# Improving genomic prediction in numerically small Red dairy cattle populations

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WAGENINGEN
UNIVERSITY & RESEARCH

100years
1918 — 2018

# Acknowledgement


ERA-NETSUSAN

**Project: ReDiverse**

**Centre for Genetic Resources, the Netherlands**

# European Red dairy breeds (ERDB)

Unique genetic variation

Well adapted to diverse environments

Robust in terms of functional and health traits

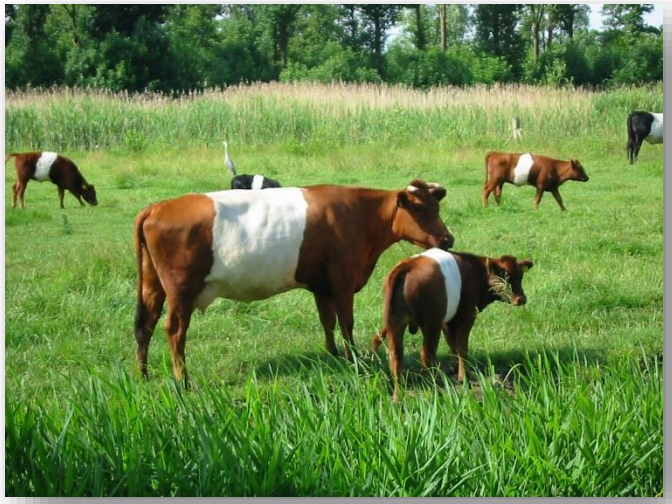
Historical and cultural value

Increasingly replaced

Genetic diversity of ERDB is endangered

# European Red dairy breeds

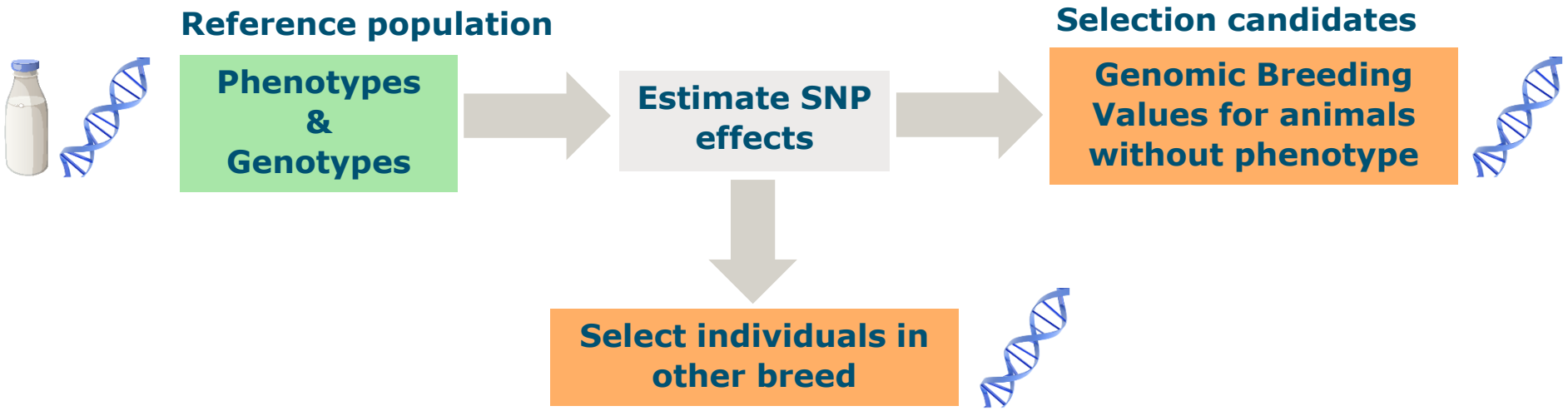
- **ReDiverse project**
- Preserve biodiversity within and between **ERDB**
- Conservation through utilization
- Increase competitiveness



# Genomic prediction

- Accelerate genetic improvement of production traits
- Genomic selection
- Increase economic perspectives for farmers
- Increase long-term perspectives ERDB

# Principle of GP




- Many of ERDB are numerically small
- **Breed-specific** RP is challenging

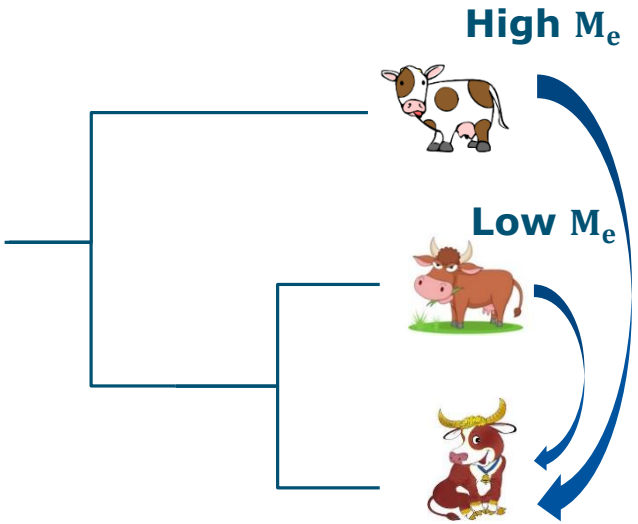
# Reference population

- Alternative - **multi-breed** RP

- Not all breeds are useful, how to prioritize?
- **We propose - Effective number of chromosome segments ($M_e$)**

