EAAP meeting 2009

Next generation genetic evaluations for European cattle population

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Outline

- Short description
    - ICAR
    - Interbull
- Status quo of genetic evaluation in Europe
- Current developments in methods
    - Genomic evaluation
- International implications
- Outlook

ICAR

- International Committee for Animal recording
  - World wide organisation for standardisation of animal recording and productivity evaluation
  - Aims:
    - promote improvement of farm animal recording and evaluations
    → formulation of definitions and standards for measurement of traits of economic importance

Interbull

- duties
  - Communication: Publications, meetings, workshops, homepage
  - Technology support to ‚members‘ (→ genetic evaluation units)
  - Conduct R&D
  - International genetic evaluations (since 1994)

Interbeef

- Research project within Interbull/ICAR → feasibility of international genetic evaluation for beef cattle

Genetic evaluation in Europe, Status quo

- Integrated systems on national scale

  ~ 1980 - 1990 → one genetic evaluation unit (GEU) per country (1-3 geneticists)
    - GEU attached to
      - Data centres
      - Herdbook organisations
      - Animal Research institutes / universities
      - State ministries of agriculture

- More complex methods from ~1995
  - Test day models
  - Survival analysis
  - Marker assisted BLUP

  → Need for more effcient systems = collaboration

  - Joint genetic evaluations (5-8 geneticists)
    - DEU/AUT/LUX
    - NLD/FLA
    - DNK/FIN/SWE

Genetic evaluation in Europe, Status quo II

- Strong interest in collaboration within Interbull
  - Exchange of knowledge with the Interbull framework
  - Compare individual bull EBVs across countries
    → Via Interbull Multiple Across Country Evaluation (MACE)
  - Since 1996 Interbull Centre is reference laboratory of bovine genetics for the EC

- Quantity and quality of
  - Pedigree data
  - Phenotypic data on nearly all traits of economic importance

led to an high standard of genetic evaluations in Europe

→ Intensive use of the portfolio of Interbull (not only production and type)

→ Total Merit Indexes are widely used

Portfolio of Interbull evaluations

1995	Production						
1999	Production	Type					
2001	Production	Type	Cellcount				
2004	Production	Type	Cellcount	Longevity			
2005	Production	Type	Cellcount	Longevity	Calving		
2007	Production	Type	Cellcount	Longevity	Calving	Fertility	
2008	Production	Type	Cellcount	Longevity	Calving	Fertility	Workability

Current developments in methods

- Status quo of the methods
- Incoporation of Genomics

Selection from about 1960 to ~ 2000

- Quantitative-genetic concepts
  - (Wright, Lush, Henderson)
    -> additiv genetic model

- Genetic evaluation
  - Separate phenotypic observations (eg 9850 kg milk) in
    - additiv genetic effect → estimated breeding value (eg. + 1430 kg M)
    - Systematic environmental effect
    - Residual effect

- Ranking based on estimated breeding values (EBVs)

