

*Will Genomics solve our problems?*

# Influence of the Environment

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# Genomic Selection: Revolution in dairy cattle breeding

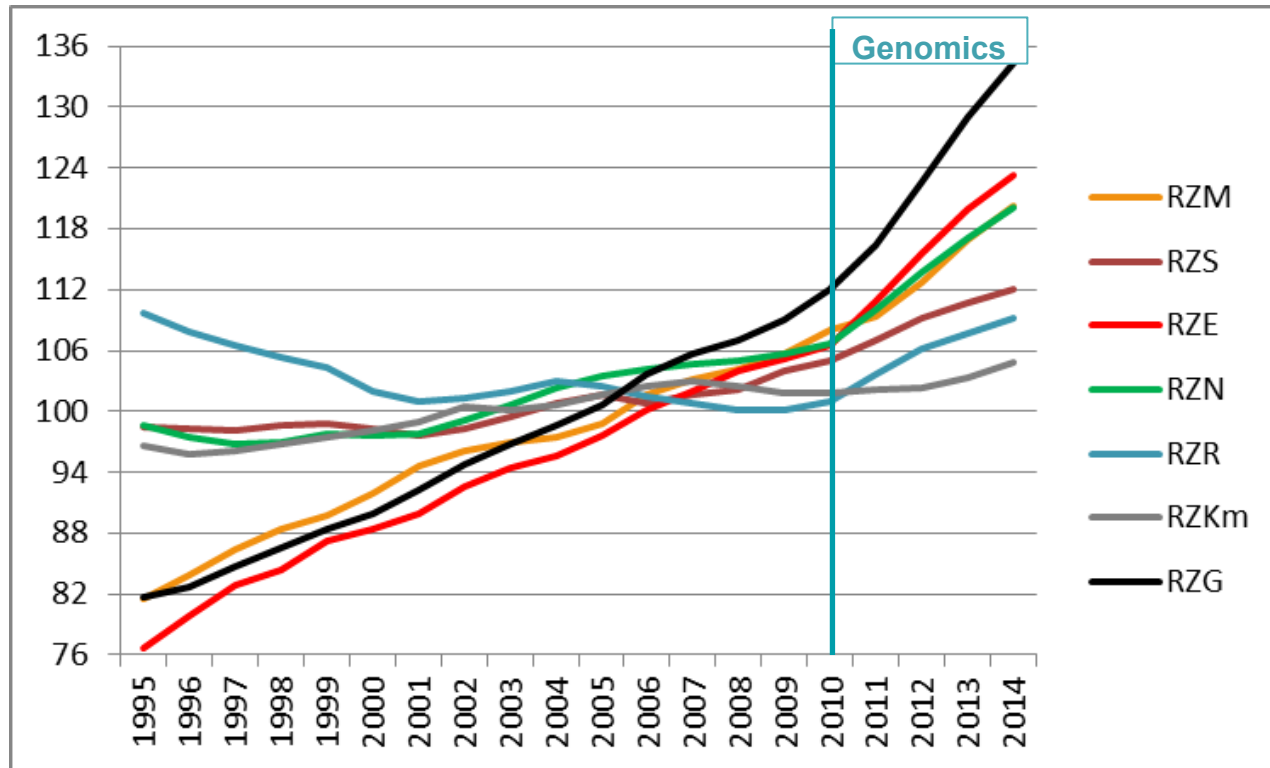
- ca. 1950 – 2009:
  - Holstein breeding based on daughter proven A.I. bulls (test-waiting-proven bull system)
  
- from 2010 onward:
  - Selection based on genomic proofs
  - Same reliability for males and females
    - >90% young sires of sons
    - >90% yearling heifers as bull dams
    - 50-90% use of young genomic A.I. bulls in cow population
  
- →Breeding based on genomic selection



# Doubled genetic progress through Genomic Selection

## Advantages Genomic Selection

- Shorter generation interval
- Effective selection of females / bull-dams for all traits



$\bar{\sigma}$  EBV of all Holstein inseminations/year:  
 1995-2008 =  $\bar{\sigma}$  +2.1 RZG ( $\cong 0.2$  s)  
 2010-2014 =  $\bar{\sigma}$  +5.1 RZG ( $\cong 0.4$  s)

Relative scale with  
 $\bar{\sigma}$  100 and s=12



## International comparability

### ■ Classical breeding values

- Exclusively available on scale of owner country
- Because phenotypic information from daughters as base for genetic evaluation only available here

