Genetic correlations between production, type and functional traits in three French dairy cattle breeds

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TOTAL MERIT INDEX in French dairy breeds

- ***approximate*** **MT BLUP animal model since 2001**

		TMI=	
Milk →	pre-adjusted Milk	Milk EBV*	1 * INEL*
SCC →	pre-adjusted SCC	SCC EBV*	+ .25 * SCC*
LPL →	pre-adjusted Longev.	FLONG EBV*	+ .25 * FLONG*
AI →	pre-adjusted Fert.	FER EBV*	+ .25 * FER*
Type →	pre-adjusted type	Type EBV*	+ .25 * TYPE*

Univariate evaluations **+ weights !**

MT-BLUP Model: $y_{pre} = m + a + e$

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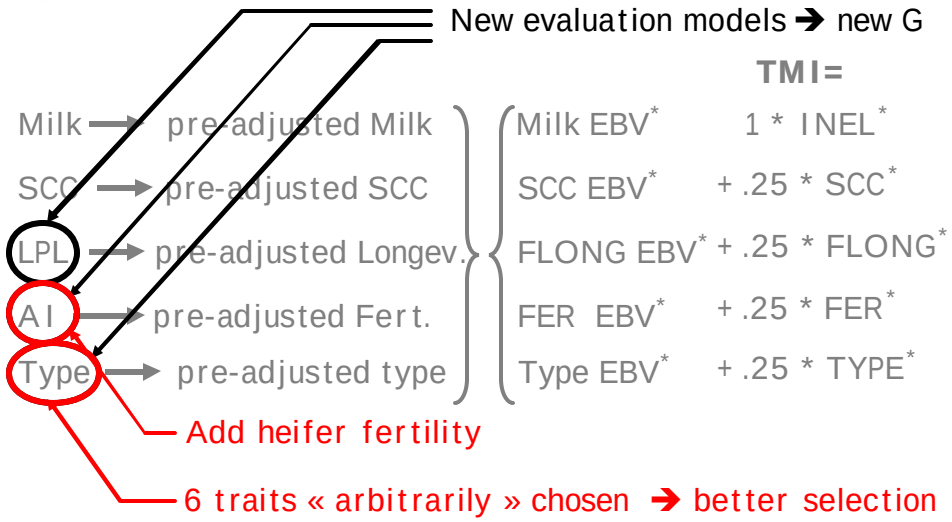
Main advantages

- Conceptually simple
- Good approximation of MT BLUP (Lassen et al, *Animal*, 2007)
- Multiple trait BLUP properties:
  - ✓ increased accuracy, less bias
  - ✓ optimal weights in TMI = economic weights
- Applicable to bulls and cows
- Combined EBVs for Longevity, Fertility, SCC

What we wanted to improve (1)



What we wanted to improve (2)

			TMI=
Milk →	pre-adjusted Milk	Milk EBV*	1 * INEL*
SCC →	pre-adjusted SCC	SCC EBV*	+ .25 * SCC*
LPL →	pre-adjusted Longev.	FLONG EBV*	+ .25 * FLONG*
AI →	pre-adjusted Fert.	FER EBV*	+ .25 * FER*
Type →	pre-adjusted type	Type EBV*	+ .25 * TYPE*

AI- REML fixing variances ← **EM-REML** → $\hat{G}$, $\hat{R}$

(Ducrocq et al, 2003, Tarrès et al, 2006
Lassen et al, 2007, *GSE*)

MT-BLUP
Model: y_{pre}= year of birth + a + e

Data for genetic parameter estimation

- AI bulls with > 10 daughters (30 for HF) with heifer fertility records
- For Holstein, extra (random) selection of one bull out of 5
- All pre-adjusted records of their daughters were included
- Estimation of genetic and residual correlations, fixing variances
- Sire model with heterogenous residual variances, AI-REML algorithm

	Daughters	Sires	Pedigree
Holstein	1,613,339	2156	7687
Montbéliarde	965,047	2204	7819
Normande	893,076	2204	6603

Type traits selection step: 1 trait at a time

Holstein

	SCC	LONG	FER
Udder support	0.05	0.12	-0.08
Udder depth	0.24	0.47	0.16
Fore Udder Att	0.08	0.25	-
Udder Height	0.05	0.26	-
Udder balance	-0.09	-0.21	-0.16
Front teat plac.	0.06	0.10	-
Teat direction	-	-	-
Teat length	-	-0.06	-0.08
Milk. Speed	-0.35	0.13	-
Stature	-	-	-0.09
Chest width	-	-0.08	-0.17

