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Genetic parameters of stearoyl coenzyme-A desaturase 9 activity estimated by test-day model

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Context

- Interest for human health
- Several authors suggested selection as a tool to modulate milk fatty acid profiles
  (e.g., Palmquist et al., 1993; Soyeurt et al. 2006)
- Around 406 FA compose the milk fat
  → need to resume the FA information

Δ^9 desaturase

- Also named stearoyl Coenzyme-A desaturase or SCD
- Able to introduce a cis-bond between carbons 9 and 10 of SFA
- Involved in the production of the majority of MONO and CLA in milk

General objective

- Study the genetic variation of Δ^9-desaturase activity in bovine milk within lactation using multitrait random regression test-day models
- Application to animal selection

Materials & Methods

- Data set
  - 6,099 spectra collected between March 2005 and July 2007
    - 1,331 primiparous Holstein cows (> 84%)
  - Milk history
    - Milk yield, %Fat, %Protein
    - 4 < DIM < 365
  - Final data set: 119,214 test-day records between 1991 and 2007
- Multi-trait random regression test-day models (3)
- Studied traits
  - Milk yield
  - Fat content
  - Protein content
  - 3 Δ^9 indices (product / substrate)

Materials & Methods

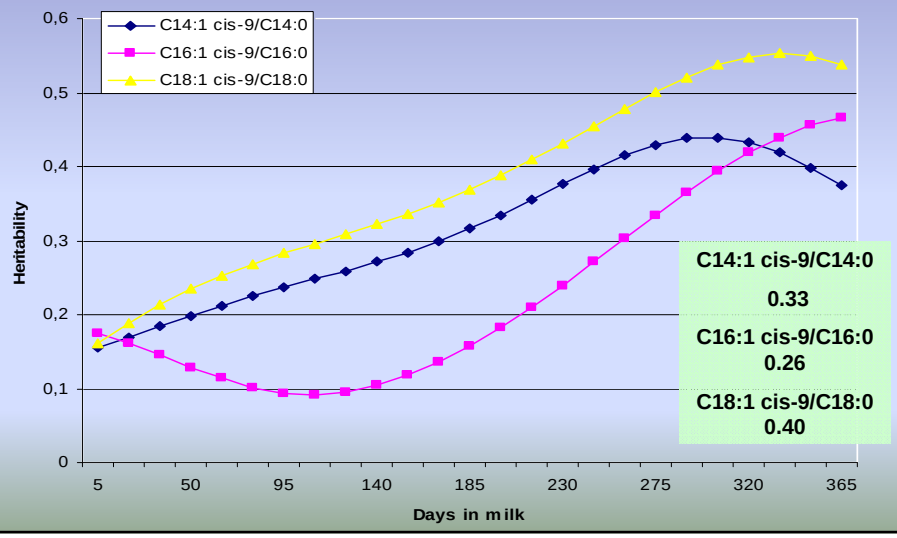
- Models:
  - Fixed effects:
    - Herd x date of test
    - Class of 15 days in milk (20)
    - Class of age (16)
  - Random effects:
    - Herd x year of calving
    - Permanent environment
    - Additive genetic effect
    - Residuals

} Second order Legendre Polynomials

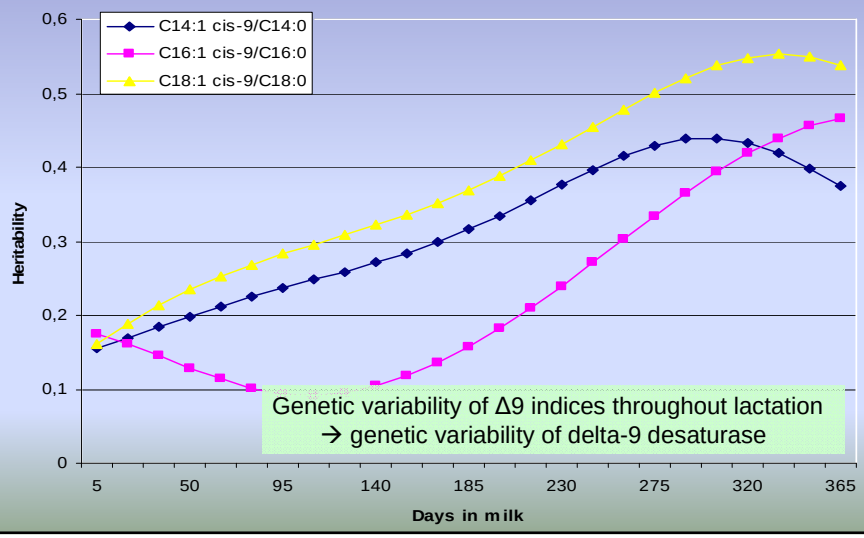
Studied traits

	N	Mean	SD
Milk (kg/day)	119,214	22.67	6.08
Fat (g/100g of milk)	119,214	4.06	0.69
Protein (g/100g of milk)	119,214	3.32	0.34
C14:1 *cis-9*/C14:0	6,099	0.10	0.02
C16:1 *cis-9*/C16:0	6,099	0.06	0.01
C18:1 *cis-9*/C18:0	6,099	1.93	0.42