■ → difficult to compare genetic level of animals across countries

■ → need for objective comparison = MACE = Multiple Across Country Evaluation

- Limitations of MACE
  - exclusively A.I. bulls from participating countries
  - Loss of information/reliability by conversion (e.g. through different trait definition)



## New possibilities for international exchange

### ■ Genomic breeding values

- Based on SNP as information source
- SNP can be exchanged easily
- and used in any national genomic evaluation system

### ■ → on the base of (exchanged) SNP on any scale

- fully comparable gEBV of foreign animals with domestic animals
- for all traits in this specific country
- independent from existence or quality of gEBV in country of origin

### ■ → no more 'conversion' necessary with loss of information

■ but

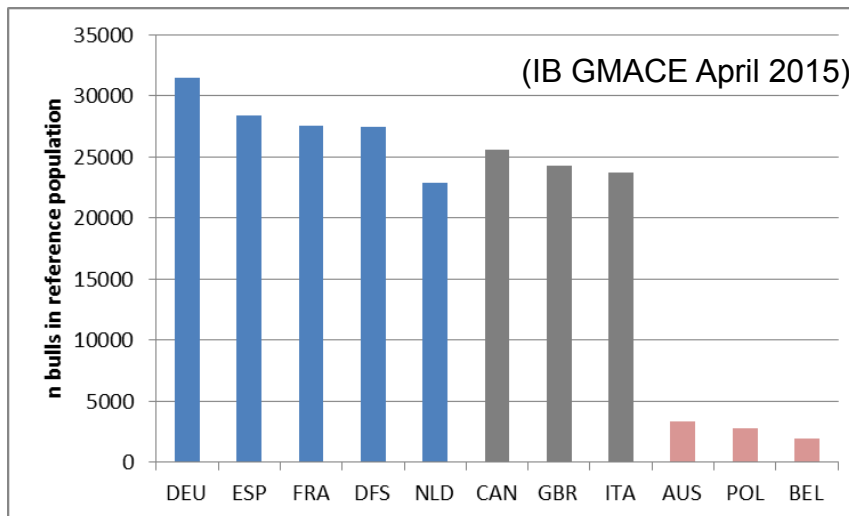
■ For correct interpretation of gEBV on foreign scale(s)

■ Good knowledge of foreign system necessary



## Reliability of genomic predictions

- Main Holstein countries work with joint bull reference populations
  - North-American Consortium: USA+CAN+ITA+GBR
  - EuroGenomics: DEU+FRA+NLD+DFS+ESP+POL
  
- Effectivity of joint reference population
  - is dependent on number of bulls



- and
- **on EBV reliability of each bull**

## Reliability of genomic predictions

- Effectivity of joint reference population
  - is dependent on number of bulls
  - **and on EBV reliability of each bull**
  
- Domestic proven reference bull = high reliability
  - Direct daughter proof
  
- Foreign reference bull = reduced reliability
  - From foreign country ‘converted ‘ daughter proof
  - Information loss by conversion dependent on Interbull correlations (MACE)

**Protein kg (IB 04-2016)**

	USA	NZL	IRL	ISR	ZAF
DEU	0.87	0.70	0.73	0.80	0.82
USA		0.70	0.75	0.83	0.80
NZL			0.84	0.76	0.70
IRL				0.68	0.73
ISR					0.83

**Longevity (IB 04-2016)**

	USA	NZL	IRL	ISR	ZAF
DEU	0.87	0.55	0.72	0.54	0.86
USA		0.56	0.76	0.66	0.88
NZL			0.56	0.40	0.66
IRL				0.44	0.87
ISR					0.53



## Reliability of genomic predictions

- → countries with many domestic proven bulls in their reference population have advantages
  - i.e. countries with high (former) test capacity: USA, DEU, .....
  
- → differences in true reliability of gEBV across countries are much bigger than for daughter proven bulls
  - A bull with 100 daughters has approx. same reliability in all countries
  
- Given national reliabilities for gEBV not necessarily reflect 'true' reliability/predictability
  - No harmonization of estimating gEBV reliability so far
  - → national reliabilities of genomic proofs are not directly comparable





## How can smaller countries use genomic selection?

- Effective own bull reference population often not possible
  - Needs thousands of daughter proven bulls for all traits
  
- Cooperation with other countries i.e. joint reference populations?
  - Precondition: participating in MACE and high correlations to partner countries
  - → often not given
  
- → hard to develop effective national bull reference population and genomics
  
- Alternative:
- Use foreign genomic system and scale for genomic selection of domestic animals



# Foreign genomics for selection of domestic animals

## ■ Advantages

- High reliability of genomic proofs
- All traits on chosen base
- Technically easy and relatively cheap

## ■ Disadvantages

- Foreign scale
- Are (differences in) gEBV on foreign scale relevant for the domestic population?

