Programe

Welcome and Introduction R. Reents

1. 13:40 – 14:10 Bull selection strategies L. Schaeffer
2. 14:10 – 14:25 Genomic selection in New Zealand, B. Harris
3. 14:25 – 14:40 Incorporation of genotype effects E. Baruch ??
4. 14:40 – 14:55 Genomic data and cooperation, P van Raden
5. 14:55 – 15:10 Genomic evaluations in the US G. Wiggans
6. 15:10 – 15:20 Distribution and location of genomic effects J. Cole
7. 15:20 – 15:30 Genomic evaluation in Holland R. van der Linde

Paper of Woodward was moved to the next IB session (16:30)

15:30 – 16:00 Diskussion

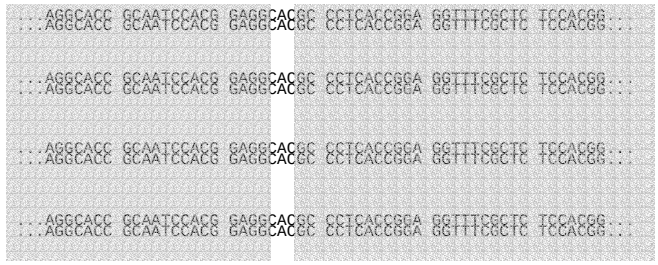
Joint session from ICAR and Interbull

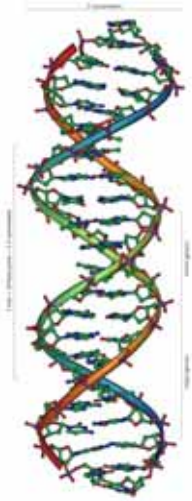
- 1st time two joint sessions of ICAR and Interbull
  - Use of Genomic Tools in Animal Breeding
  - Impact of New Technologies on Performance Recording and Genetic Evaluation
- Aim: Present and discuss topics that are of relevance for both organisations

Introduction

- Structure and function of Chromosomes known since 1953 ➔
  - Watson and Crick

Tier 1:
Tier 2:
Tier 3:
Tier n:





- Statistical models to estimate breeding values (EBV) used
  - Lush, Wright, Henderson etc.

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‚Conventional' genetic evaluation

- Elements
  - Pedigree data
  - Performance data
    - Production, type etc
  - Arteficial insemination
    - Datastructure for across herd genetic evaluation
  - Computing power and algorithms

    ➔ BLUP procedures, that give very reliable EBVs from bulls after a progeny test (95 –99 % reliability)

- Very sucessfull tool in the last 40 years
  - These results for individual bulls have been input to Interbull, that converted the figures from country of first test to foreign scales

but

- Expensive
- EBV of young animals ➔ parent agerage (PI) r^2 ~ 30 - 40%
- R^2 of cows much lower than bulls

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Very recent ➔ genotyping of single nucleotid polymorphisms (SNP)

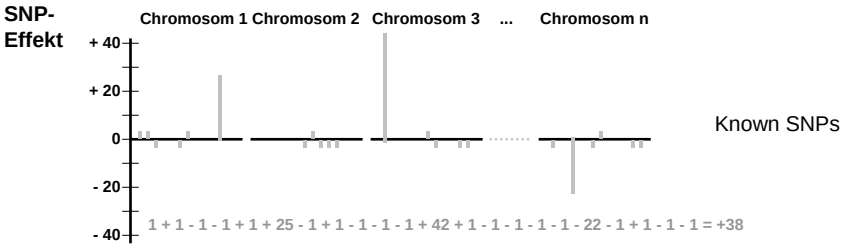
- Genotyp = „Allels“ at a given location
- State of the art technology
  ➔ ~ 50.000 SNPs from an individual animal for 200 EUR

e. g. Position: Chromosom 6 # 43.675.239

Practical application

- 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
  - r^2 significantly higher than parent average
  - r^2 of cows same as bulls
- Select among these young animals

Genomic breeding value



Genomic evaluation will come

But

- Performance recording ?
- Pedigree data ?
- Ownership of information ?
- Which kind of collaboration to make best use of this new technology ?
- Marketing of animals with genomic evaluations in foreign countries ?
- Role of Interbull ?
- ...

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