



Genetic parameters for major milk proteins in three French dairy cattle breeds

M. Brochard, M.P. Sanchez, A. Govignon-Gion, M. Ferrand, M. Gelé, D. Pourchet, G. Miranda, P. Martin, D. Boichard

www.phenofinlait.fr

phenofinlait@idele.fr

PhénoFinlait

Context

Expectations of consumers evolve:
Improve the human nutritional value and functionalities of cow milk
Common interest for Dairy industry, breeding and genetic sectors



Fine milk composition
Global approach (feeding, genetics...) to develop tools for breeders

Basis for genomic selection



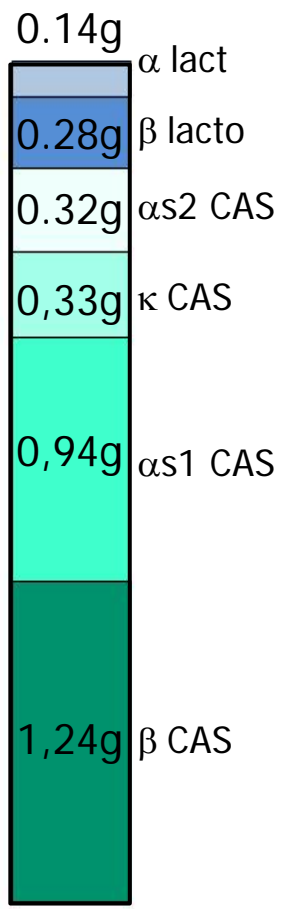
Record the data and estimate the genetic variability

Protein composition (Montbéliard)