## ■ How important are 'genotype-environment-interactions'?

- Science hardly detected major interactions
- Low genetic correlations in MACE e.g. between proofs from grazing and intensive systems seem to indicate differences
  - but often weak genetic links
  - and differences in trait definitions



## How can smaller countries use genomic selection?

- Countries without own genetic evaluation
  - gEBV on foreign scale give chance for advanced selection in own population
  - And to compare genetic quality of own population to other populations/countries
  
- Countries with classical genetic evaluations but without genomics
  - Possibility to double genetic progress by genomic selection
  
- How to select the 'right' country scale
  - Most effective reference population
  - Good genetic links to own population
  - All for domestic population important traits available
  - Similar production systems
  
- Genomic selection based on effective foreign genomics is superior compared to own genomics with limited (true) reliability



## How can smaller countries use genomic selection?

- Genomics on foreign country scale: effective but ...
- ... it's not my scale
  - e.g. classical domestic EBV and foreign gEBV on different scales (diff. traits)
- Possible solution for countries with domestic classical evaluation
  - Genotype your (few) proven bulls and sent SNP to foreign genomic system
  - Use the relation of domestic EBV and foreign gEBV for calibration/conversion of foreign gEBV to domestic scale
  - Ranking of animals by gEBV and relative distance between animals is not changed



Redbull P (gRZG 117)  
1st German genomic young RDC bull  
Based on gEBV from DFS system

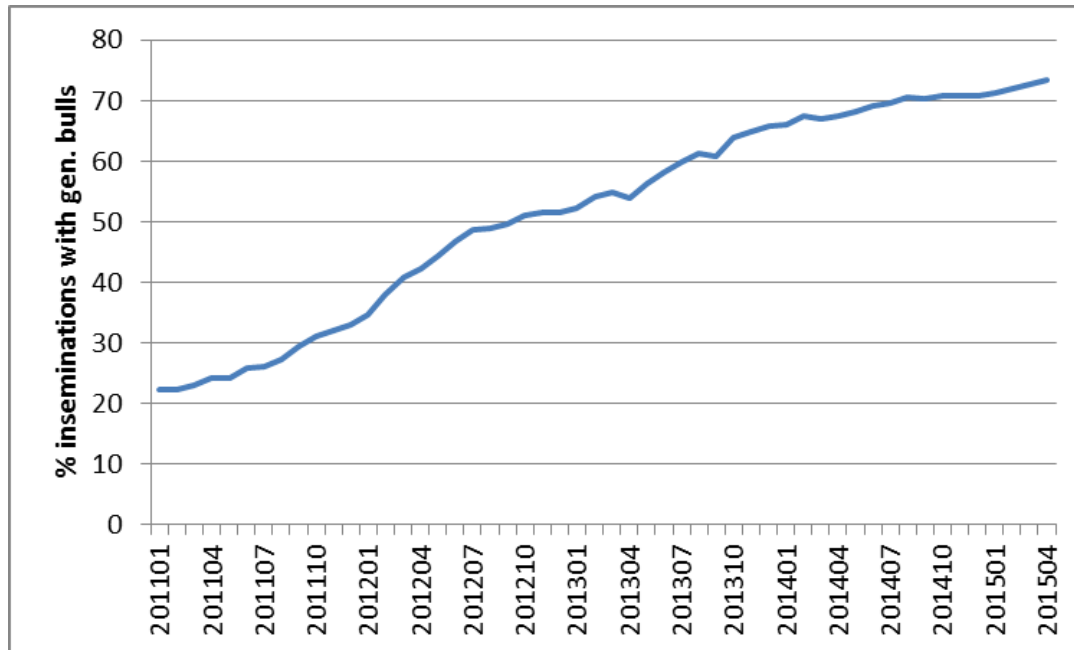
## Cow reference population as chance?