Results: Heritability

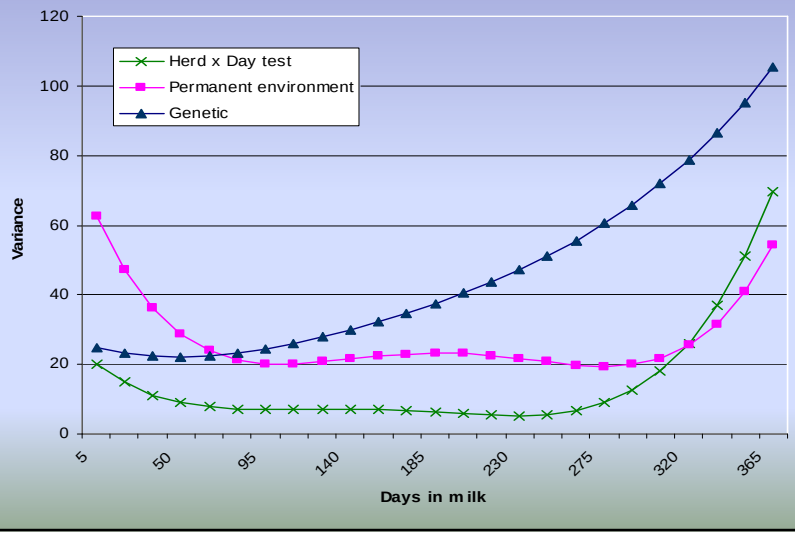


Results: Heritability

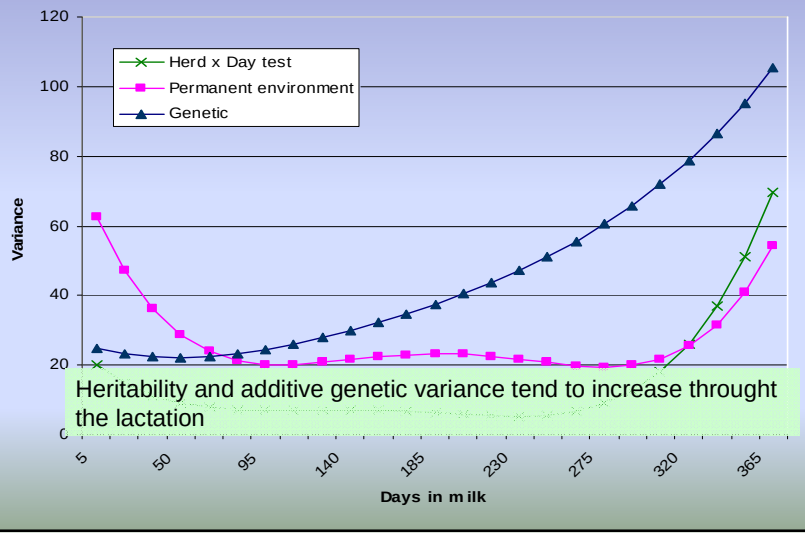


Genetic variability of Δ9 indices throughout lactation
→ genetic variability of delta-9 desaturase

Results: Variance components

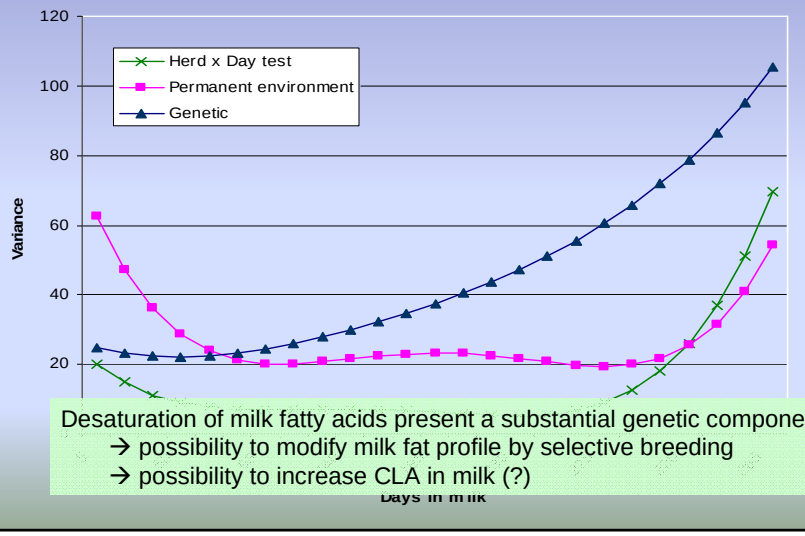


Results: Variance components



Heritability and additive genetic variance tend to increase throught the lactation

Results: Variance components



Desaturation of milk fatty acids present a substantial genetic component

→ possibility to modify milk fat profile by selective breeding

→ possibility to increase CLA in milk (?)