100g milk



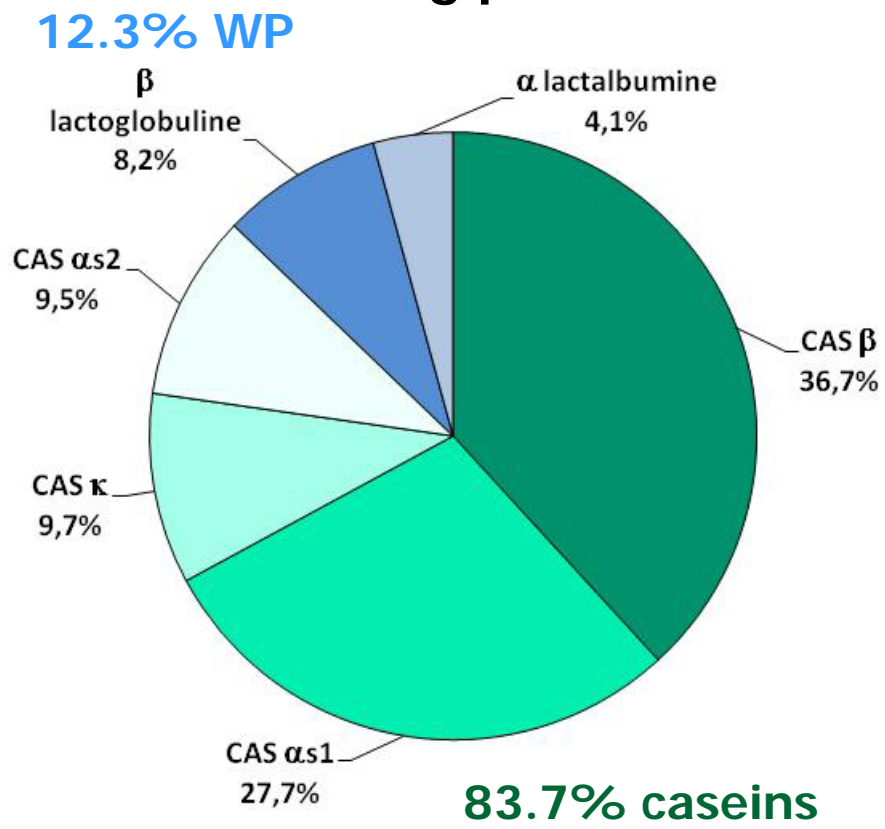
3.37g proteins



0.42g WP

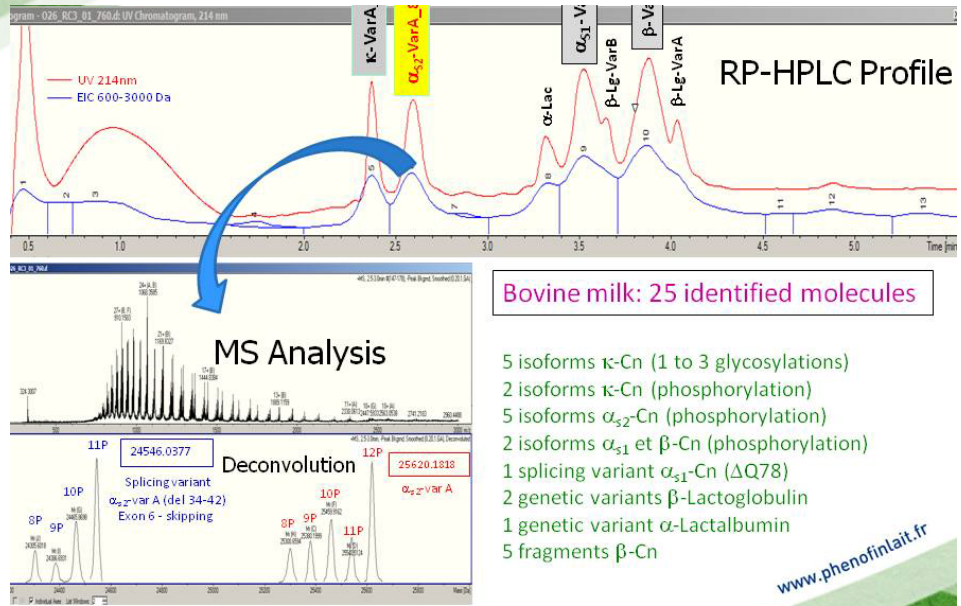
2.83g caseins

100g proteins



Total Casein + Whey protein (WP) = 96% (≠ 100%) due to proteolyse (10%, partly distributed over native proteins)

Main protein milk composition: analysis tools

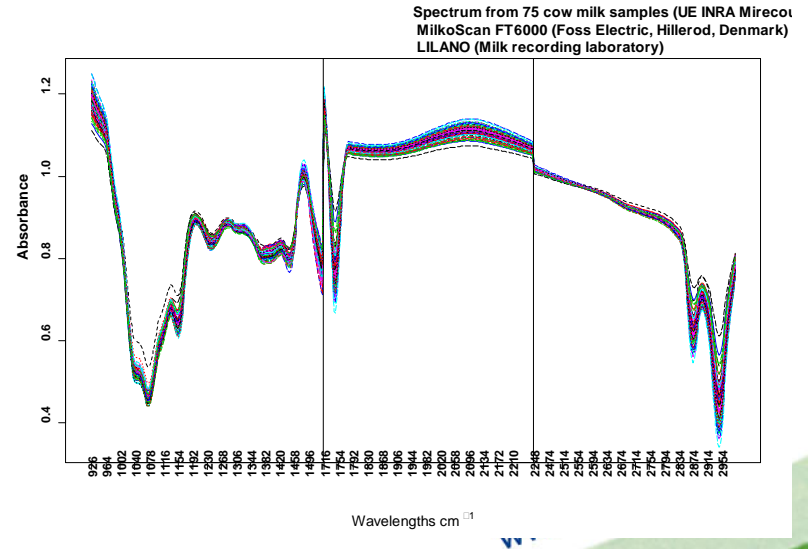


Bovine milk: 25 identified molecules

- 5 isoforms κ -Cn (1 to 3 glycosylations)
- 2 isoforms κ -Cn (phosphorylation)
- 5 isoforms α_2 -Cn (phosphorylation)
- 2 isoforms α_1 et β -Cn (phosphorylation)
- 1 splicing variant α_1 -Cn ($\Delta Q78$)
- 2 genetic variants β -Lactoglobulin
- 1 genetic variant α -Lactalbumin
- 5 fragments β -Cn

« Reference » method (*Miranda et Martin, Inra-GABI*):
 LC-MS: liquid chromatography coupled with mass spectrometry

