Genomic Data and Cooperation Result in Faster Progress

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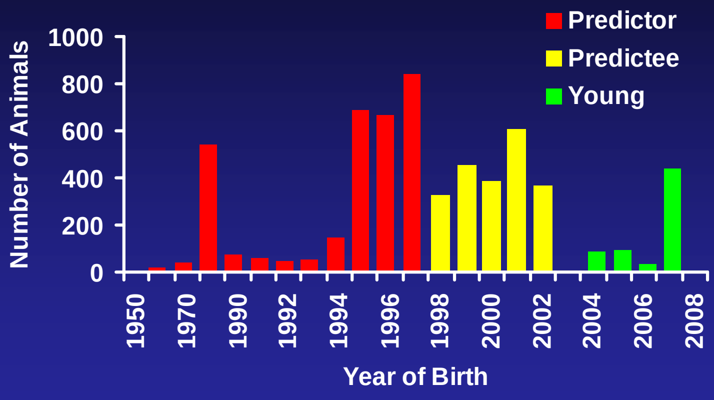
Experimental Design

- Predict April 2008 daughter deviations from August 2003 PTAs
  - Similar to Interbull trend test 3
  - 3576 older Holstein bulls
  - 1759 younger bulls (total = 5335)
- Genomic predictions computed for 27 traits: 5 yield, 5 health, 16 conformation, and Net Merit

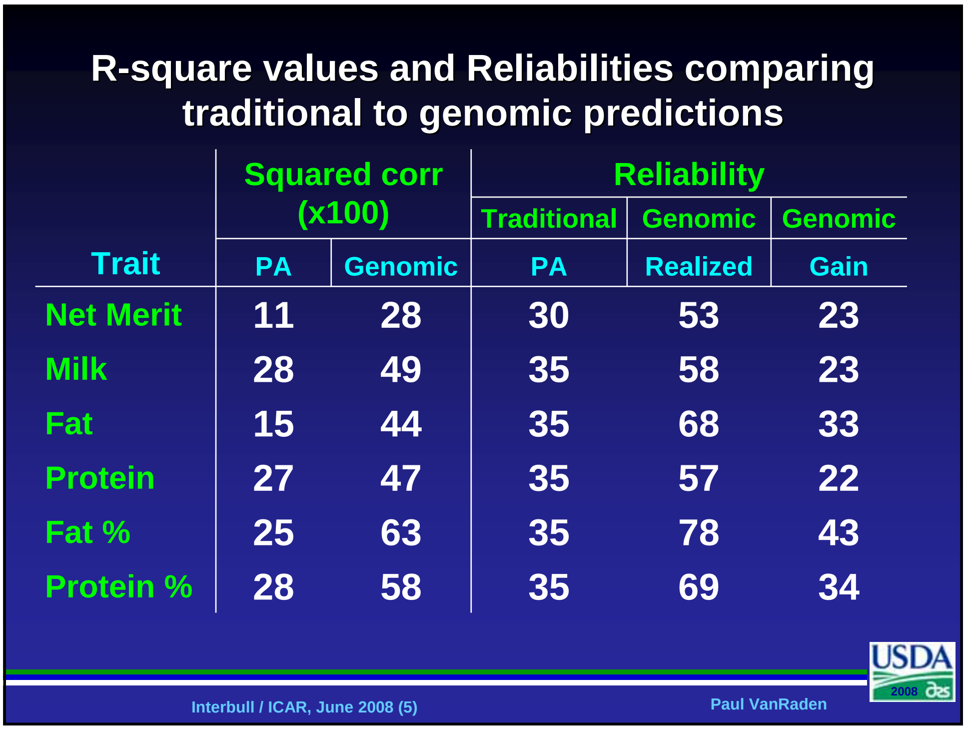
Genotyped Animals (n=6005)