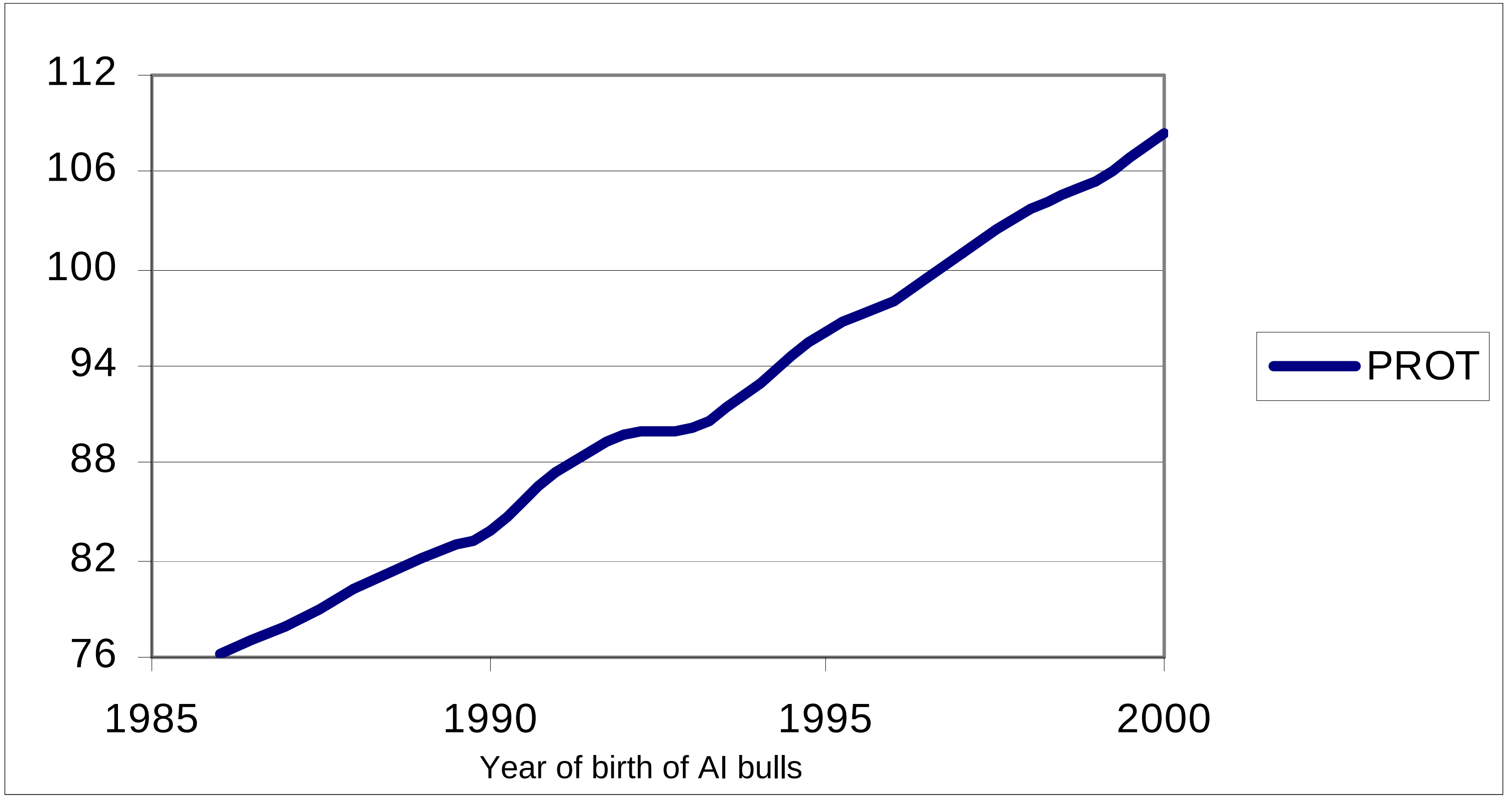
Selection on EBVs

- Necessary elements
  - Phenotypic observations
    - Milk yield, somatic cell counts, type traits, etc.
  - Pedigree data
  - Data structure (across herds/environments)
    - Artificial insemination gives optimal structure to estimate EBVs that rank the animals best and unbiased in many environments
  - Algorithms (Henderson, Schaeffer&Kennedy, Misztal, etc) and computing power
    - ➔ BLUP methodology, which result in highly reliable EBVs (85-99%) for bulls with a **progeny test of 100-150 daughters**
    - ➔ Transformation of these EBVs since 15 years via Interbull MACE
      - ➔ **Bulls that are marketed worldwide**
        - ➔ **Intensively used**

Genetic trend in Holstein bulls

(MACE Evaluation Interbull, Holstein AI bulls (50,000);
Mean = 100, SD = 10; Data Sept. 2007, Berglund, 2008)