- The future will be cow reference populations
  - Because less new daughter proven bulls and highly pre-selected
  - Only possibility to introduce new traits
- Projects in some countries
  - NLD: *FokerijdataPlus*
  - DEU: *KuhVision*
  - USA: *Clarifide plus*
  - ...
- Cow reference population
  - Genotyped 'commercial' cows with many genotyped herd mates
  - With well recorded pedigree and performance data
  - 5-8 cows just as effective as 1 daughter proven bull with 100 daughters
  - → e.g. 50,000-80,000 cows are as effective as 10.000 reference bulls
  - → could be possible for populations without long history of bull testing programs
  - → could enable new co-operations



# Future of Genomics from West-European perspective

- Selection in breeding programs 100% based on genomics
  - Almost 100% use of young genomic sires of sons
  - intensive selection of bull dams among genotyped yearling heifers
  - Intensive selection among resulting male candidates to become A.I. bull
- Use of young bulls for >2/3 of inseminations



DEU (2015):  
 >70% young bulls  
 15 most used bulls: 10 young bulls



**Goaway**  
 (Gold Chip x MOM x Bolton)  
**32,160 1<sup>st</sup> inseminations 2015**  
**#1 use of all HOL bulls in DEU**



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- Use of young bulls for >2/3 of inseminations
  
- Introduction of new functional traits by cow reference populations
  - More direct health traits
  - Feed efficiency
  
- Classical data collection from DHI/classification and genetic evaluation remain important
  - For validation of genomic predictions



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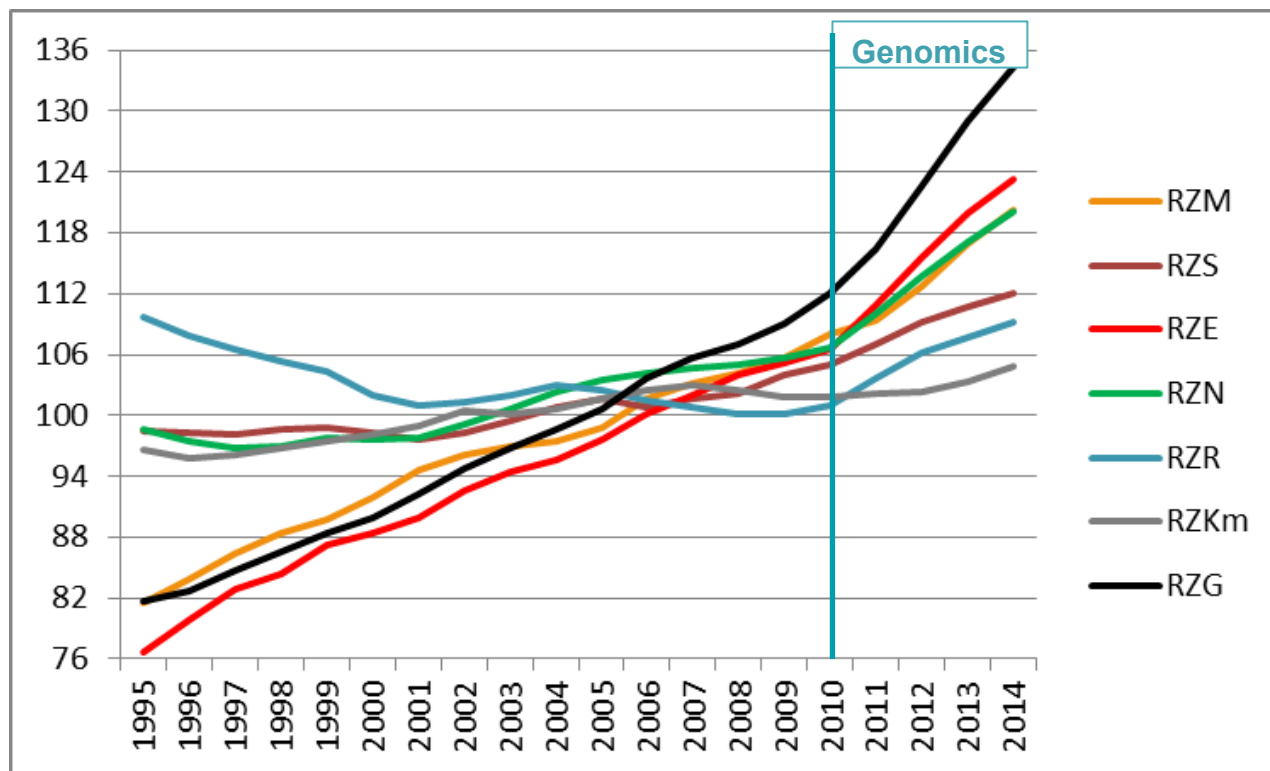
IT-Solutions for Animal Production



