



ReDiverse: Biodiversity within and between European Red Dairy Breeds – Conservation through utilization

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**IRDBF Conference 2019
26th March 2019**



Outline

- Motivation
- Objectives of ReDiverse
- Involved partners
- Work packages
- Expected outcomes of ReDiverse



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Motivation

- European Red Dairy Breeds (ERDB) represent a unique source of genetic diversity
 - complex histories of gene flow and connectedness
 - local adaptation to various environments
 - cultural heritage

- ERDB are well known for superior functional characteristics
 - high fertility
 - outstanding udder health
 - low incidence of stillbirth
 - good conformation of legs and claws



C.P. Tordsen

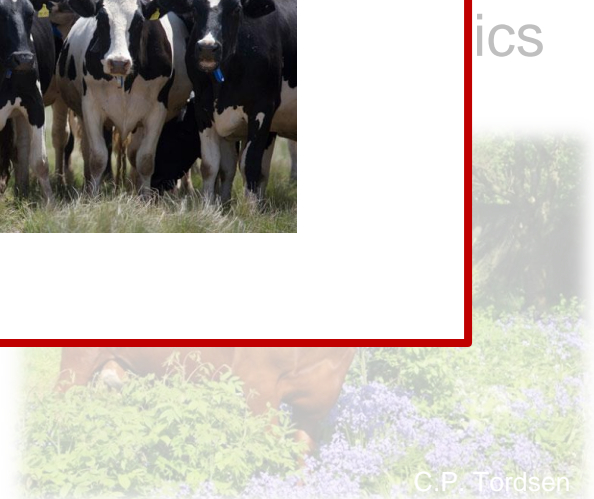
Motivation

- European Red Dairy Breeds (ERDB) represent a unique source of genetic diversity

Despite their qualities, ERDB are increasingly replaced by higher yielding breeds (e.g., Holstein Friesian)



