipavlou G., Hatziplis D., Koumas A., Mavrogenis A., Papachristoforou C., Miltiadou D.* (2012) *J. Dairy Sci.* 95:3419–3427

ACAA2 association with milk traits

Confirmed previous association of **ACAA2 with milk yield** in an extended population of Chios

ACAA2 is associated with milk protein %

	all lactations milk yield	1 st lactation milk yield	milk protein percentage	milk fat percentage	milk protein yield	milk fat yield
a ¹ ±SE	6.81±2.95	10.61±3.56	-0.05±0.02	-0.03±0.03	0.23±0.18	0.28±0.17
p ²	0.021*	0.003*	0.003*	0.370	0.200	0.100
d ³ ±SE	8.67±3.53	13.02±4.26	0.02±0.02	0.04±0.04	0.41±0.21	0.46±0.21
p ⁴	0.014*	0.002*	0.41	0.322	0.048*	
% V _p due to SNP ⁵	0.62%	2.25%	1.68%	0.3	44%	

ACAA2 is NOT associated with milk fat% and is associated with fat yield

Dilution effect

Results from 742 animals from all sheep farms keeping data on milk yield and milk composition

Trait	all lactations milk yield ¹	1 st lactation milk yield ¹	milk protein percentage	milk fat percentage	milk protein yield	milk fat yield
Genotyped means±SE ²						
CC	245.23±4.44 ^c	170.21±5.28 ^a	5.29±0.02 ^a	5.19±0.05	8.78±0.25	12.87±0.26 ^c
CT	260.71±2.76 ^c	193.85±3.33 ^d	5.23±0.01 ^c	5.20±0.03	9.42±0.16	13.62±0.17 ^d
TT	258.85±3.88 ^b	191.44±4.77 ^c	5.20±0.02 ^c	5.14±0.04	9.23±0.25	13.44±0.23 ^b

ACAA2 association with milk traits

PROJECT TITLE:

IMPROVEMENT OF LIPID FRACTION IN OVINE MILK AND HALLOUMI CHEESE, TOWARDS HEALTHIER LOCAL PRODUCTS

Collection of milk samples

4 Chios Farms → 1st 171 ewes

→ 2nd 118 ewes

→ 3rd 94 ewes

→ 4th 46 ewes

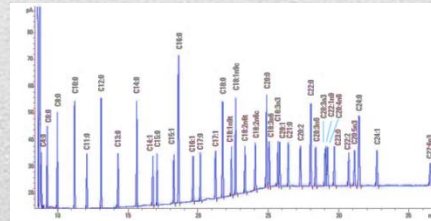
Total **429** Chios ewes

At least 3 samplings/animal

~1300 milk samples

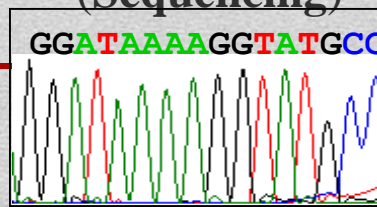
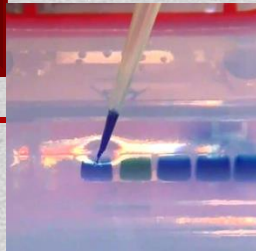
MILK → fat, protein, lactose

fame → fatty acid profile (**GC-MS**)

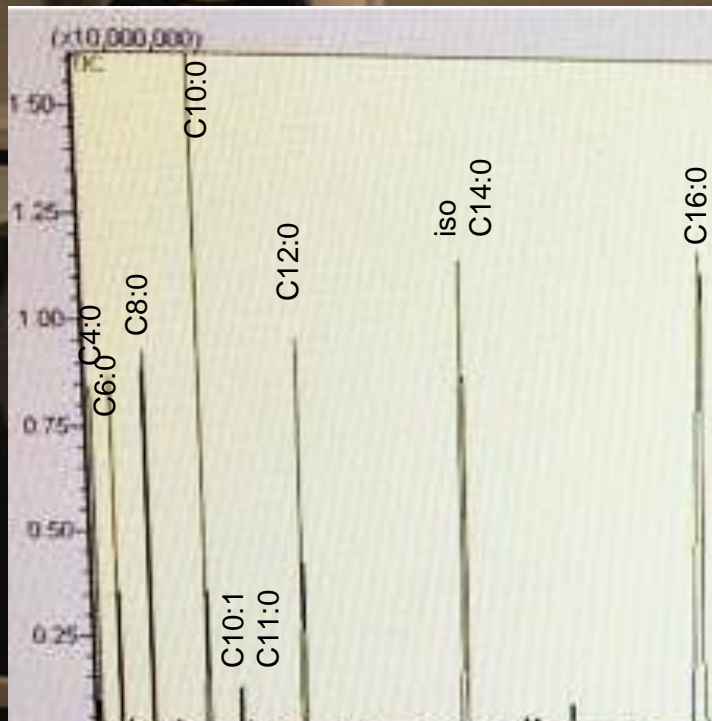


~430 blood samples

→ DNA extraction → Genotyping
(**Sequencing**)