# Doubled genetic progress through Genomic Selection

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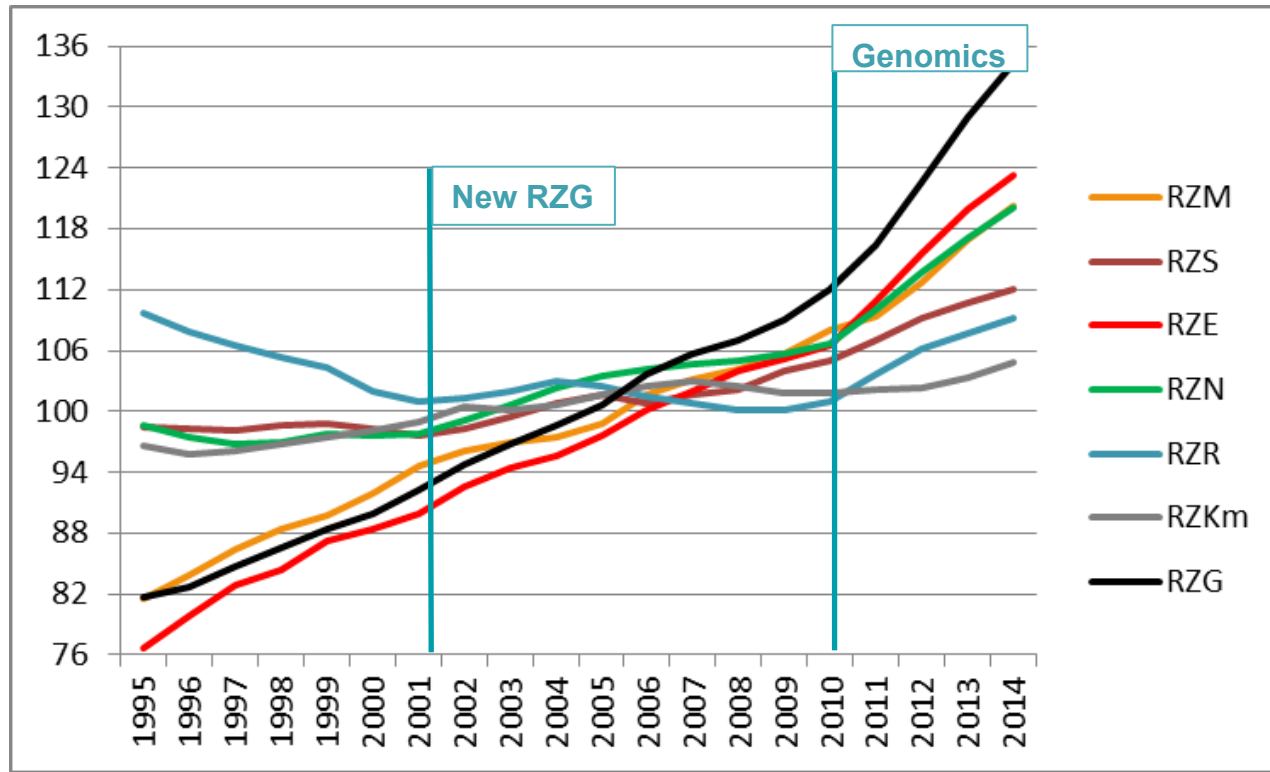


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## If genomic predictions are correct/unbiased



## Reliability of genomic predictions

- Predicting ability of breeding values is expressed by ‘reliability’
  - ‘Reliability’ is estimated
- Good international harmonization for classical breeding values
  - e.g. among countries in Interbull
- Given reliabilities for genomic breeding values are not comparable:

Country	n bulls ref. Pop.	rel. production	rel. conformation
DEU	27829	73%	52%
FRA	27273	64%	63%
NLD	26532	69%	62%
DNK	25636	70%	75%
ESP	25290	68%	71%
CAN	25056	71%	67%
USA	25056	73%	71%
GBR	23759	68%	66%
ITA	23259	75%	69%
CHE	ca. 3000	64%	62%
IRL	ca. 3000	65%	?
POL	2748	75%	65%

*Reference populations 12-2014*

- → for conversion gEBV Interbull ‘adjusts’ national rel. with size reference pop.



## The role of Interbull in Holstein Genomics

- Interbull converts daughter proofs to all participating country scales (MACE)
  - the base for using foreign bulls as reference bulls
  
- Interbull approves national genomic evaluation systems
  
- Interbull converts genomic proofs to all participating country scales (GMACE)
  - To countries having no national genomics
  - To countries with national genomics
  - → loss of reliability through conversion dependent on country correlations
  
- → for countries with national genomics: exchange of SNP and direct gEBV from the national evaluation system results in higher gEBV reliability