- good conformation of legs and claws





Importance of genetic diversity

Genetic diversity – a resource deserving protection

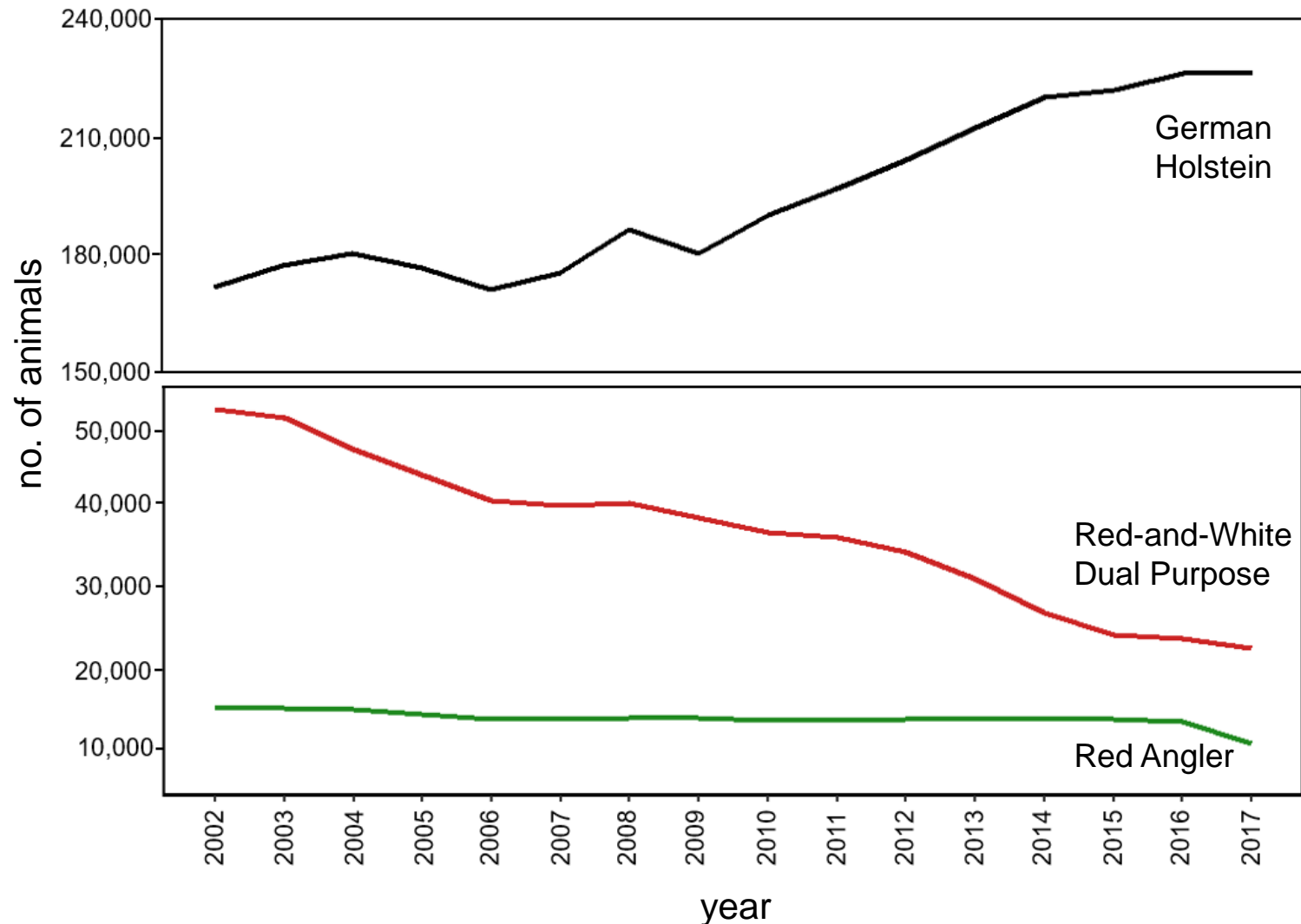
- Animal genetic diversity is a unique and irreplaceable heritage
- Essential for maintaining the adaptability to changing environments
- Insurance future breeding options
- Genetic diversity in livestock declines significantly
- Globally, 16% of all livestock breeds have been lost during the last 100 years (Scherf, 2000)

Utilization will ensure conservation!



Dairy breeds in Northern Germany

Development of dairy cows under milk recording in Schleswig Holstein



(LKV, 2017)



Dairy breeds in Northern Germany

Table: Average performances of breeds (LKV SH, 2017)