EBV



PROT=Protein yield

Jorjani, 2008

but

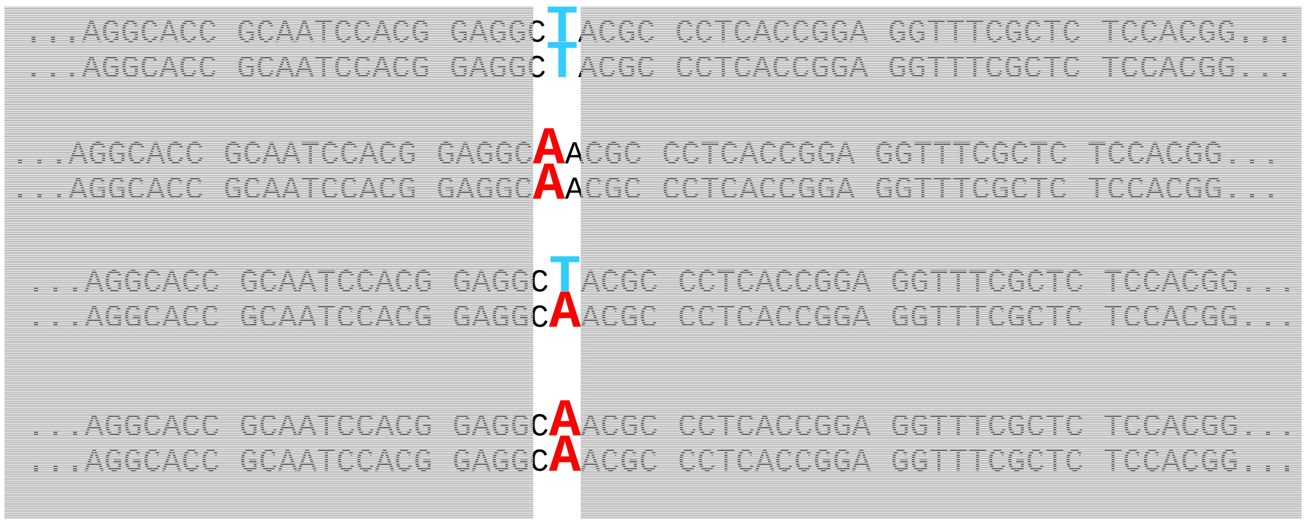
- Genetic gain / costs
  - High generation interval due to progeny test
    - ➔Expensive
    - ➔Genetic gain per year not very high
  - Reliability of a pedigree index (=0,5 EBV sire + 0.5 EBV dam) is low (25 – 35%)
    - Max r^2 PI = 50% -> both parents r^2 = 100%
    - Rest of 50% -> Mendelian sampling
  - Reliability of a cow EBV < lower as r^2 of a bull EBV

- Aim:
  - Increase the reliability of EBVs of young animals

- Solution → use of genomic informationn

SNP - genotyping

- SNP = Single-nucleotide polymorphism
- Genotype = Which alleles of the nucleotides **A-T,C-G** an animal carries
- Genome = contains 3 billion base pairs
- Ca. 50.000 SNPs at a cost of about 200 EUR



		Genotype:
Anim. 1:	...AGGCACC GCAATCCACG GAGGCTACGC CCTCACCGGA GGTTTCGCTC TCCACGG... ...AGGCACC GCAATCCACG GAGGCTACGC CCTCACCGGA GGTTTCGCTC TCCACGG...	**TT**
Anim. 2:	...AGGCACC GCAATCCACG GAGGCAACGC CCTCACCGGA GGTTTCGCTC TCCACGG... ...AGGCACC GCAATCCACG GAGGCAACGC CCTCACCGGA GGTTTCGCTC TCCACGG...	**AA**
Anim. 3:	...AGGCACC GCAATCCACG GAGGCTACGC CCTCACCGGA GGTTTCGCTC TCCACGG... ...AGGCACC GCAATCCACG GAGGCAACGC CCTCACCGGA GGTTTCGCTC TCCACGG...	**AT**
Anim. n:	...AGGCACC GCAATCCACG GAGGCAACGC CCTCACCGGA GGTTTCGCTC TCCACGG... ...AGGCACC GCAATCCACG GAGGCAACGC CCTCACCGGA GGTTTCGCTC TCCACGG...	**AA**