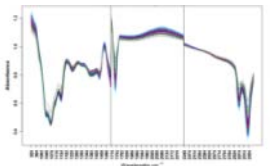
Mid infrared spectra (**MIR**)
 = large scale use for milk analysis (DHI): Fat and protein content.
 « Easy » to implement, very few additional cost
 (*Ferrand et al*)





Milk protein composition at a large scale

MIR routinely collected



Equations

α -lactalbumin
 β -lactoglobulin

α s1-casein
 α s2-casein
 β -casein
 κ -casein

Whey proteins (WP)

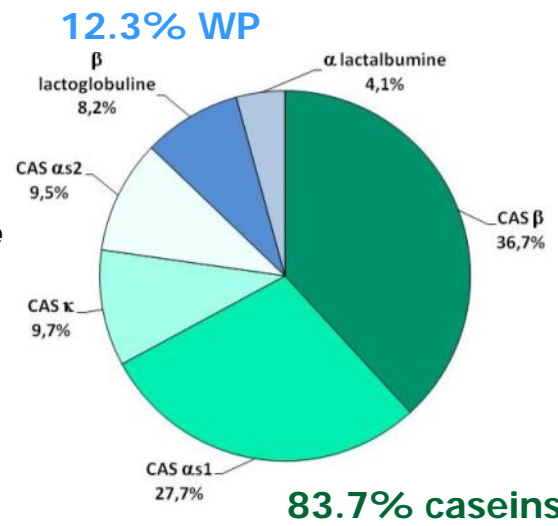
Caseins

in g/100g milk
= % milk

in g/100g protein
= % protein



100g proteins
ex. in Montbéliarde



	R ²	Relative error
Caseins	80 - 92%	4 - 8%
WP	60 - 70%	12 - 14%

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Data

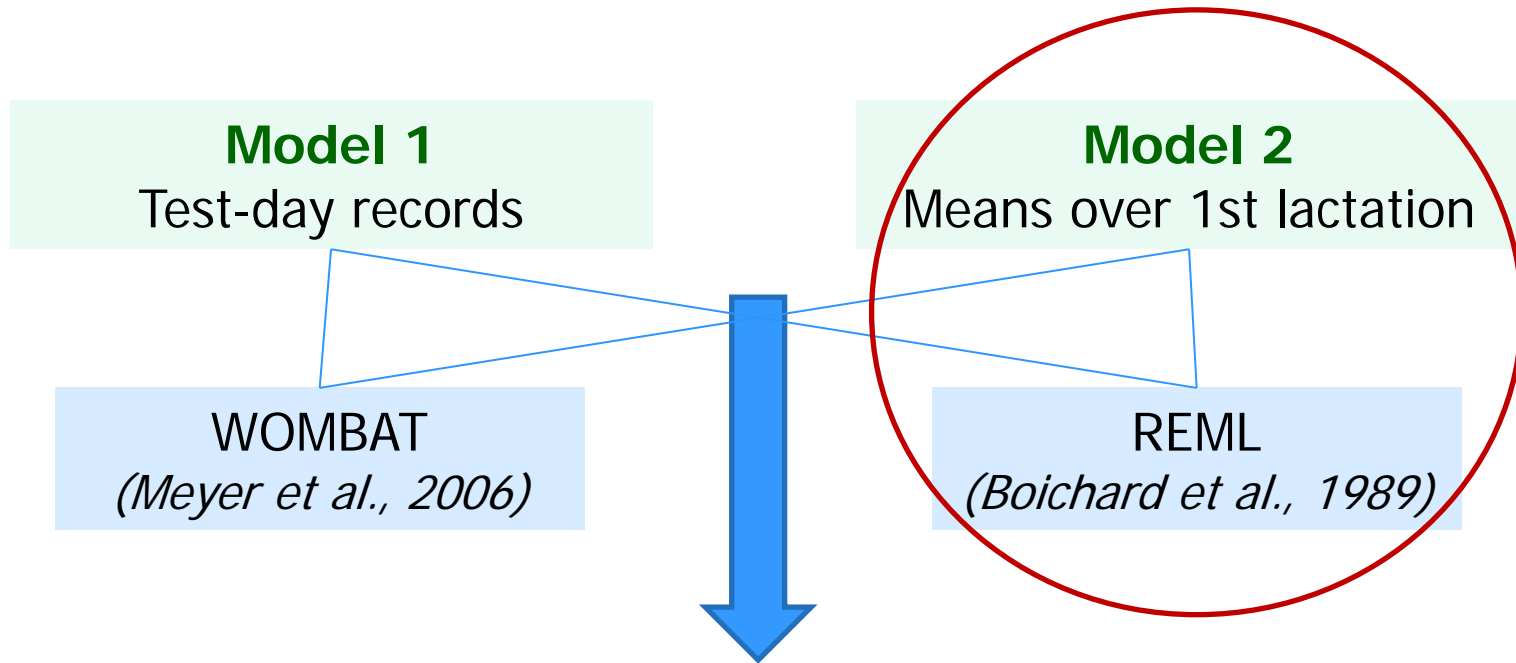
Breed	All lactations	1st lactations	
	MIR spectra	MIR spectra	Cow
Montbéliarde (MO)	589 016	181 515	36 042
Normande (NO)	117 323	37 668	9 668
Holstein (HO)	150 285	47 325	11 767
Total	856 624	266 508	57 477