	SCC	LGF	FER
Body Depth	-0.11	-0.21	-0.35
Angularity	-0.19	-0.16	-0.31
Rump length	-	-	0.12
Rump width	-	-0.08	-0.13
Rump angle	-	0.12	0.27
Rear leg set	-0.06	-0.10	-
Rear Leg Rear	-	-	-0.13
Heel depth	0.08	-	0.11
Foot angle	-	-	-0.07
Locomotion	-	0.12	-0.11
Temperament	-0.06	-	-0.11

-	]-0.05,0.05[	[0.15,0.25[ ]-0.25,-0.15]	[0.25,0.35[ ]-0.35,-0.25]	>0.35 <-0.35

12 traits: early predictors of functional traits

Holstein

	Milk yield	Somatic cell	Longevity	Heifer Fert.	Cow Fertility
Milk yield	1				
Somatic Cell	-0.09	1			
Longevity	0.11	0.50	1		
Heifer Fertility	-0.12	0.20	0.37	1	
Cow Fertility	-0.22	0.25	0.48	0.67	1
Milking Speed	-	-0.37	0.17	0.09	
Udder depth	-0.23	0.27	0.41	-	0.14
Fore Udder	-0.13	0.07	0.21	-	-
Rump angle	0.06	-	0.13	0.18	0.24
Body depth	0.15	-0.17	-0.19	-	-0.27
Angularity	0.22	-0.22	-0.08	0.08	-0.20
Locomotion	0.12	-	0.10	-	-0.10

-	]-0.05,0.05[	[0.15,0.25[ ]-0.25,-0.15]	[0.25,0.35[ ]-0.35,-0.25]	>0.35 <-0.35

Most correlations consistent between breeds

	Holstein	Montbéliarde	Normande
➢ Longevity – SCC	0.50	0.40	0.46
➢ Longevity – Cow fertility	0.48	0.43	0.37
➢ Longevity - Udder depth	0.41	0.55	0.43
➢ Longevity – Body depth	-0.27	-0.16	
➢ Heifer – Cow fertility	0.67	0.68	0.65
➢ Milk yied – Cow fertility	-0.22	-0.22	-0.28

Main breed differences

	Holstein	Montbéliarde	Normande
➢ Milking speed - SCC	-0.37	-0.08	-0.32
➢ Milking speed - Longevity	0.17	0.42	0.21

➔ Holstein closer to (or beyond?) optimum milking speed?

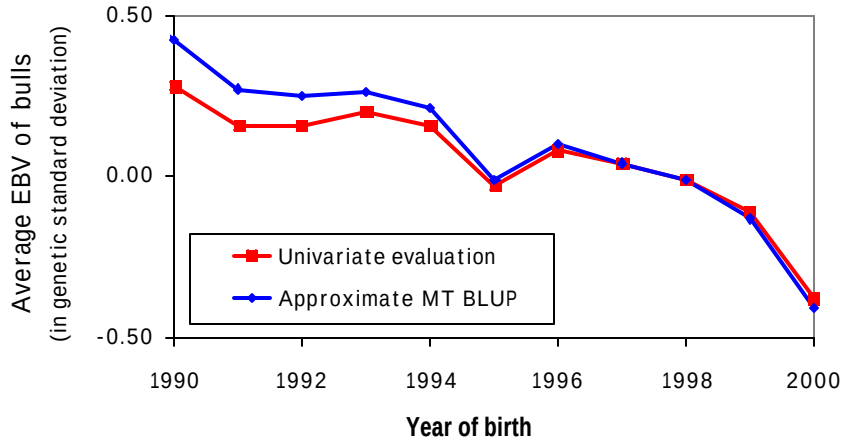
➢ Longevity – Locomotion	0.10		
- overall feet and leg score		0.26	0.21

➔ individual feet and leg traits are poor early predictors

➢ Poor type predictors of cow fertility in Montbéliarde and Normande

Influence on genetic trends

Example: Cow fertility (conception rate) in Holstein



Increase in reliability

- Example: Functional longevity of Montbéliarde AI bulls

Year of birth	Average reliability x 100		
	Univariate analysis	Increase when including other functional traits	Increase when including functional + type traits
1994	77	+1	+4
1996	73	+2	+6
1998	66	+3	+9
1999	60	+4	+12
2000	47	+6	+18
2001	37	+7	+20

Conclusion

- Official TMI for bulls and cows computed using an approximate MT BLUP animal model with 12 traits
- Holstein breed: >13 million animals evaluated
  >9 million with at least one record
- Improved functional trait evaluations for both sexes through the use of information from early predictors
- New choice of type traits as early predictors
- Consistent genetic correlations between breeds with some interesting exceptions