Results: Relationships

Genetic correlation

Phenotypic correlation

	Milk	Fat content	Protein content
C14:1 cis-9/C14:0	0.52 0.07	-0.43 -0.31	-0.28 -0.10
C16:1 cis-9/C16:0	0.13 -0.05	-0.28 -0.10	-0.02 -0.02
C18:1 cis-9/C18:0	0.59 0.23	-0.72 -0.31	-0.54 -0.26

Results: Relationships

Negative correlation with fat and protein contents
→ Milk payement (?)

	Milk	Fat content	Protein content
C14:1 cis-9/C14:0	0.52 0.07	-0.43 -0.31	-0.28 -0.10
C16:1 cis-9/C16:0	0.13 -0.05	-0.28 -0.10	-0.02 -0.02
C18:1 cis-9/C18:0	0.59 0.23	-0.72 -0.31	-0.54 -0.26

Application

- Sort sires according to their breeding values for the different studied traits:
  - C14:1 cis-9/C14:0
  - C16:1 cis-9/C16:0
  - C18:1 cis-9/C18:0
  - %MONO (g/100g of fat)
  - %SAT (g/100 g of fat)

  } Previous presentation

- Comparison among the lists of sires obtained for all traits

Application: Relationships (Spearman correlations)

	C14:1 cis-9 /C14:0	C16:1 cis-9 /C16:0	C18:1 cis-9 /C18:0
C14:1 cis-9/C14:0	1	0.40	0.63
C16:1 cis-9/C16:0		1	0.16
C18:1 cis-9/C18:0			1

Values of correlations among Δ^9 indices were expected higher

→ Complexity of the studied traits

Application: example

C14:1 cis-9 /C14:0	C16:1 cis-9 /C16:0	C18:1 cis-9 /C18:0
Sire 1	Sire 5	Sire 2
Sire 2	Sire 4	
Sire 3	Sire 18	Sire 6
Sire 4	Sire 1	Sire 1
Sire 5		Sire 16
Sire 6	Sire 9	Sire 4
Sire 7		Sire 12
Sire 8		Sire 9
	Sire 7	Sire 5
Sire 10	Sire 15	
Sire 11		Sire 3
	Sire 17	
Sire 13	Sire 6	Sire 13
Sire 14		Sire 14
Sire 15	Sire 14	Sire 7

Most of sires observed in the C14 top 15 are the same in the C16 and C18 top 15

But the ranks are different

C14:1 cis-9 /C14:0	C16:1 cis-9 /C16:0	C18:1 cis-9 /C18:0
Sire 1	Sire 5	Sire 2
Sire 2	Sire 4	
Sire 3	Sire 18	Sire 6
Sire 4	Sire 1	Sire 1
Sire 5		Sire 16
Sire 6	Sire 9	Sire 4
Sire 7		Sire 12
Sire 8		Sire 9
	Sire 7	Sire 5
Sire 10	Sire 15	
Sire 11		Sire 3
	Sire 17	
Sire 13	Sire 6	Sire 13
Sire 14		Sire 14
Sire 15	Sire 14	Sire 7

Application: example

C14:1 cis-9 /C14:0	C16:1 cis-9 /C16:0	C18:1 cis-9 /C18:0	Mono (g/100g of fat)	Sat (g/100g fat)
Sire 1	Sire 5	Sire 2	Sire 19	Sire 1
Sire 2	Sire 4		Sire 2	Sire 11
Sire 3	Sire 18	Sire 6		Sire 8
Sire 4	Sire 1	Sire 1	Sire 6	Sire 9
Sire 5		Sire 16		Sire 7
Sire 6	Sire 9	Sire 4	Sire 9	
Sire 7		Sire 12	Sire 8	Sire 18
Sire 8		Sire 19	Sire 12	
	Sire 7	Sire 5	Sire 5	Sire 15
Sire 10	Sire 15		Sire 1	
Sire 11		Sire 3		Sire 5
	Sire 17			
Sire 13	Sire 6	Sire 13	Sire 17	Sire 2
Sire 14		Sire 14	Sire 3	Sire 10
Sire 15	Sire 14	Sire 7		Sire 17

Conclusions and perspectives

- Potential improvement of Δ^9 activity and subsequently of the milk fat composition
  - by breeding and animal selection
- Perspectives
  - Increase of data base
  - Sires used today are they in the top15?
    - Estimation of genetic parameters for FA for all of the Walloon cows in the milk recording

Thank you for your attention

Acknowledgments

DGA project: D31-5593 (section 1)

AWE

Milk committee (Battice)

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