Data for genetic parameters estimation

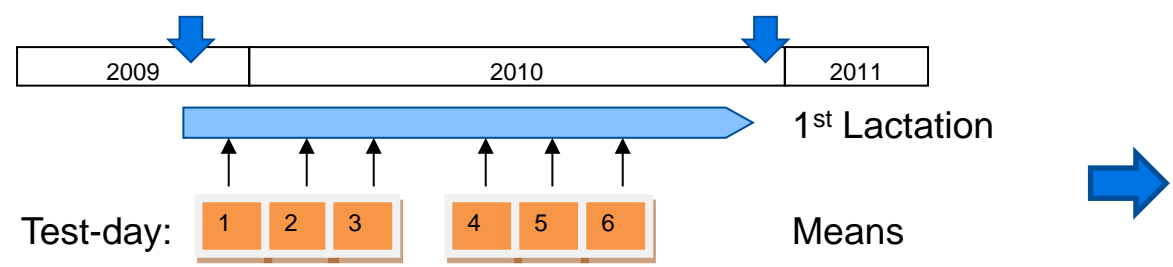
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2 models & 2 softwares



Very similar results between models X softwares
→ model2 * REML is the fastest combination, efficient for genetic correlation computations (results shown thereafter)

Model 2 – means over 1st lactation



Means
 At least 3 test-day NO & HO
 At least 7 test-day MO

$$y = X\beta + Za + e$$

Fixed effects
 herd
 calving month_year
 spectrometer

Random effects
 animal (0, $G \sigma_a^2$)
 residual (0, $I \sigma_e^2$)

Heritability estimates (%) – Montbéliard

	<i>g /100g milk</i>	<i>g /100g prot</i>
Total Casein	57	73
α s1 casein	54	67
α s2 casein	54	58
β casein	66	42
κ casein	48	61
Whey protein	61	61
α lactalbumin	57	72
β lactoglobulin	86	79

High h^2 estimates especially for β -lactoglobulin



Heritability estimates (%) – Holstein

	<i>g /100g lait</i>	<i>g /100g prot</i>	<i>Schopen* et al. 2008 g / 100g prot</i>
α s1 casein	30	53	47
α s2 casein	29	31	73
β casein	27	39	25
κ casein	32	54	64
α lactalbumin	31	44	55
β lactoglobulin	61	71	80

* LC analysis method

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Genetic coefficient of variation (σ_g/μ) % - Montbéliard

	<i>g /100g prot</i>	<i>g /100g milk</i>
Total Casein	0,3	3,7
α s1 casein	0,6	3,5
α s2 casein	0,9	4,2
β -casein	0,6	3,7
κ -casein	2,1	4,3
Whey protein	3,0	5,6
α -lactalbumin	2,8	4,5
β -lactoglobulin	6,4	8,6

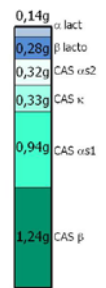
Higher CV for proteins expressed in milk and for β -lactoglobulin