As of April 2008



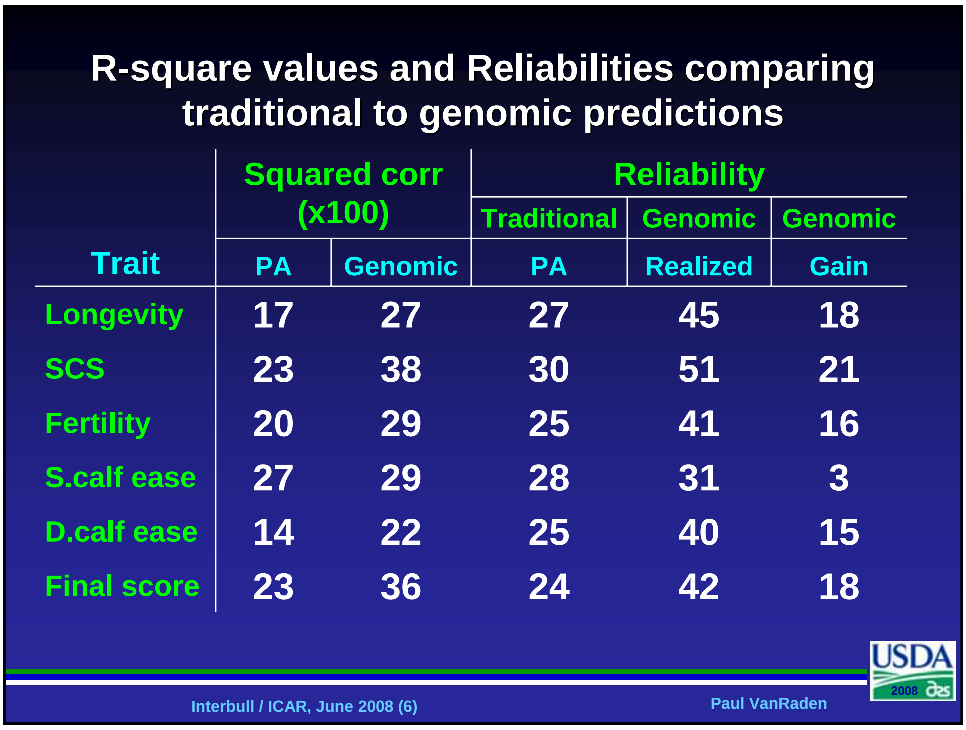
Genomic Data and Methods

- **38,416** markers for each bull
- **Direct** genomic evaluation
  - Inversion for linear prediction, REL
  - Iteration for nonlinear prediction
- **Combined** genomic evaluation
  - 3 x 3 selection index combining direct genomic PTA, traditional PA or PTA, and subset PA or PTA by REL



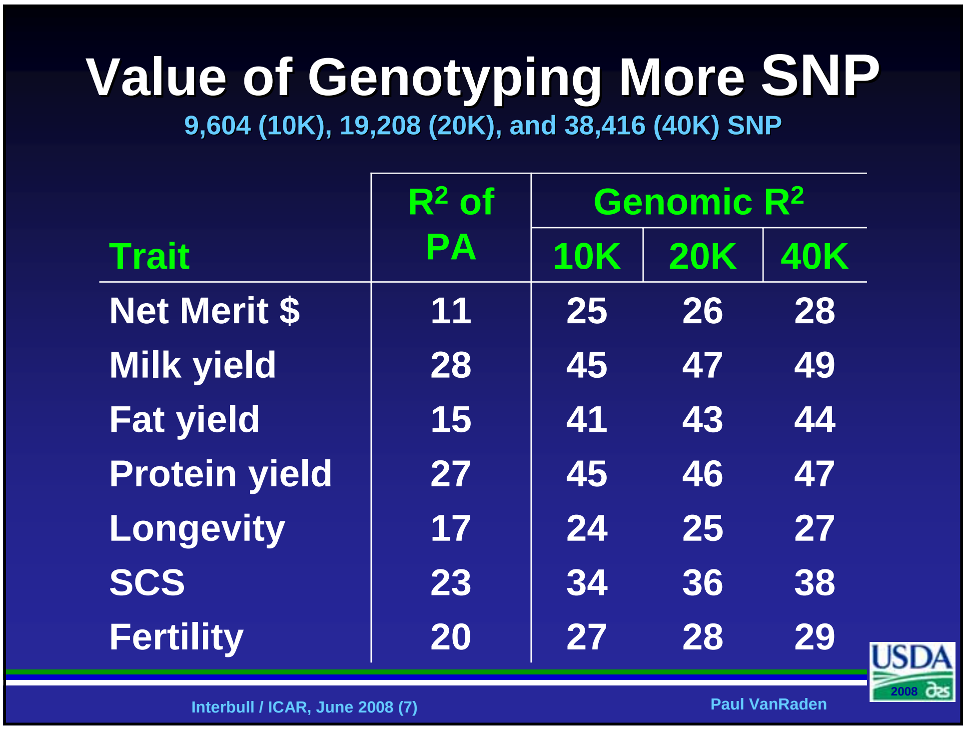
R-square values and Reliabilities comparing traditional to genomic predictions

	Squared corr (x100)		Reliability		
			Traditional	Genomic	Genomic
Trait	PA	Genomic	PA	Realized	Gain
Net Merit	11	28	30	53	23
Milk	28	49	35	58	23
Fat	15	44	35	68	33
Protein	27	47	35	57	22
Fat %	25	63	35	78	43
Protein %	28	58	35	69	34