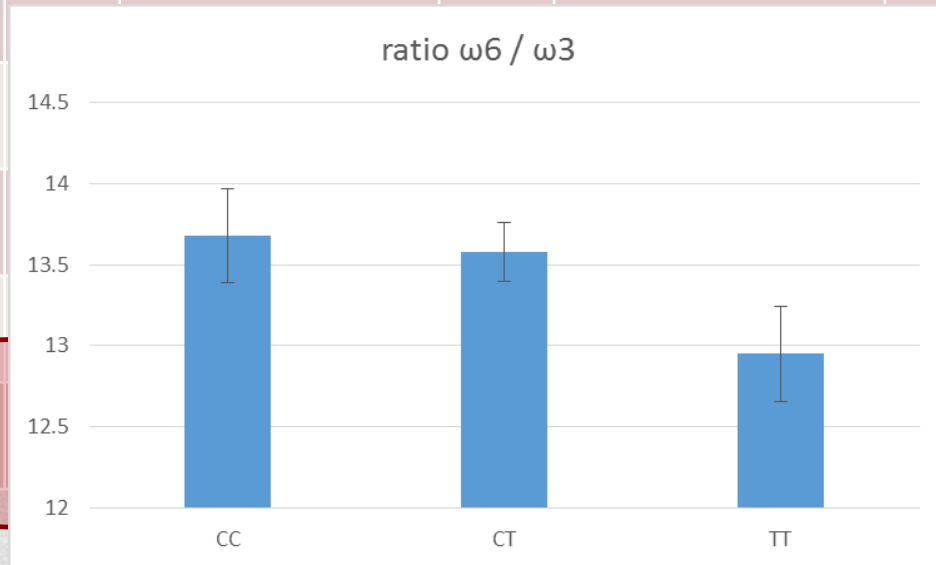
GCMS RESULTS



FAME	mean %w/w	sd	FAME	mean %w/w	sd
C4:0	3.27	1.56	C16:1 cis9	0.92	0.55
C5:0	0.04	0.02	iso C17:0	0.34	0.15
C6:0	3.18	1.56	C16:1 other	0.44	0.29
C7:0	0.07	0.04	anteiso C17:0	0.49	0.32
C8:0				0.57	0.23
C9:0				0.21	0.11
C10:0			mean		
C10:1	FAME		%w/w	sd	
C11:0	SFA	72.93	7.21	2.14	3.00
C12:0	SCFA (4C-10C)	18.98	8.67	18.70	5.23
C12:1cis9	mammary origin C4-C14	35.96	10.70	0.96	0.61
C13:0	MCFA (12C-14C)	16.86	2.83	0.45	0.28
iso C14:0	LCFA(16C-24C)	36.00	5.24	0.14	0.09
C14:0	MUFA	22.42	5.70	2.72	1.10
iso C15:0	PUFA	3.85	1.54	0.17	0.11
C14:1	UFA	26.25	6.88	0.08	0.04
ant C15:0	C<16	64.81	9.89	0.27	0.13
cis10 C15:1	C>16	34.39	9.55	0.30	0.22
C15:0			Linoleic acid (9Z, 11E)	0.56	0.31
iso C16			cis-11-C20:1	0.16	0.12
C16:0			C20:4ω6	0.21	0.10
			C22:0	0.14	0.07
			cis_13_C22:1_ω9	0.15	0.08

ACAA2 association with FA profile

Trait	CC ²	n	CT ²	n	TT ²	n
C9:0	0.113 ^c ± 0.004	191	0.109 ^c ± 0.002	526	0.115 ^d ± 0.004	238
C11:0	0.136 ± 0.005					
C12:1 cis-9	0.152 ^d ± 0.005					
C13:0	0.089 ± 0.003					
ω6/ω3	13.67 ^c ± 0.29					