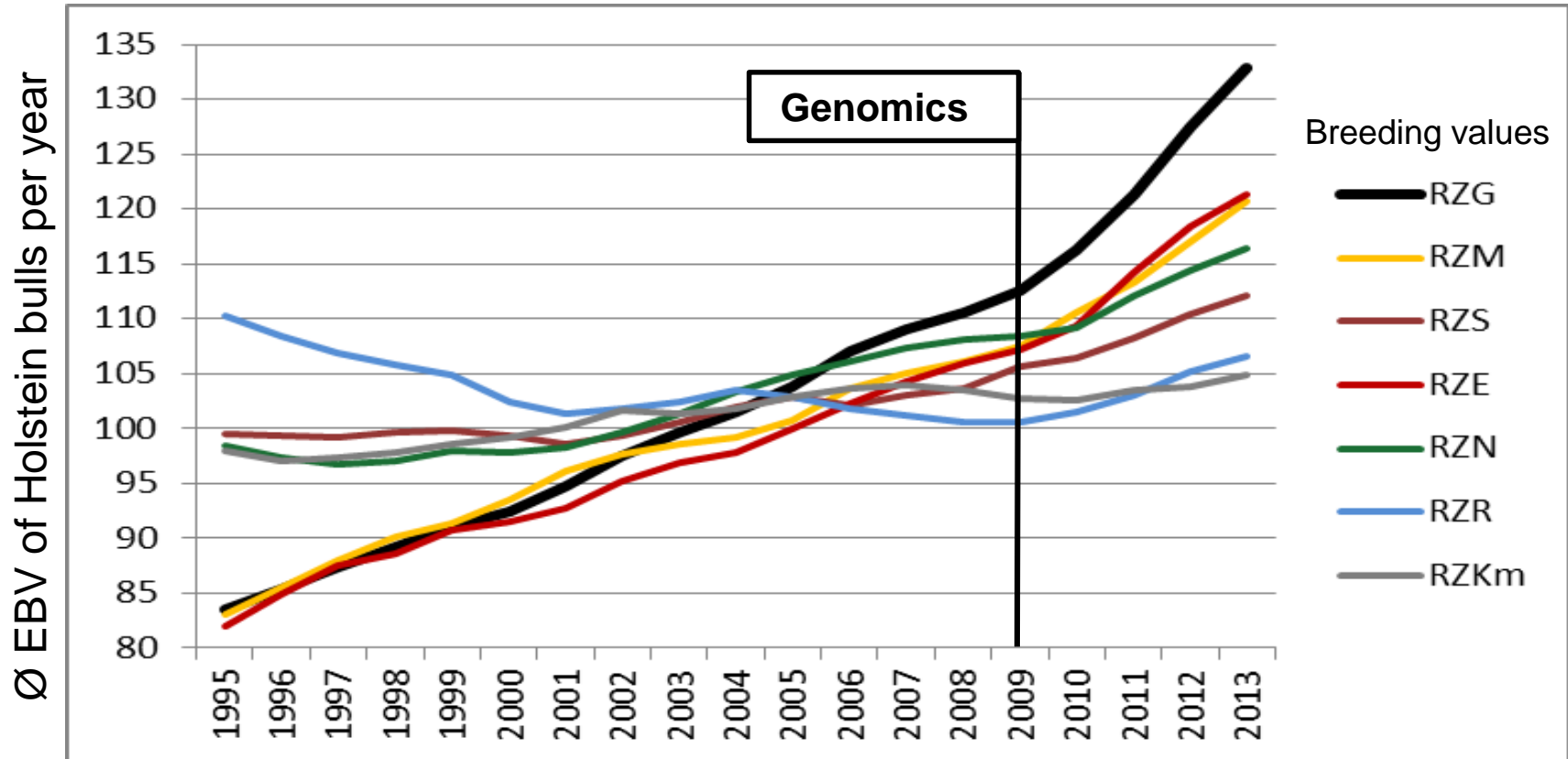
	Red Angler	Red-and-White Dual Purpose	German Holstein
Number of animals in milk recording (2017, SH)	10,257	20,730	233,003
Milk yield (kg)	7,766	6,771	8,804
Fat %	4.60	4.34	4.09
Protein %	3.61	3.50	3.41





Impact of genomic breeding

Genetic gain in German Holstein



(Reinhardt, 2014)

RZG 1995-2008 = $\emptyset + 2.1$ per year
RZG 2010-2013 = $\emptyset + 5.1$ per year

Genomic selection has doubled genetic progress



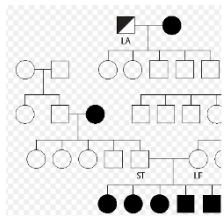
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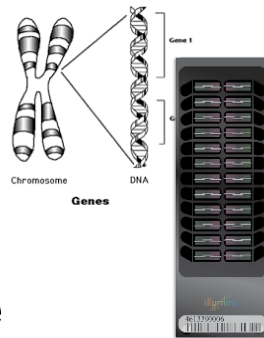


ReDiverse – Main objectives

Development and implementation of methods and strategies for sustainable use of genetic diversity provided by European Red Dairy Breeds

