

Improving genomic prediction in numerically small Red dairy cattle populations

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Acknowledgement



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

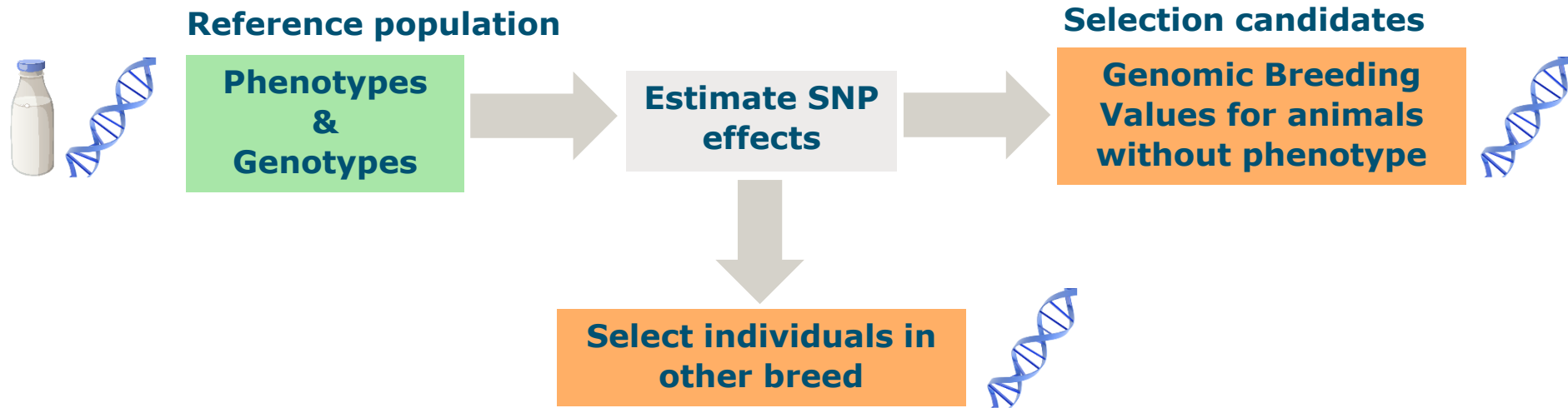
- **ReDiverse project**
- Preserve biodiversity within and between **ERDB**
- Conservation through utilization
- Increase competitiveness



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

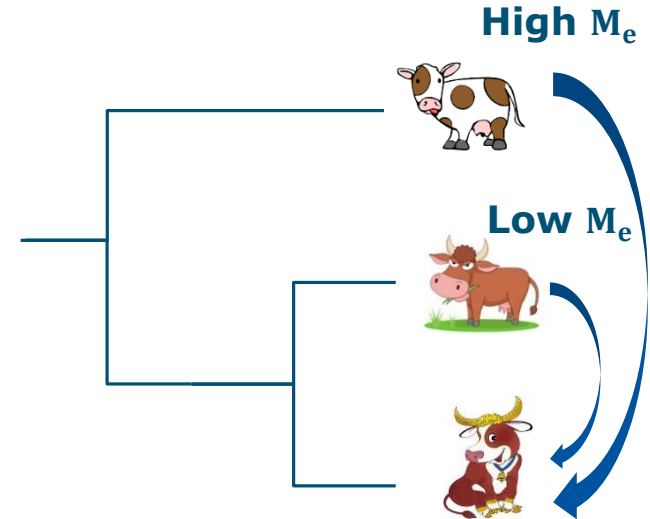


- Not all breeds are useful, how to prioritize?
- We propose - Effective number of chromosome segments (M_e)**

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	Netherlands	17,771
Dutch Red Friesian	Netherlands	700
Deep Red	Netherlands	1,563
Groningen White Headed	Netherlands	2,488
Improved Red	Netherlands	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



$$M_{e,w} = \frac{1}{\text{Var}(G_{ij} - A_{ij})}$$

$$M_{e,a} = \frac{1}{\text{Var}(G_{pop1ipop2j} - A_{pop1ipop2j})}$$

Objectives

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

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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

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

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

Results

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

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

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

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

Results

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

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

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

		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!