Genomic evaluation of dairy cattle health

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What are health and fitness traits?

- Health and fitness traits do not generate revenue, but they are economically important because they impact other traits.
- Examples:
  - Poor fertility increases direct and indirect costs (semen, estrus synchronization, etc.).
  - Susceptibility to disease results in decreased revenue and increased costs (veterinary care, withheld milk, etc.)

Increased emphasis on functional traits

Relative emphasis on traits in index (%)

Trait	PD$ 1971	MFP$ 1976	CY$ 1984	NM$ 1994	NM$ 2000	NM$ 2003	NM$ 2006	NM$ 2010
Milk	52	27	-2	6	5	0	0	0
Fat	48	46	45	25	21	22	23	19
Protein	…	27	53	43	36	33	23	16
PL	…	…	…	20	14	11	17	22
SCS	…	…	…	-6	-9	-9	-9	-10
UDC	…	…	…	…	7	7	6	7
FLC	…	…	…	…	4	4	3	4
BDC	…	…	…	…	-4	-3	-4	-6
DPR	…	…	…	…	…	7	9	11
SCE	…	…	…	…	…	-2	…	…
DCE	…	…	…	…	…	-2	…	…
CA$	…	…	…	…	…	…	6	5

Challenges with health and fitness traits

- Lack of information
  - Inconsistent trait definitions
  - No national database of phenotypes
- Low heritabilities
  - Many records are needed for accurate evaluation
  - Rates of change in genetic improvement programs are low

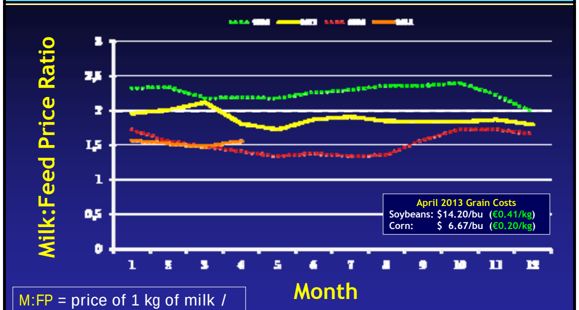
What does "low heritability" mean?

P = G + E

The percentage of total variation attributable to genetics is small.
- CA$: 0.07
- DPR: 0.04
- PL: 0.08
- SCS: 0.12

The percentage of total variation attributable to environmental factors is large:
- Feeding/nutrition
- Housing
- Reproductive management

Why are these traits important?



April 2013 Grain Costs
Soybeans: $14.20/bu (€0.41/kg)
Corn: $ 6.67/bu (€0.20/kg)

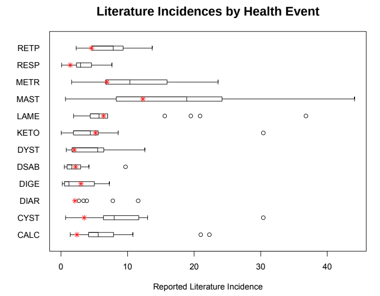
M:FP = price of 1 kg of milk / price of 1 kg of a 16% protein ration

How does genetic selection work?

$$\Delta G_{year} = \frac{\sqrt{\text{reliability}} \times \text{selection intensity} \times \sqrt{\text{genetic variance}}}{\text{generation interval}}$$

- ΔG = genetic gain each year
- reliability = how certain we are about our estimate of an animal's genetic merit (genomics can ↑)
- selection intensity = how "picky" we are when making mating decisions (management can ↑)
- genetic variance = variation in the population due to genetics (we can't really change this)
- generation interval = time between generations (genomics can ↓)

Incidence of disease in on-farm data



The red asterisk indicates the mean ID/LIR from the data over all lactations. The box plots represent the ID/LIR based on literature estimates (figure from Parker Gaddis et al., 2012, J. Dairy Sci. 95:5422–5435).

Health event data for analysis

Health event	Records	Cows	Herd-years
Cystic ovaries	222,937	131,194	3,369
Digestive disorders	156,520	97,430	1,780
Displaced abomasum	213,897	125,594	2,370
Ketosis	132,066	82,406	1,358
Lameness	233,392	144,382	3,191
Mastitis	274,890	164,630	3,859
Metritis	236,786	139,818	3,029
Reproductive disorders	253,272	151,315	3,360
Retained placenta	231,317	138,457	2,930

Genetic and genomic analyses

Single-trait genetic	Multiple-trait genetic	Multiple-trait genomic
MAST, METR, LAME, KETO, RETP, CYST, DSAB		1) MAST, METR, LAME, KETO 2) RETP. CYST, DSAB
Fixed parity, year-season		
Random sire, herd-year		
Numerator relationship matrix, A		Blended matrix, H
ASReml	THRGIBBS1F90	

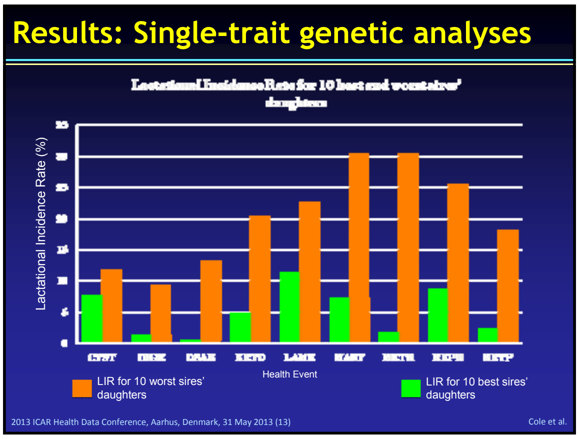
Genetic analyses included only pedigree and phenotypic data.
Genomic analyses included genotypic, pedigree, and phenotypic data.