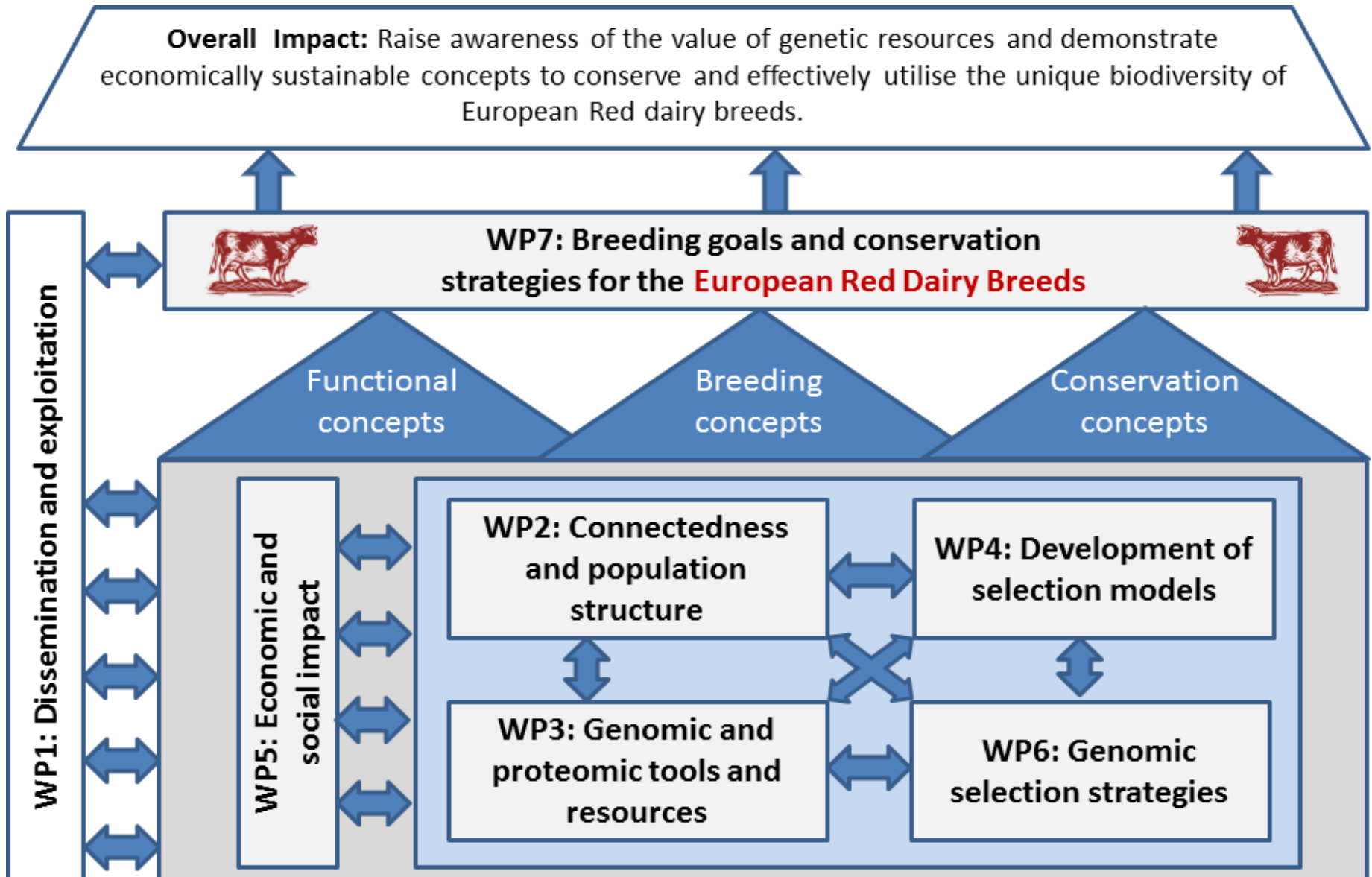


- Investigation of population structure and genetic composition of Red dairy breeds
- Genetic analyses
 - Cooperative reference population
 - Breed-specific SNP-Chip
- Proteomic analyses → Identification and characterization
- Design and evaluation of breeding programs to ensure genetic gain and genetic diversity
- Exploration of farmers' preferences keeping Red Dairy breeds