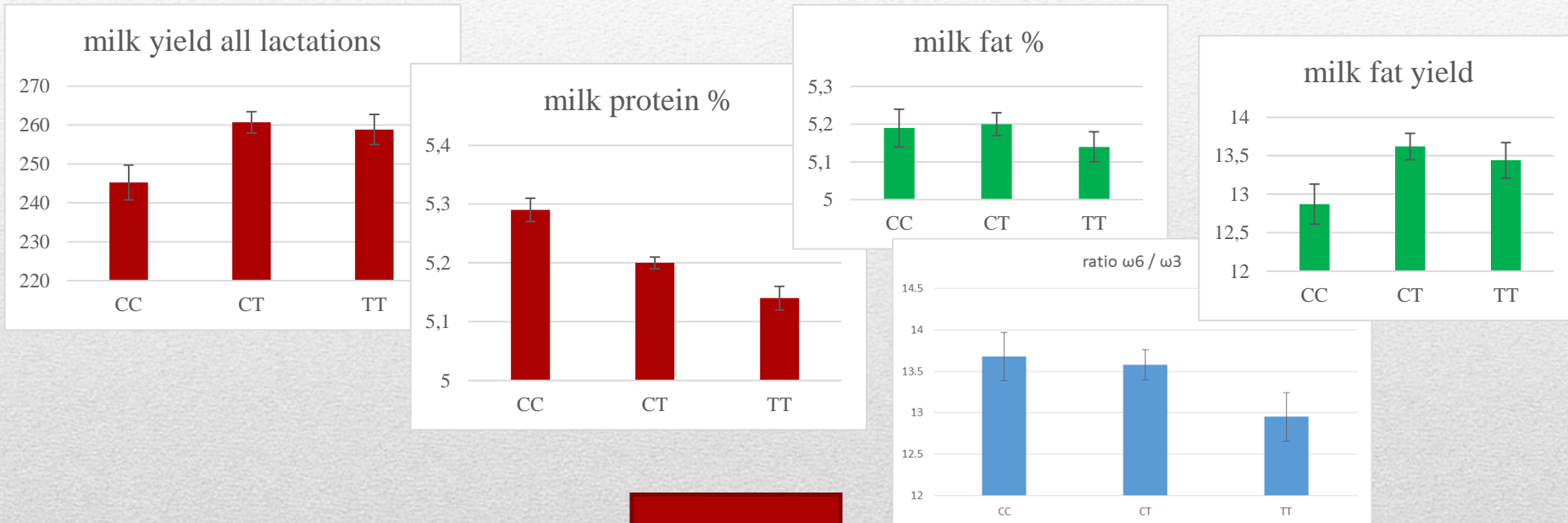
**ACAA2 WAS ASSOCIATED WITH
ω6/ω3 RATIO**

Simoni Symeou^a, Ouranios
Tzamaloukas^a, Georgios Banos^{b,c},
Despoina **Miltiadou**^a
ACAA2 and *FASN* polymorphisms
affect fatty acid profile of Chios
sheep milk; under reviewing in
Journal of Dairy Research

ACAA2 association with FA profile

ACAA2 IS ASSOCIATED WITH DAIRY TRAITS

TT and CT animals produce more milk with lower protein percentage, higher fat yield
 CC animals produce less milk with higher protein percentage, TT animals with higher $\omega 6/\omega 3$ ratio



ACAA2 3UTR SNP is the causative mutation?

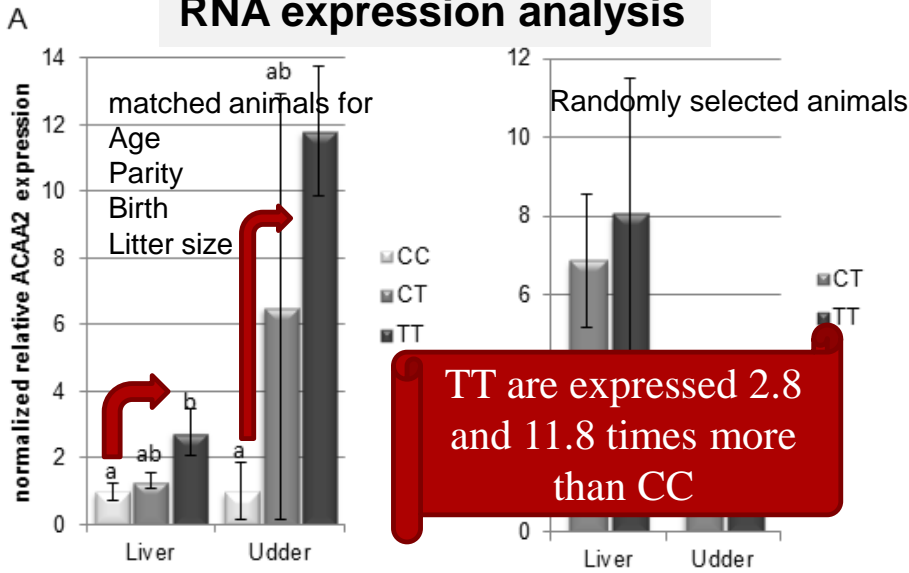
Effect observed

ACAA2 3UTR SNP is in linkage or LD with the causative mutation?

