

Does the fatty acid profile in Churra sheep milk show additive genetic variation?

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Introduction

- Ideal diet regarding FA composition
 - 30% SFAs
 - 60% MUFAs
 - 10% PUFAs
- Sheep milk is far from having this composition
 - 66% SFAs
 - 28% MUFAs
 - 6% PUFAs

Objective

- It could be possible through animal breeding to modify FA profile in sheep milk?
 - Increasing MUFAs and PUFAs %
 - Reducing SFAs %
 - Increasing concentration of healthy FAs
 - I.E.: CLA, $\omega 6$ and $\omega 3$

Material & Methods

- Animals
 - 4,100 milk samples
 - 976 ewes (sired by 15 rams)
 - 3,524 pedigree records
 - 14 commercial herds

Material & Methods

- Records
 - FA composition in the milk samples
 - Proportion of a particular FA with respect to the total amount of FAs (Fat)
- FA content was determined by gaseous chromatography
 - Fat was extracted using Bligh and Dyer's method
 - Methylation of FAs with NaOCH_3
 - HP 6890 series GC system chromatographer

Statistical Methods

- Animal repeatability models

- Model I (DIC)

$$y_{hklij} = HTD_h + DIM_k + Age_l + p_i + a_i + e_{hklij}$$

$$DIC = 2E^0 \left[-2 \log(p(\mathbf{y} | \boldsymbol{\theta})) \right] + 2 \log(p(\mathbf{y} | E[\boldsymbol{\theta}]))$$

- Model II (Bayes Factor)

$$y_{hklij} = HTD_h + DIM_k + Age_l + p_i + u_i \cdot \sigma_a + e_{hklij}$$

$$BF = \frac{p(\mathbf{y} | \sigma_a \neq 0)}{p(\mathbf{y} | \sigma_a = 0)} = \frac{p(\sigma_a = 0)}{p(\sigma_a = 0 | \mathbf{y})}$$

$$p(\mathbf{u}) \sim MVN(0, \mathbf{A} \times 1)$$

$$p(\sigma_a) \sim Unif(0, \sigma_p)$$

Trait statistics

Trait ¹	Mean	Std. Dev.	CV
C _{8:0}	3.45	0.46	13.29
C _{10:0}	8.60	1.40	16.26
C _{12:0}	5.37	1.13	21.12
C _{14:0}	10.18	1.45	14.28
C _{16:0}	22.05	2.42	11.00
C _{18:0}	10.48	2.20	20.95
C _{16:1 c9}	1.64	0.34	20.78
C _{18:1 t11}	2.53	0.46	18.14
C _{18:1 c9}	15.36	2.25	14.66
C _{18:2 c9,c12}	3.47	0.62	17.85
C _{18:3 c9,c12,c15}	1.23	0.54	43.68
C _{18:2 c9,t11} (CLA)	0.89	0.44	48.87

Heritabilities

Trait	Genetic model		Non Genetic model		
	h^2	p^2	r^2	DIC Diff.	BF
$C_{8:0}$	0.05(0.02)	0.03(0.02)	0.07(0.01)	-22.18	>100
$C_{10:0}$	0.07(0.03)	0.05(0.02)	0.11(0.01)	-22.11	>100
$C_{12:0}$	0.07(0.03)	0.06(0.03)	0.13(0.02)	-22.47	>100
$C_{14:0}$	0.08(0.03)	0.04(0.02)	0.11(0.01)	-30.35	>100
$C_{16:0}$	0.04(0.01)	0.01(0.01)	0.04(0.01)	-25.53	>100
$C_{18:0}$	0.08(0.02)	0.03(0.03)	0.11(0.01)	-33.32	>100
$C_{16:1} \text{ c9}$			0.05(0.01)	-5.30	0.429
$C_{18:1} \text{ t11}$	0.02(0.01)	0.02(0.01)	0.04(0.01)	-11.43	3.39
$C_{18:1} \text{ c9}$			0.05(0.01)	-2.00	0.053
$C_{18:2} \text{ c9,c12}$	0.11(0.04)	0.07(0.03)	0.17(0.02)	-24.79	>100
$C_{18:3} \text{ c9,c12,c15}$			0.06(0.01)	-3.54	0.40
$C_{18:2} \text{ c9,t11 (CLA)}$			0.04(0.01)	-0.74	0.10

Heritabilities

- All the SFAs have a low heritability
- Those UFAs having a heritability different from zero do not have an endogenous biosynthesis

Discussion & Conclusions

- Few genetic variation is involved in the FA composition of Churra milk fat
 - Particularly in the endogenous biosynthesis of UFA
 - Ratio CLA/trans-vaccenic (proxy of $\Delta 9$ -desaturase activity) do not have an heritability different from zero.
 - Few alleles have been detected for the gene controlling this enzyme.
 - It seems to exist genetic variation in the ruminal biosynthesis of UFA, i.e. Linoleic Acid.

Discussion & Conclusions

- Our data come from commercial herds
 - No limitations in the ordinal of lactation
 - No limitations in the lactation period
 - No limitations in the season of the year
 - High environmental variation that could not be properly removed with our model, since it may be interacting with genes (GxE interaction)

Implications

- For modifying FA profile in Churra milk fat thought genetic selection it seems that evaluating candidates based on the assumptions from the infinitesimal model is not an appropriate alternative, particularly for increasing the concentration of UFAs.

Thank you for your attention !!