Methods: Single-trait genetic analysis

- Estimate heritability for common health events occurring from 1996 to 2012
- Similar editing applied
  - US records
  - Parities 1 to 5
  - Minimum/maximum constraints
- Lactations lasting up to 400 days
- Parity considered first versus later

Methods: Multiple-trait genomic analyses

- Multiple-trait threshold sire model using single-step methodology (Aguilar et al., 2011)
  - THRGIBBS1F90 with genomic options
  - Default genotype edits used
    - 50K SNP data available for 7,883 bulls
    - Final dataset included 37,525 SNP for 2,649 sires



Results: Single-trait genetic analyses

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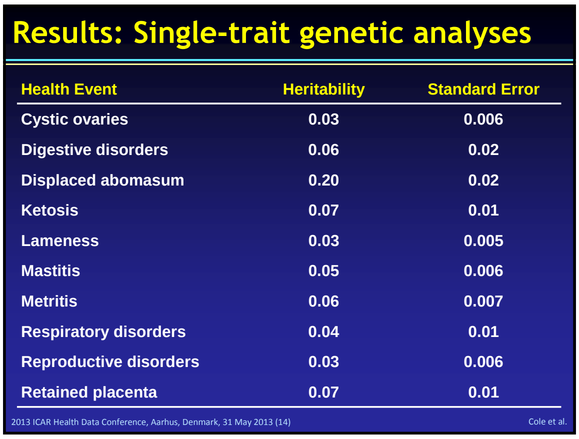

Results: Single-trait genetic analyses

Health Event	Heritability	Standard Error
Cystic ovaries	0.03	0.006
Digestive disorders	0.06	0.02
Displaced abomasum	0.20	0.02
Ketosis	0.07	0.01
Lameness	0.03	0.005
Mastitis	0.05	0.006
Metritis	0.06	0.007
Respiratory disorders	0.04	0.01
Reproductive disorders	0.03	0.006
Retained placenta	0.07	0.01

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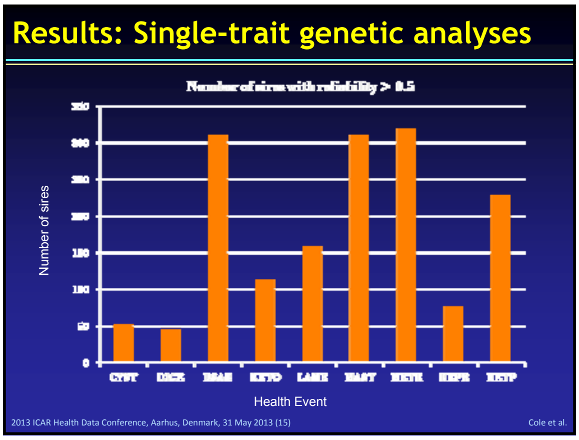

Results: Single-trait genetic analyses

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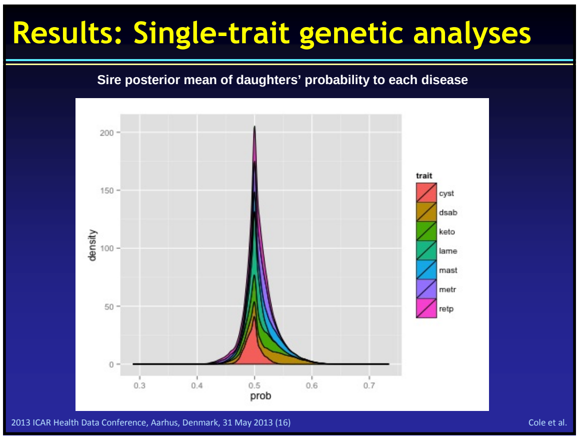

Results: Single-trait genetic analyses

Sire posterior mean of daughters' probability to each disease

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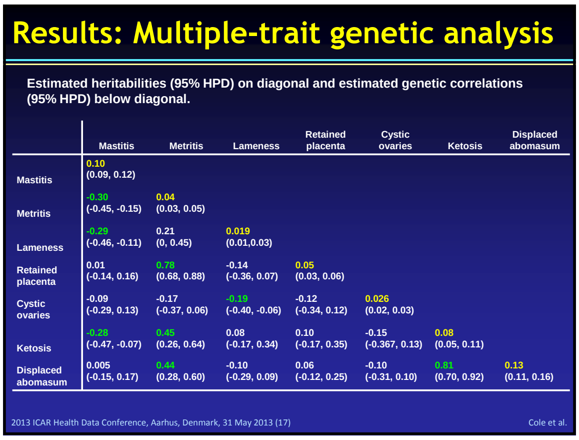

Results: Multiple-trait genetic analysis

Estimated heritabilities (95% HPD) on diagonal and estimated genetic correlations (95% HPD) below diagonal.

