Optimization of genomic diversity in a gene bank for Dutch cattle breeds

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IMAGE
Innovative Management of
Animal Genetic Resources

Centre for Genetic Resources (CGN)

Introduction: gene banks

- Ex situ conservation of genetic diversity

- Three main reasons:

    1. Market or environmental changes

    2. Safeguard

    3. Opportunities for research

- Prioritization may be needed because of limited resources

Introduction: Dutch cattle

- Dutch cattle population in 1975:
    - 70% Dutch Friesian (DF)
    - 28% Dutch Red and White (MRY)
    - 2% Groningen White Headed (GWH)

- Nowadays 98% Holstein Friesian

- Possible loss of genetic diversity in small populations

Introduction: Dutch gene bank

- Genetic material from all native Dutch breeds stored in a national gene bank

- Maximization of genetic diversity based on pedigree data
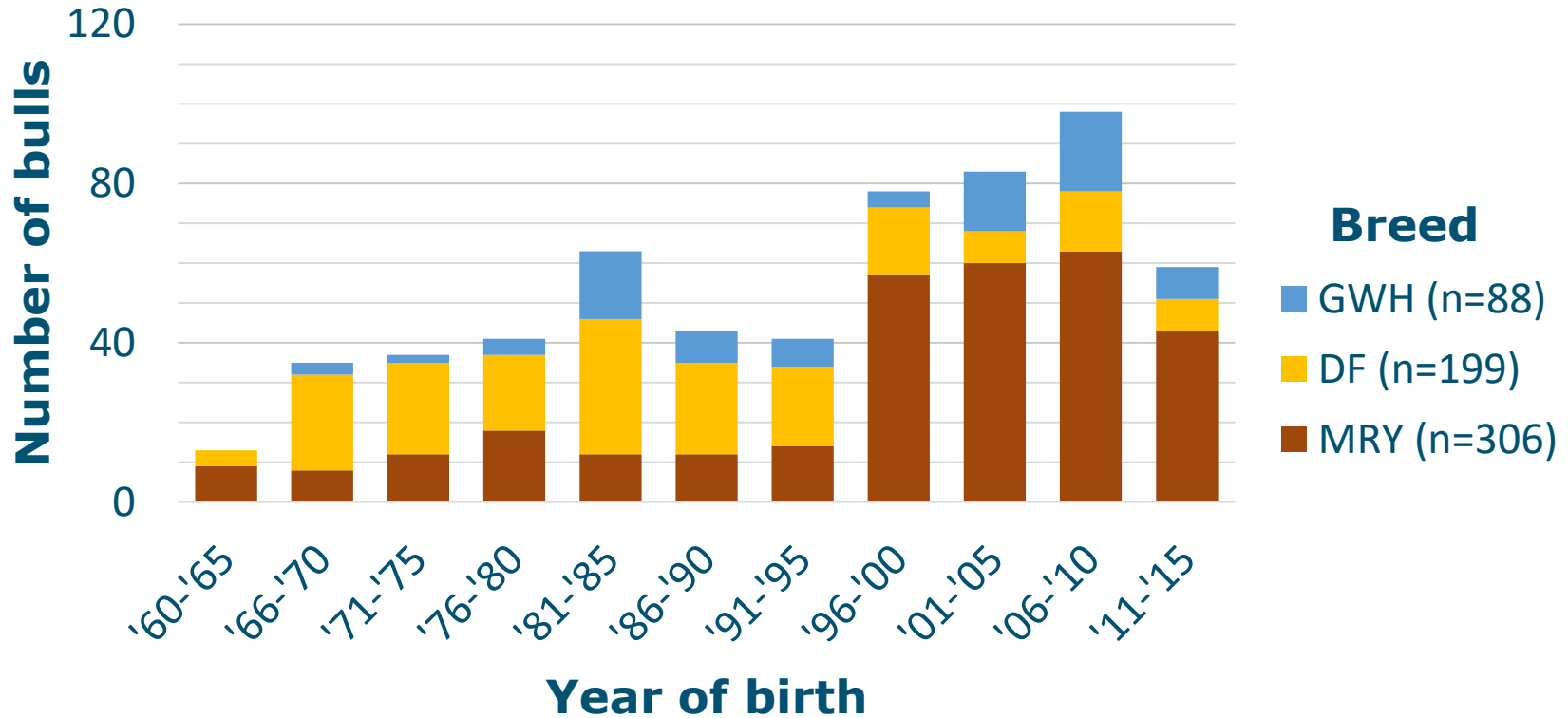
- Recently, all bulls genotyped