Genetic correlations – Normandie

	α s1 cas	α s2 cas	β cas	κ cas	α lact	β lacto
α s1 casein		0.98	0.95	0.89	0.71	0.59
α s2 casein			0.96	0.92	0.69	0.57
β casein				0.85	0.68	0.58
κ casein					0.74	0.31
α lacta						0.27
β lacto						

g / 100 g milk

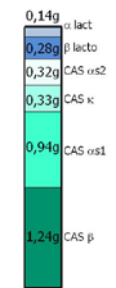


All genetic correlations >0

Genetic correlations – Montbéliard

	α s1 cas	α s2 cas	β cas	κ cas	α lact	β lacto
α s1 casein		0.94	0.96	0.84	0.69	0.51
α s2 casein			0.95	0.88	0.72	0.46
β casein				0.83	0.70	0.47
κ casein					0.80	0.10
α lacta						0.18
β lacto						

g / 100 g milk



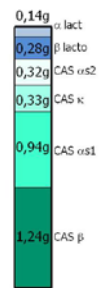
The different caseins are highly correlated to each other
 Co-regulations through BTA6 genes cluster?



Genetic correlations – Montbéliard

	α s1 cas	α s2 cas	β cas	κ cas	α lact	β lacto
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α lacta						0.18
β lacto						

← g / 100 g milk



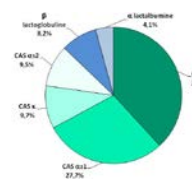
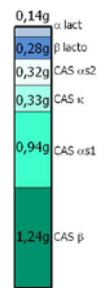
Moderate correlations between β lactoglobulin et caseins



Genetic correlations – Holstein

	α s1 cas	α s2 cas	β cas	κ cas	α lact	β lacto
α s1 casein		0.96	0.94	0.87	0.72	0.39
α s2 casein	0.04		0.95	0.88	0.71	0.39
β casein	-0.48	-0.37		0.84	0.75	0.39
κ casein	0.14	0.36	-0.31		0.80	0.07
α lacta	-0.01	-0.09	0.25	0.46		-0.01
β lacto	-0.19	-0.22	-0.20	-0.66	-0.52	

g / 100 g milk



g / 100 g proteins

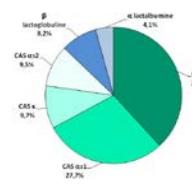
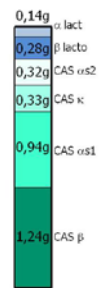
Correlations = 0 or < 0 due to mathematical relationships ($\Sigma = 100\%$!)



Genetic correlations – Holstein

	α s1 cas	α s2 cas	β cas	κ cas	α lact	β lacto
α s1 casein		0.96	0.94	0.87	0.72	0.39
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κ casein	0.14	0.36	-0.31		0.80	0.07
α lacta	-0.01	-0.09	0.25	0.46		-0.01
β lacto	-0.19	-0.22	-0.20	-0.66	-0.52	

g / 100 g milk



g / 100 g proteins

β Lacto and caseins negatively correlated

Conclusions

h^2 from MIR spectra
 $\approx h^2$ ref. meth. (LC)

MIR spectra useful
« phenotypes » for
genetic selection

High h^2 and
genetic variability
available

For all proteins
and especially
for β lacto.

Correlations >0 or
 <0 regarding unit

All proteins
linked to each
other

Genetic selection can modulate protein composition of cow milk, for instance it is possible to

↘ β lactoglobulin and ↗ several caseins at the same time

Next step

Genetic parameters estimation

Model improvement: Random Regression model to account for variation of genetic parameters along the lactation

QTL detection → SANCHEZ Marie-Pierre et al presentation,

" Whole genome scan to detect QTL for major milk proteins in three French dairy cattle breeds"

~ **8 000** cows in 3 breeds genotyped (Labogena)



7 500
54K snp chip
(Illumina)

+



500 7K snp chip (Illumina)
and imputation

Authors

M Brochard, MP Sanchez, A Govignon-Gion, M Ferrand, M Gelé,
D Pourchet, P Martin, G Miranda, D Boichard

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