

## Future Animal Improvement Programs Applied to Global Populations

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## Topics

- Brief history of past improvement programs
- National and global goals
- Genetic x environment interaction
- International genomic evaluation
  - Exchange of GEBVs or genotypes
- Use of new reproductive tools

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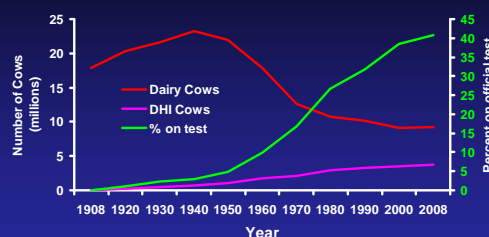
## Step 1: Collect Data

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## Cows Tested 1908-2008



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## Step 2: Analyze Data Bull proof (pounds) from 1916

	Dtr Milk	Dtr Fat	Dam Milk	Dam Fat
1	6976	276	4422	171
2	8602	292	5976	217
3	7631	280	1923	84
4	6640	248	4011	147
5	7121	253	5492	198
6	6901	298	6123	248
7	6622	236	5048	190
Avg	7580	282	5426	206

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## Traits Evaluated by U.S. and Interbull

Trait	USA	ITB	Trait	USA	ITB
Milk, fat	1936	1995	Calving	2000	2005
Protein	1978	1995	Stillbirth	2006	2005
Conf.	1978	1999	Fertility	2003	2007
Cell count	1994	2001	M speed	???	2009
Longevity	1994	2004	???	???	???

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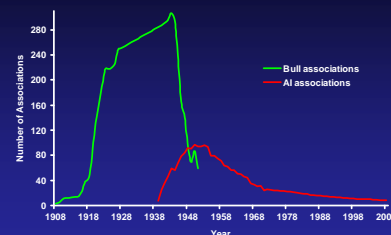
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### Step 3: Select Animals



### Number of U.S. Bull Associations



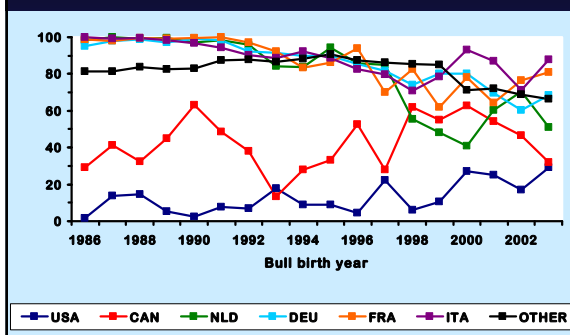
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### Percent Bulls with Foreign Sire

Powell et al, 2009 JDS (abstract)



### Global Scale, Global Index

Powell and VanRaden, 2002 JDS 85:1863

- **Advantages**
  - Much simpler foreign marketing
  - Focus on international economics
  - Weighted average of national goals
- **Disadvantages**
  - Less national progress if  $\text{corr} < 1.0$
  - Removes "home field" advantage (removes protectionism)

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### Current EBV Exchange



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### Tropical Breeding Programs

- **Traits** needed by tropical cattle
  - Tolerate heat and humidity
  - Consume low cost forage or pasture
  - Resist parasites and disease
- **Parameters** needed for prediction
  - $\text{Corr}$  (tropical, temperate) performance
  - $\text{Corr}$  among tropical environments
  - Can 1 tropical breed fit many markets?
  - Is Taurus / Indicus recombination loss too large to use synthetics? (Rutledge, 2001)

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## Genotype by Environment Interaction

Zwald et al, 2003 JDS 86:376

- Model **environment** or **country**?
  - GxE exists within large countries
  - Little GxE for neighbor countries
  - Requires central control of all data
- Factors affecting **global GxE**
  - Temperature, rainfall, herd yield, herd size, persistency, calving age, seasonal calving



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## Genotype by Environment within USA

- Include GxE regressions in national models
  - Heat tolerance
  - High / low input herds
- Extrapolate to more extreme environments outside USA
  - Coefficients of regressions larger
  - Changes in rank will be magnified