	Mastitis	Metritis	Lameness	Retained placenta	Cystic ovaries	Ketosis	Displaced abomasum
Mastitis	0.10 (0.09, 0.12)						
Metritis	-0.30 (-0.45, -0.15)	0.04 (0.03, 0.05)					
Lameness	-0.29 (-0.46, -0.11)	0.21 (0, 0.45)	0.019 (0.01,0.03)				
Retained placenta	0.01 (-0.14, 0.16)	0.78 (0.68, 0.88)	-0.14 (-0.36, 0.07)	0.05 (0.03, 0.06)			
Cystic ovaries	-0.09 (-0.29, 0.13)	-0.17 (-0.37, 0.06)	-0.19 (-0.40, -0.06)	-0.12 (-0.34, 0.12)	0.026 (0.02, 0.03)		
Ketosis	-0.28 (-0.47, -0.07)	0.45 (0.26, 0.64)	0.08 (-0.17, 0.34)	0.10 (-0.17, 0.35)	-0.15 (-0.367, 0.13)	0.08 (0.05, 0.11)	
Displaced abomasum	0.005 (-0.15, 0.17)	0.44 (0.28, 0.60)	-0.10 (-0.29, 0.09)	0.06 (-0.12, 0.25)	-0.10 (-0.31, 0.10)	0.81 (0.70, 0.92)	0.13 (0.11, 0.16)

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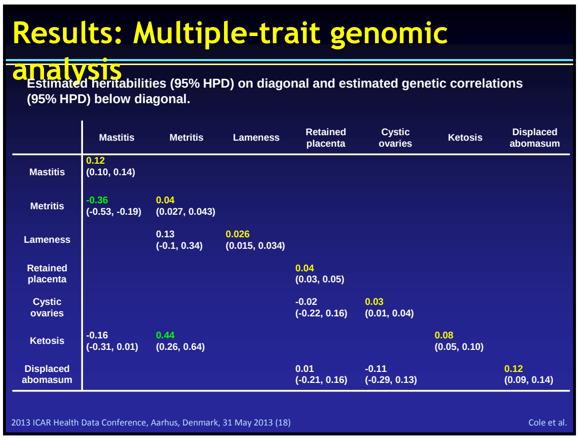

Results: Multiple-trait genomic analysis

Estimated heritabilities (95% HPD) on diagonal and estimated genetic correlations (95% HPD) below diagonal.

	Mastitis	Metritis	Lameness	Retained placenta	Cystic ovaries	Ketosis	Displaced abomasum
Mastitis	0.12 (0.10, 0.14)						
Metritis	-0.36 (-0.53, -0.19)	0.04 (0.027, 0.043)					
Lameness		0.13 (-0.1, 0.34)	0.026 (0.015, 0.034)				
Retained placenta				0.04 (0.03, 0.05)			
Cystic ovaries				-0.02 (-0.22, 0.16)	0.03 (0.01, 0.04)		
Ketosis	-0.16 (-0.31, 0.01)	0.44 (0.26, 0.64)				0.08 (0.05, 0.10)	
Displaced abomasum				0.01 (-0.21, 0.16)	-0.11 (-0.29, 0.13)		0.12 (0.09, 0.14)

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Reliability with and without genomics

Mean reliabilities of sire PTA computed with pedigree information and genomic information, and the gain in reliability from including genomics.

Event	EBV Reliability	GEBV Reliability	Gain
Displaced abomasum	0.30	0.40	+0.10
Ketosis	0.28	0.35	+0.07
Lameness	0.28	0.37	+0.09
Mastitis	0.30	0.41	+0.11
Metritis	0.30	0.41	+0.11
Retained placenta	0.29	0.38	+0.09

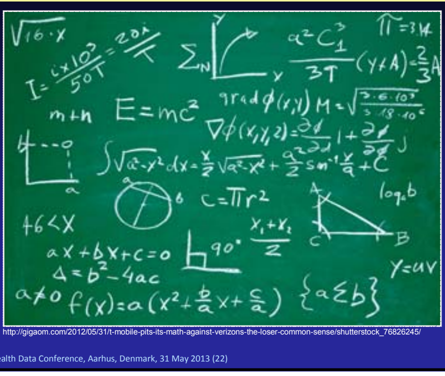
What do we do with these PTA?

- Focus on diseases that occur frequently enough to observe in most herds
- Put them into a selection index
- Apply selection for a long time
  - There are no shortcuts
- Collect phenotypes on many daughters
  - Repeated records of limited value

Conclusions

- The data stored in on-farm computer systems are useable for genetic evaluation
- We can compute PTA for bulls with many daughters
  - Genomics improves reliabilities
- Multiple-trait analysis may help improve reliabilities

Questions?



http://gigaom.com/2012/05/31/t-mobile-pits-its-math-against-verizons-the-loser-common-sense/shutterstock_76826245/