Objective

Characterize and optimize
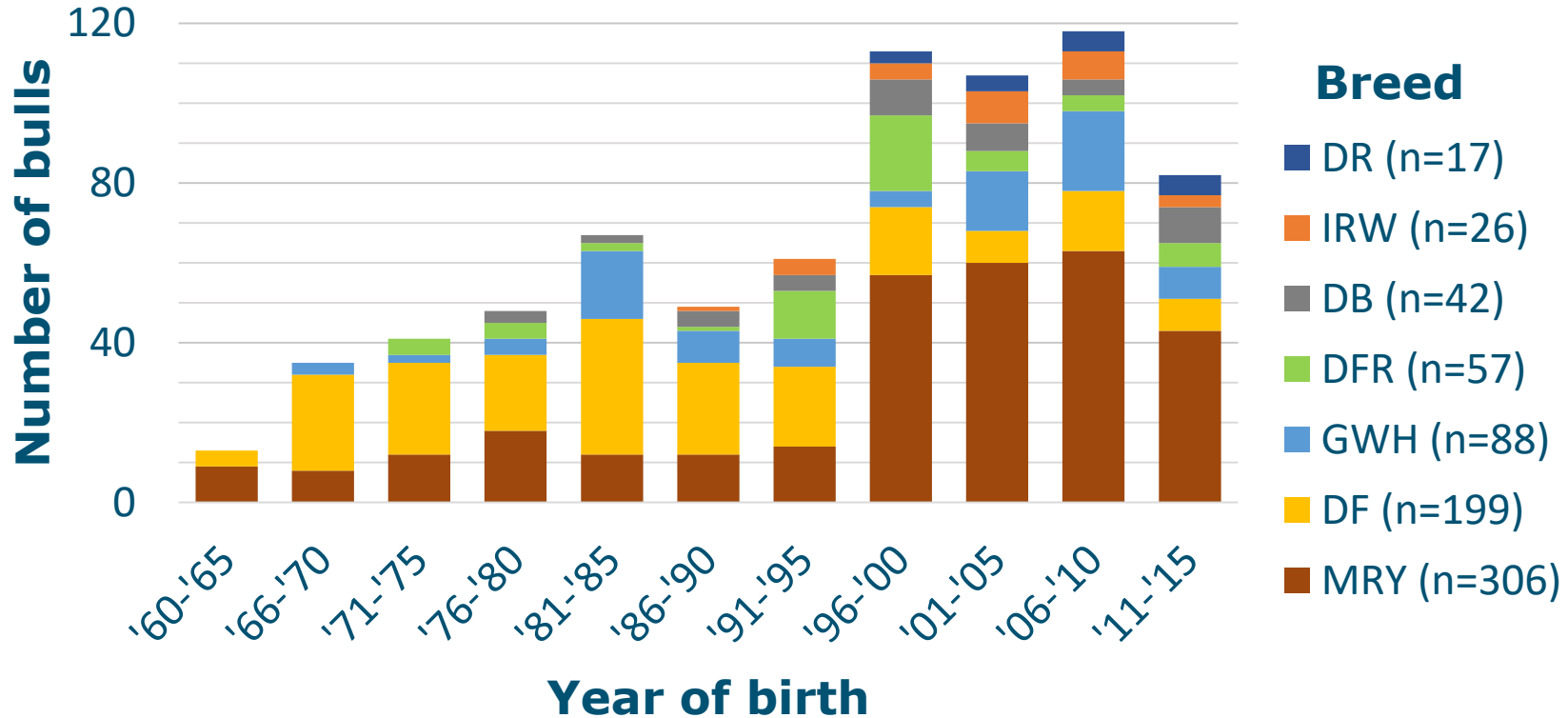genomic diversity in the Dutch gene bank for native cattle