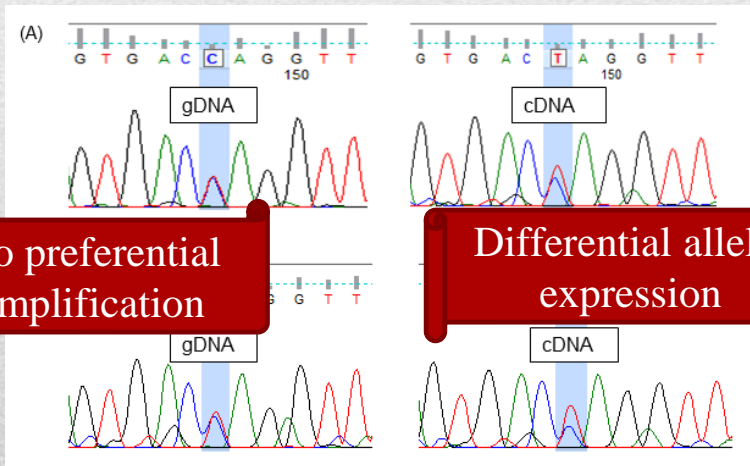


No aminoacid change, may affect the expression of the gene

RNA expression analysis

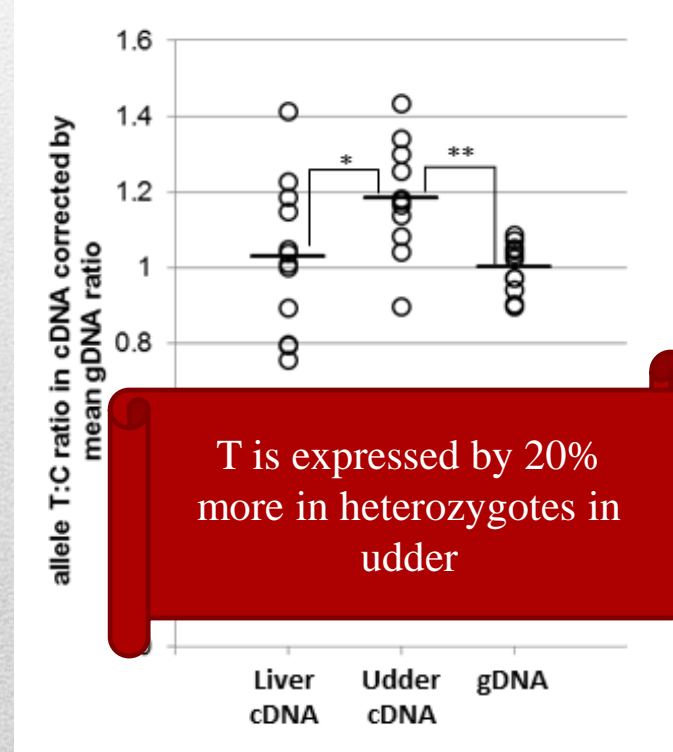


TT are expressed 2.8 and 11.8 times more than CC



No preferential amplification

Differential allelic expression



T is expressed by 20% more in heterozygotes in udder

Comparison of gDNA and cDNA from heterozygous animals

Functional ACAA2 study

Conclusions

- The variants in the 3'UTR of the *ACAA2* gene are associated
 - with milk yield
 - protein percentage
 - fat yield
 - $\omega 6/\omega 3$ ratio
- are differentially expressed in homozygous ewes of each allele and
- exhibit AEI within heterozygotes in a tissue specific manner

=>suggesting the existence of a cis-acting regulatory DNA mechanism.



↑ mRNA expression => likely ↑ *ACAA2* activity => ↑ energy and carbon substrates for lactation and FA synthesis

My colleagues in Animal and Dairy Science

- Dr Ouranios Tzamaloukas
- Dr Michael Orford

Our PhD students

- Simoni Symeou
- Constantina Constantinou



Undergraduate students
Farm technical staff



Our partners

Prof. Georgios Banos



Dr. Ariadne-Hager
Theodorides



Dr Dimitris Hatziplis



Dr. Georgia Hatzipavlou



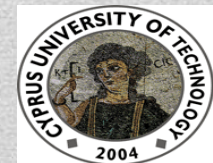
Acknowledgments



• **Partner institutions**



• **Funding bodies**



Acknowledgments

Thank you for your attention !