| Breed | Country | Herd-book animals |
|---|---|---|
| Modern Angeln Dairy Cattle | Germany | 10,000 |
| Traditional Angeln Dairy Cattle | Germany | 150 |
| Red and White Dual Purpose | Germany | 4,000 |
| Vorderwälder Cattle | Germany | 6,600 |
| Hinterwälder Cattle | Germany | 600 |
| Rotes Höhen Cattle | Germany | 1,500 |
| Modern Red Danish Dairy Cattle | Denmark | 40,000 |
| Traditional Red Danish Dairy Cattle | Denmark | ~200 |
| Swedish Red and White Cattle | Sweden | 130,000 |
| Swedish Polled | Sweden | ~1,200 |
| Finnish Ayrshire | Finland | 190,000 |
| Estonian Red | Estonia | 18,000 |
| Lithuanian Red | Lithuania | 30,295 |
| Latvian Brown | Latvia | 44,280 |
| Meuse-Rhine-Yssel | Netherland | 17,771 |
| Dutch Red Friesian | Netherland | 700 |
| Deep Red | Netherland | 1,563 |
| Groningen White Headed | Netherland | 2,488 |
| Improved Red | Netherland | 1,283 |

# $M_e$




- Indicator of relatedness
- Directly predict expected accuracy
- $M_e$ - within the population and across two populations
- Within $M_e$ - Chrom segments that are segregating independently
- Across $M_e$ - consistency of LD between populations/breeds

$$M_{e,w} = \frac{1}{Var(G_{ij} - A_{ij})} \qquad M_{e,a} = \frac{1}{Var(G_{pop1_i pop2_j} - A_{pop1_i pop2_j})}$$

# Objectives

- Estimate
  - $M_e$ within breeds
  - $M_e$ between each pairwise combination of breeds

| Breed | Country | Herd-book animals |
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# Data & Analysis

- BovineSNP50 data - 38,991 SNPs after QC
- Individual call rate > 90%, SNP call rate >95%, MAF > 5%
- Data on 5 breeds - CGN, WUR

| Breed | N |
|---|---|
| MRY | 423 |
| Groningen White Headed (GWH) | 129 |
| Dutch Belted (DB) | 41 |
| Dutch Friesian (DF) | 352 |
| Deep Red (DR) | 44 |

- $M_e$ - calc_grm

http://www.dairydreams.co.uk/our-cows/

https://resource.wur.nl/en/show/Meet-the-Dutch-heritage-cattle-breeds.htm

http://www.regionalcattlebreeds.eu/publications/documents/5384_Brandrood_Engels.pdf

# Results

| | MRY | GWH | DB | DF | DR |
|---|---|---|---|---|---|
| **MRY** | 293 | | | | |
| **GWH** | | 151 | | | |
| **DB** | | | 104 | | |
| **DF** | | | | 212 | |
| **DR** | | | | | 149 |

# Results

| | MRY | GWH | DB | DF | DR |
|---|---|---|---|---|---|
| **MRY** | 293 | | | | |
| **GWH** | 17906 | 151 | | | |
| **DB** | 14883 | 16315 | 104 | | |
| **DF** | 16452 | 10890 | 7625 | 212 | |
| **DR** | 3662 | 17516 | 17047 | 14560 | 149 |

- MRY and DR are most closely related
- DF was most closely related to DB
- For GWH, DF was the closest breed
- The most distant relationships DR and DB, DR and GWH, and GWH and MRY

# Results

- Adding individuals from other breed
- To obtain the same increase in accuracy

$$n_{P,2} = \frac{h_1^2}{h_1^2} \frac{M_{e_{1,2}}}{M_{e_1}} n_{P,1}$$

$$r_{G_{1,2}=1}$$

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| | | Population 2 | | | | |
|---|---|---|---|---|---|---|
| | | **MRY** | **GWH** | **DB** | **DF** | **DR** |
| **Population 1** | **MRY** | **1** | 61 | 51 | 56 | 13 |
| | **GWH** | | | | | |
| | **DB** | | | | | |
| | **DF** | | | | | |
| | **DR** | | | | | |

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- To obtain the same increase in accuracy

$$n_{P,2} = \frac{h_1^2}{h_1^2}\frac{M_{e_{1,2}}}{M_{e_1}} n_{P,1}$$

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| | | Population 2 | | | | |
|---|---|---|---|---|---|---|
| | | **MRY** | **GWH** | **DB** | **DF** | **DR** |
| **Population 1** | **MRY** | **1** | 61 | 51 | 56 | 13 |
| | **GWH** | 119 | **1** | 108 | 72 | 116 |
| | **DB** | 144 | 158 | **1** | 74 | 165 |
| | **DF** | 78 | 51 | 36 | **1** | 81 |
| | **DR** | 25 | 117 | 114 | 97 | **1** |

# Conclusions

**$M_e$:**

- Shows high variability in relatedness
- Shows which breeds to use in multi-breed RP

**Multi-breed RP:**

- Should be much larger than single-breed RP
- Beneficial for some small breeds (DR)

**Thank you!**