Material

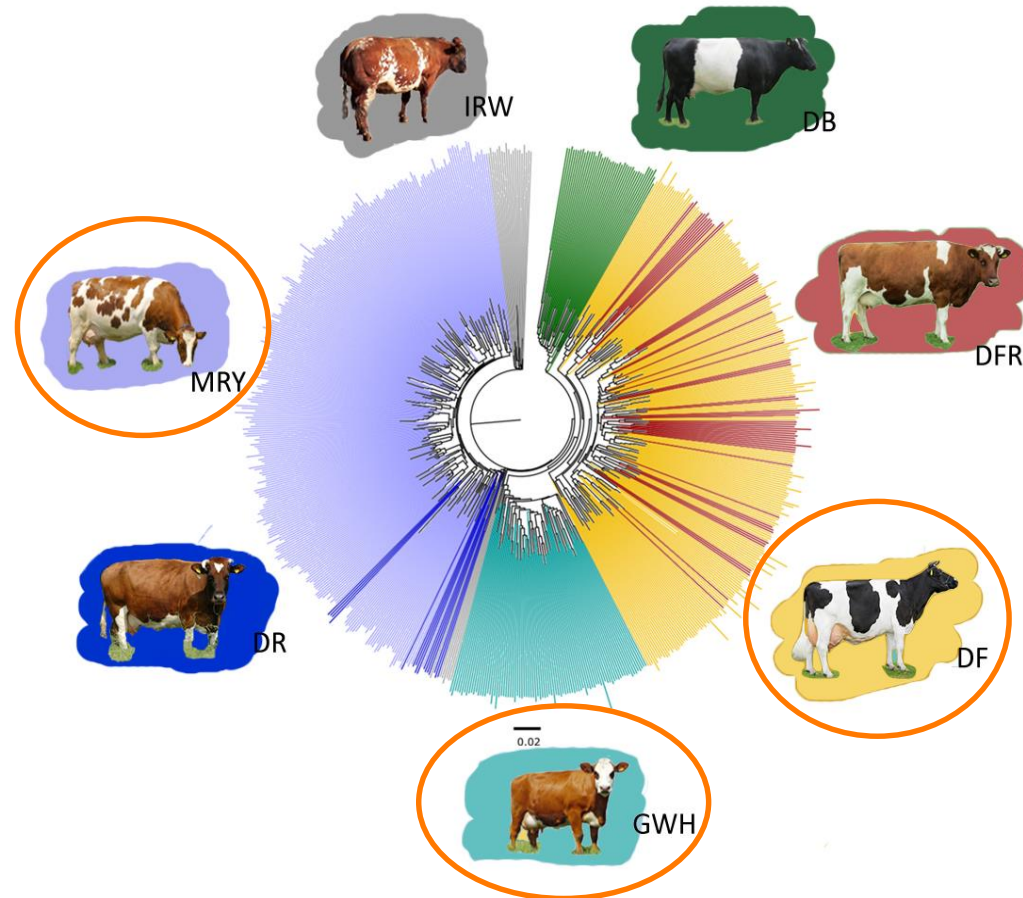# Material

All bulls genotyped at 50k

Methods: characterization

- Genomic similarity between all bulls (IBS)

- Neighbour-joining tree based on genetic distance (1-IBS)

- Unique diversity; method by Eding et al. (2002)

	Breed 1	Breed 2	Breed 3	Breed ...
Breed 1				
Breed 2				
Breed 3				
Breed ...				

Results: neighbour-joining tree

- Dutch Friesian Red (DFR) highly similar to Dutch Friesian (DF)

- Deep Red (DR) and Improved Red and White (IRW) founded by lines within MRY

Results: unique diversity

- Little diversity unique to a single breed

- Improved Red and White (IRW) bulls most unique, in the past some crossing with Belgian Blue cattle
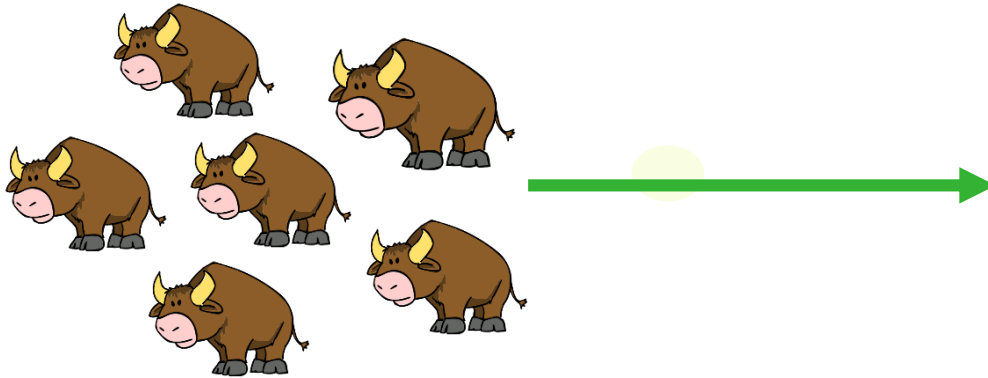
	Unique diversity (%)
DB	0.093
DF	0.023
DFR	0.015
DR	0.033
GWH	0.099
IRW	0.199
MRY	0.016

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Methods: optimization

- Optimal contribution selection by Gencont
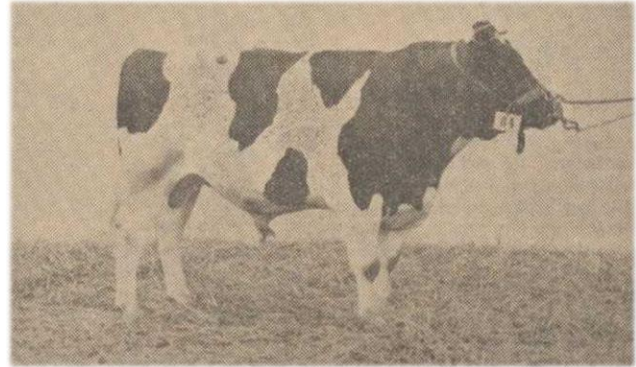
- Reducing mean genomic similarity

Results: optimization across all breeds

- In total 72 out of 718 bulls with optimal contribution higher than zero

- Older bulls were selected as well, across and within breeds

Birthyear	Contribution
1960-1969	8%
1970-1979	7%
1980-1989	22%
1990-1999	22%
2000-2009	21%
2010-2019	20%

Results: optimization within breeds

Breed	Current (%)	Optimal (%)	Difference (%)
DB	69.1	68.0	-1.13
DF	68.2	66.4	-1.79
DFR	69.6	68.6	-1
DR	68.1	67.9	-0.28
GWH	71.1	69.4	-1.62
IRW	67.5	66.8	-0.71
MRY	68.7	67.1	-1.55

Conclusions

- Little diversity is unique to a single breed in the gene bank

- Old bulls contribute considerably to diversity

- In retrospect, we could reduce the mean similarity within each breed with 0.28%-1.79% using optimal contributions

Thank you for your attention!

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