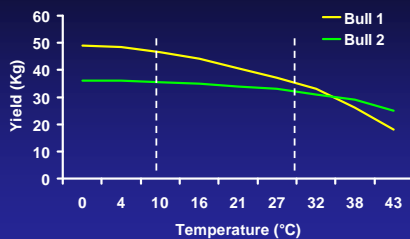


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## Heat Tolerance

Ravagnolo and Misztal, 2000



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## Step 4: Genomics

- **Actual** results
- **International** genomic evaluation
  - Simple conversion formulas
  - Exchange of genomic EBVs via G-MACE
  - Multi-country exchange of genotypes
- **Future** chips



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## Actual 50K Results

- Correlation of predicted Mendelian sampling from Nov 2004 and actual from Aug 2009 is about .5
- Bull with highest predicted Net Merit in Nov 2004 is now ranked 4<sup>th</sup> of 1925 for NM\$ phenotype (Man O Man)
- Highest predicted Net Merit in Jan 2009 now 2nd for NM\$ phenotype (Freddie)



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## Genotype Exchange Options

- **Country pairs** exchange genotypes
  - Each computes GEBVs using joint data
  - Small countries get GEBV from large
- **All countries** combine genotypes
  - One or many copies of genotype file?
  - Centralized or decentralized GEBV service?
  - How many genotypes must each submit?
  - How many phenotypes must each submit?
  - Are GEBVs on 25 scales really needed?



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## Genomic Evaluation - GMACE

- Exchange **GEBVs** (not genotypes)
  - Each country computes GEBVs separately
  - GMACE accounts for any data sharing
  - GEBVs from different countries have residual correlations due to common bulls
- Similar to **conventional MACE**
- Less benefit than combining genotypes



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## Multi-Country Combined Genotypes

- **Evaluation options**
  - Foreign data included via MACE, then single-trait genomic evaluation, **OR**
  - Domestic and foreign data evaluated using multi-country genomic model
- **Advantages of multi-trait model**
  - Phenotypic and genomic both multi-trait
  - Domestic data weighted more than foreign
  - More accurate ranking than G-MACE



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## Multi-Country Computation with combined genotype files

- **USA-CAN, 2 trait model**
  - 10,129 HO with data, 11,815 without
  - Block-diagonal solver converged in 250 iterations (similar to single-trait)
  - 11 hours using 2 processors
- **Global Brown Swiss, 9 countries**
  - All 8,073 proven bulls simulated
  - 30 hours using 9 processors



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## Proven Bull Reliability

Simulated BS bulls on home country scale

Country	Traditional		Genomic	
	Nat'l	MACE	Nat'l	Multi-trait
<b>DEU</b>	81	82	84	84
<b>CHE</b>	91	91	91	92
<b>USA</b>	80	81	83	88
<b>CAN</b>	71	86	72	90



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## Young Bull Reliability

120 simulated BS bulls sampled in USA

Country	Traditional		Genomic	
	Nat'l	MACE	Nat'l	Multi-trait
<b>DEU</b>	4	11	64	69
<b>CHE</b>	14	17	65	73
<b>USA</b>	20	20	55	70
<b>CAN</b>	1	14	9	61



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## Holstein Simulation Results

World population, single-trait methods

- 40,360 older bulls to predict 9,850 younger bulls in Interbull file
- **50,000** or **100,000 SNP**; 5,000 QTL
- Reliability vs. parent average REL
  - Genomic REL =  $\text{corr}^2(\text{EBV}, \text{true BV})$
  - **81% vs 30%** observed using **50K**
  - **83% vs 30%** observed using **100K**



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## Lower and Higher Density Chips

- **384 marker** low-cost assay
  - 96 parentage + 288 selected for Net Merit \$
  - Available in fall 2009
- **600,000 marker** chip
  - Expected to be available in 2010
- **3 billion full sequence** of individual
  - Blackstar (most related to HO breed)
  - Already done by USDA Bovine Functional Genomics Lab