Eg position on chromosome 6 # 43.675.239

Use in practical application

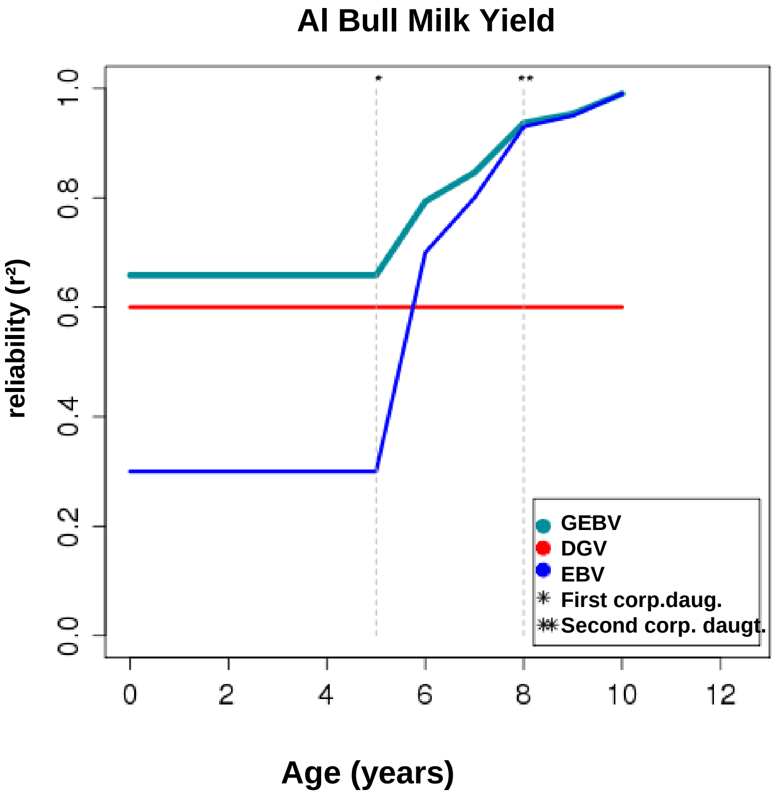
- Lab is an important part, BUT
  SNP data has per se no information on ‚traits‘

Steps:

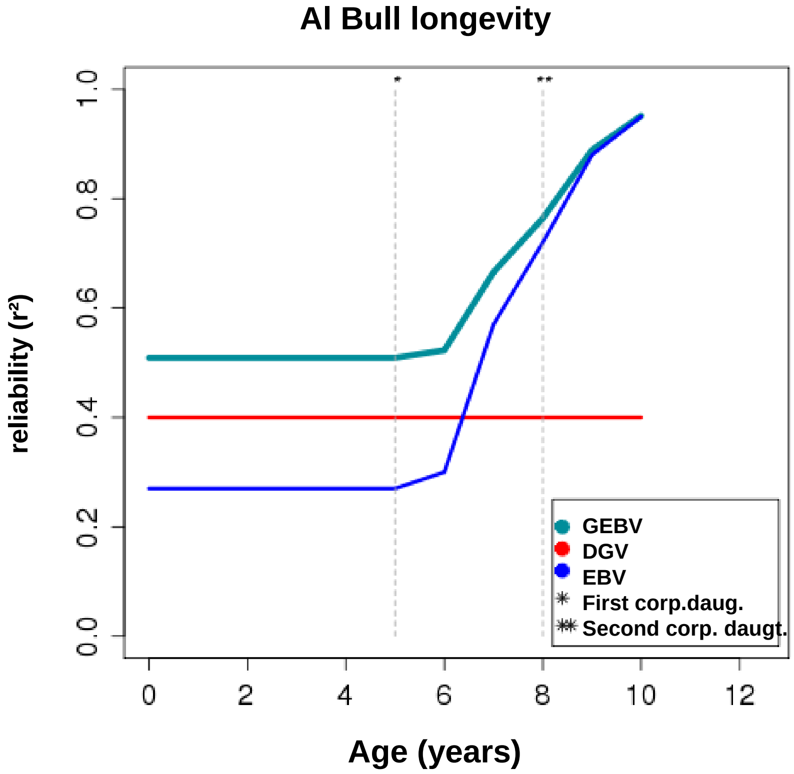
- Genotype animals that have reliable EBVs from ‚conventional‘ genetic evaluation
- Calculate regression formulas so that SNPs explain well the conventional EBV
- Use the regression formulas derived by historic data to evaluate young animals
- Select among these young animals