ReDiverse – Structure of project





European Red Dairy Breeds



Breed	Herdbook animals
Meuse–Rhine–Yssel	17,771
Groningen White Headed	2,488
Deep Red	1,563
Dutch Red Friesian	700

Breed	Herdbook animals
Finnish Ayrshire	190,000
Swedish Red and White Cattle	130,000
Modern Red Danish Cattle	40,000



Breed	Herdbook animals
Modern Angeln Cattle	10,257
Red and White Dual Purpose	2,846
Vorderwald Cattle	6,050
Hinterwald Cattle	600

Breed	Herdbook animals
Latvian Brown	44,280
Lithuanian Red	30,295
Estonian Red	18,000





Outline

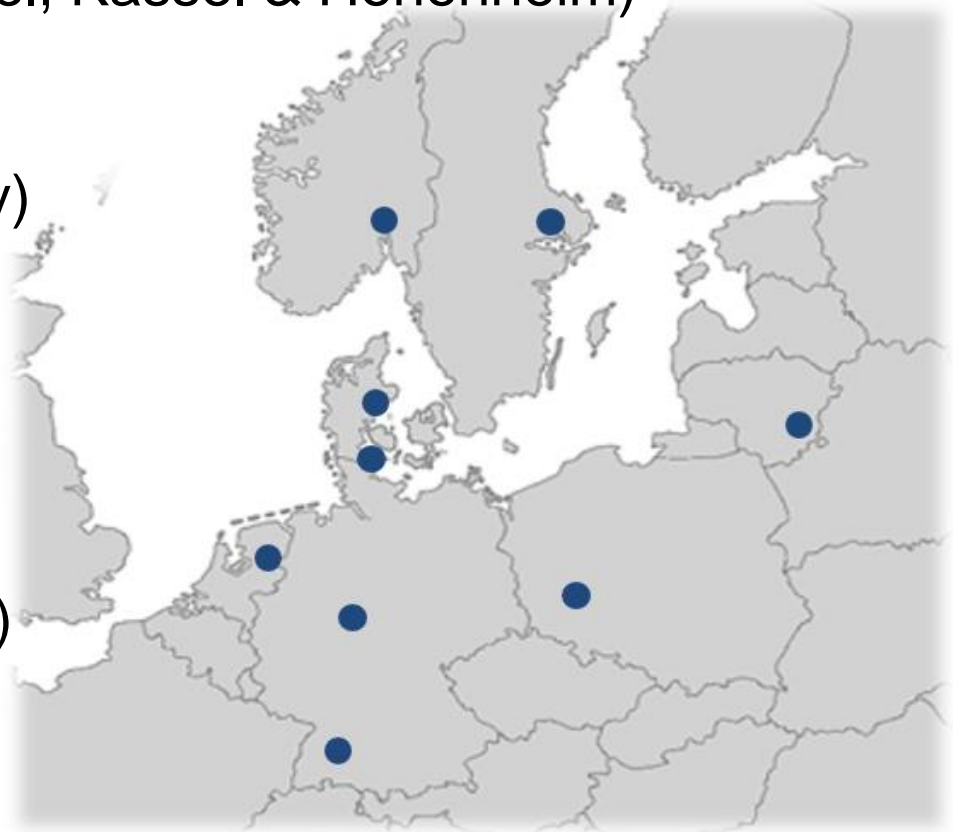
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Involved partners

Scientific partners

- Germany (Universities of Kiel, Kassel & Hohenheim)
- The Netherlands (WUR)
- Denmark (Aarhus University)
- Sweden (SLU, Interbull)
- Norway (NMBU)
- Lithuania (LUHS)
- Poland (Wroclaw University)