R-square values and Reliabilities comparing traditional to genomic predictions

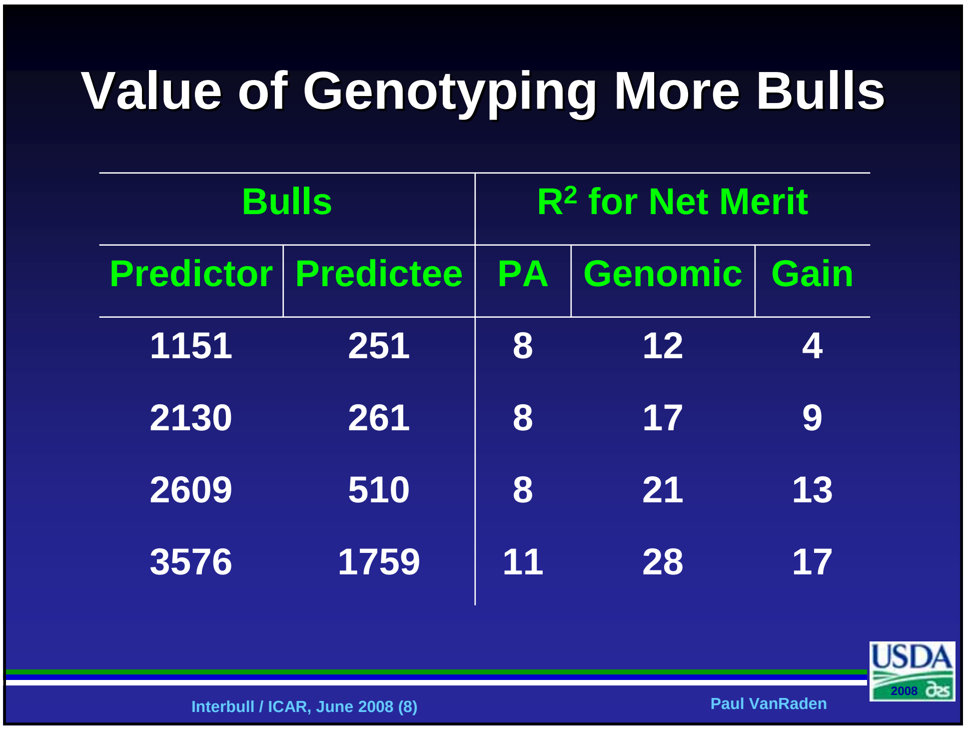
	Squared corr (x100)		Reliability		
			Traditional	Genomic	Genomic
Trait	PA	Genomic	PA	Realized	Gain
Longevity	17	27	27	45	18
SCS	23	38	30	51	21
Fertility	20	29	25	41	16
S.calf ease	27	29	28	31	3
D.calf ease	14	22	25	40	15
Final score	23	36	24	42	18



Value of Genotyping More SNP

9,604 (10K), 19,208 (20K), and 38,416 (40K) SNP

Trait	R^2 of PA	Genomic R^2		
		10K	20K	40K
Net Merit $	11	25	26	28
Milk yield	28	45	47	49
Fat yield	15	41	43	44
Protein yield	27	45	46	47
Longevity	17	24	25	27
SCS	23	34	36	38
Fertility	20	27	28	29



Value of Genotyping More Bulls

Bulls		R^2 for Net Merit		
Predictor	Predictee	PA	Genomic	Gain
1151	251	8	12	4
2130	261	8	17	9
2609	510	8	21	13
3576	1759	11	28	17

Expected vs Observed Reliability

- Reliability for predictee bulls
  - Traditional PA: 27% average across traits
  - Genomic: 63% expected vs. 50% observed
  - Observed range 78% (fat pct) to 31% (SCE)
  - PTA regressions .8 to .9 of expected
- REL and PTA adjustments
  - Multiply genomic daughter equivalents by .7 to make expected closer to observed
  - For example, 16 * .7 = 11
  - Include polygenic effect, less than 5%

Simulated Results

World Bull Population

- 15,197 older and 5,987 younger bulls from all countries in Interbull file
- 40,000 SNP and 10,000 QTL (heavy tail)
- Provided timing, memory test
- Reliability vs parent average REL
  - REL = corr^2 (EBV, true BV)
  - 80% vs 34% expected for young bulls
  - 72% vs 30% observed in simulation

Genetic Progress

- Assume 60% REL for net merit
  - Sires mostly 2 instead of 6 years old
  - Dams of sons mostly heifers with 60% REL instead of cows with phenotype and genotype (66% REL)
- Progress could increase by >50%
  - 0.37 vs. 0.23 genetic SD per year
  - Reduce generation interval more than accuracy

Conclusions

- Genomic predictions significantly better than parent average ($P < .0001$) for all 27 traits tested
- Gains in reliability equivalent on average to 11 daughters with records
  - Analysis used 3576 historical bulls
  - April data included 5285 proven bulls
- R^2 increases with more bulls and SNPs

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