→ Genetic gain doubled

Increase in reliability of the BVs for AI bulls



AI Bull Milk Yield



AI Bull longevity

Potential of genomic evaluation

- **Genomic evaluation is a very useful additional tool, but it can only be used if**
  - **Sophisticated conventional genomic evaluation**
    - **Large amount of phenotypic data is collected on all traits of interest**
    - **Reliable pedigree information**

- **Full potential of genomic selection can only be gathered if MORE phenotypic data is collected**
  - **Functional traits (well defined eg by the ICAR WG ‚Functional Traits‘)**
  - **New traits → e.g. composition of milk**

Collaboration is key factor

Areas for future research

- Optimal statistical model
- Combination of conventional EBVs and direct genomic EBVS (DGV) → genomic EBVS (GEBVs)
- Bias due to preselection of bulls on GEBVs in conventional genetic evaluation
- More dense SNP chips
- Structure and size of reference population
    - Pooling of reference samples across countries
- (Best use of GEBVs in breeding programes)

Size of reference sample, van Raden, IB meeting, Jan 2009

Gain in reliability over PA in US (shared genotypes with Canada)

	Bulls		Reliability Gain	
	Predictor	Predicted	NM$	27 trait avg
	2130	261	13	**17**
	2609	510	17	**18**
Cows:	**3576**	1759	23	**23**
947	**4422**	2035	20	**28**
1916	**6184**	7330	31	**30**

International Comparisons

- **Status Quo (progeny tested bulls):**
  - BLUP national genetic evaluations
    - highly reliable EBVs (85-99%) for bulls with a **progeny test of 100-150 daughters**
  - BLUP national genetic evaluations
    - Transformation of these EBVs since 15 years via Interbull MACE

      ➔**Bulls that are marketed worldwide**

- **Genomic evaluation**
  - Young bulls have reliabilities of 60-65%
    - ~10-15 daughters
    - GEBVs on the national scale (exporting country)

- **How well does genomic evaluation work**
- **How to compare these bulls (GEBVs) internationally?**

Interbull / ICAR meeting 27.1. - 30.1.2009

- Interbull workshop (27. - 28.1.2009, 101 participants)
  - Report Task Force (→ 7 experts from genetic evaluation centres)

Results Interbull Workshop 27.1. - 28.1.2009

- Report Task Force Genomic Evaluation
  - Methodology works
  - but: assignment of an unbiased reliability measure for the genomic EBVs is not achieved yet → clear tendency to overestimate the r²
    - Approximation of r²:
      use prediction formula for group of bulls with genotypes and conventional EBVs, but were **not** part of the reference population
      → basis of validation procedure

- Urgent need for Interbull validation procedure
  - Genomic evaluation system → unbiased DGV and GEBV
  - Unbiased r² for DGV and GEBV

  → Both relevant for approval within EC

- Urgent need for Interbull services to transform GEBVs

International Comparisons of GEBVs

1. **Conversions via conversion formulas**
   - GEBVimport = A + b*GEBVexport
     - Undesirable solution, large regression effect, no G*E interaction considered

2. **GMACE**
   - Like MACE, GEBV instead of EBVs
     - desirable solution, considerable regression effect, G*E interaction considered

3. **Use of importing countries formula**
   - Statistically best solution
     - Prerequisite: importing countries genetic evaluation unit allows incorporation of foreign genotypes

1. and 2. can only be done within Interbull framework

3. Bilateral or within Interbull

Outlook

- Enourmeous development of the methodology during the last years

- North America / Ozeania have been very fast in incorporation of genomics
  - Large amount of public funding
  - Europe → delay 1-2 years
    - Need to avoid similar situation in future
      → high density chips, low density chips etc.

- Make best use of good infrastructure in Europe
  - Investment in collection of phenotypic data for ‚new' traits

- Dairy cattle breeding is still a farmers owned business
  - Risk that agribusiness companies take over control due to new technologies

Summary

- Genomics leads to significant changes in genetic evaluation
- Significant changes also in structure of breeding programes
- Clear need for more collaboration within Europe
  - Best done in the Interbull/ICAR framework
- ICAR / Interbull allow cooperation also on a world wide basis with other continents where needed

Thank you for your attention