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## Embryo Selection

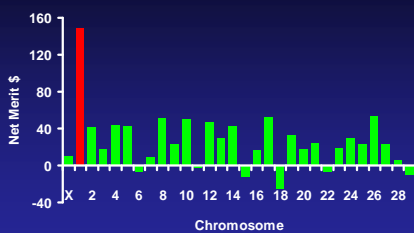
- **In vitro embryos** from heifers before puberty
  - Further reduce generation interval
- **Frozen, genotyped embryo** market
  - Cost of genotyping < cost of ET
  - Could replace AI if accuracy high
- **Very rapid generation turnover**
  - Velogenetics not yet feasible



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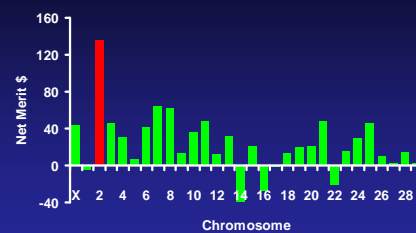
## Best Chromosome 1 Co-Op Boliver Lisha



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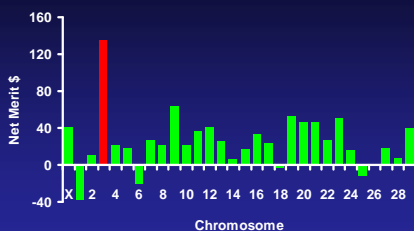
## Best Chromosome 2 Kellercrest Earnit Hank



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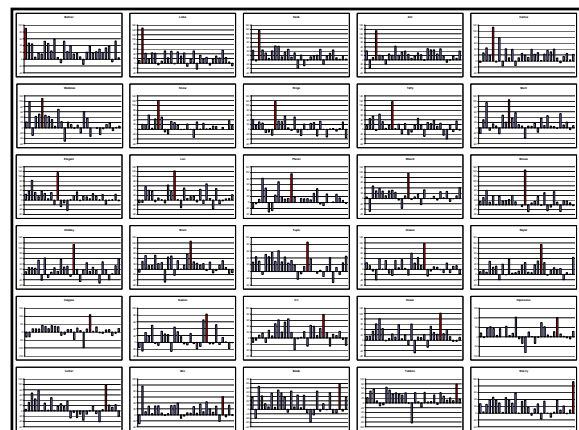
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## Best Chromosome 3 Wesselcrest Sidney Aric



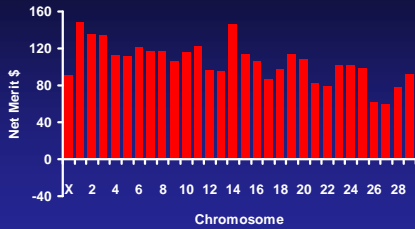
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## Best Chromosomes 1-30

Genomics Extraordinaire, +3148 Net Merit \$



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## Step 5: Crossbreeding

- **Composite** population
  - Select best alleles from any breed
  - Increase genetic SD, long term gain
- **Perpetual F1** crossbred
  - For example, JE x HO F1 embryos inserted into JE x HO F1 cows
  - Maximize heterosis and uniformity
  - Similar to breeding of hybrid corn

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## Step 6: Transgenics

Brophy et al, 2003, Wall et al, 2005

- Insert **polled** gene into **horned** cow
  - Faster than traditional breeding
  - Are resulting animals transgenic?
  - Similar events occur naturally
- Insert desired genes from **different species**
  - Large investment needed to prove safe
  - Global marketing will be difficult because of within-country politics

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## Breeding Companies

- **Poultry, swine**
  - **Closed**, private breeding populations
  - Central control and vertical integration
- **Dairy, beef cattle**
  - **Open** exchange of breeding stock
  - Producers choose using genetic rankings
- Almost no patents or intellectual property

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## Conclusions

- Local data collection and selection programs have become international
- **Global** genomic evaluations possible
  - Conversion formulas for young bulls
  - G-MACE to exchange GEBVs
  - Multi-country genomic evaluation increases reliability
- Advanced technologies require more investment and organization

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## Acknowledgments

- **Interbull Genomics Task Force** for ideas on global evaluation
  - Pete Sullivan, Georgios Banos, Esa Mantysaari, Mario Calus, Vincent Ducrocq, Zengting Liu, Hossein Jorjani, and João Dürr
- **Tabatha Cooper** for preparing slides on individual chromosome selection