Involved partners

Industrial partners

- CRV
- Geno
- Rinderzucht Schleswig Holstein eG
- Viking Genetics
- Lithuanian Red Cattle Improvement Association
- Animal Breeders Association of Latvia





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WP 2 – Genetic connectedness + population structure



Leader WP2: Dirk-Jan De Koning, SLU Sweden

- Investigation of population structure and genetic connectedness
 - Determination of genomic relationships and distances between breeds
- Investigation of phenotype recording schemes between ERDB
 - Defining clear phenotypes which will be recorded across countries within a reasonable time
 - Harmonization of recording schemes
- Determination of recent migration from other breeds
- Identification of key animals for further genotyping and sequencing



WP 2 – Genetic connectedness + population structure

Numbers of pedigree information per sex and reporting country

	FEMALE	MALES	TOTAL
Lithuania	9 789	9 211	19 000
Denmark, Sweden, Finland	4 855 904	1 490 092	6 345 996
Netherlands	2 217 343	256 627	2 473 970
Germany	4 089	815	4 904
Latvia	58 025	4 517	62 542
Poland	6 893	713	7 606
Norway	1 648 872	445 426	2 094 298
TOTAL	8 800 915	2 207 401	11 008 316

(S.Nyman & A.M.Johansson, 2018)

Verification of pedigree information ➡ 3 009 686 duplicates



WP 2 – Genetic connectedness + population structure

Existing evaluation schemes for Red dairy breeds per trait/country

Trait/ Country	Production	Udder health	Conformation	Longevity	Calving ease	Female fertility	Workability
Lithuania	X	X					
Denmark, Sweden, Finland	X	X	X	X	X	X	X
Netherlands	X	X	X	X	X	X	X
Germany	X	X	X	X	X	X	X
Latvia	X	X					
Poland							
Norway	X	X	X	X	X	X	X

(S.Nyman & A.M.Johansson, 2018)



WP 3 – Development of genomic and proteomic tools

Leader WP3: Bernt Guldbrandtsen, Aarhus University

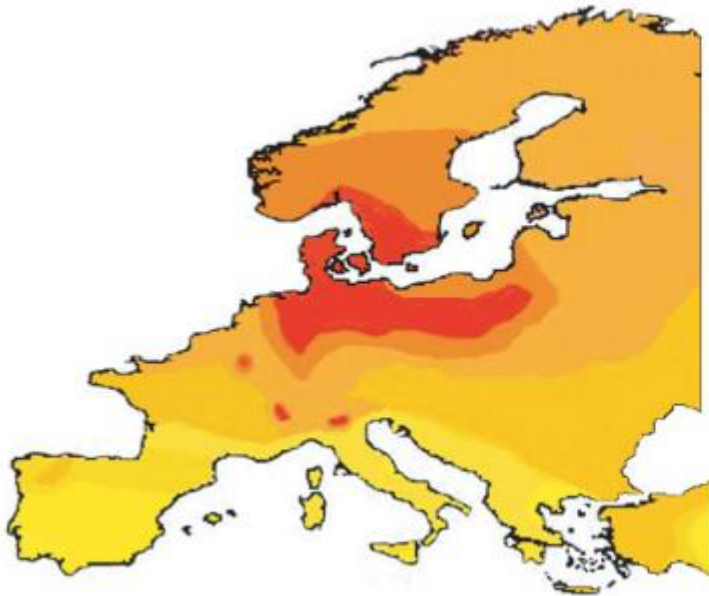


- Analysis of genomic data with respect to patterns of milk protein variants
 - Investigation of implications for human health
- Design of a SNP chip customized for ERDB
 - Improved QTL results
 - Promotion of milk protein variants
 - Support of genomic prediction
- Identification of breed differences at sequence level
- Improve the understanding how admixture is detectable in genomic data

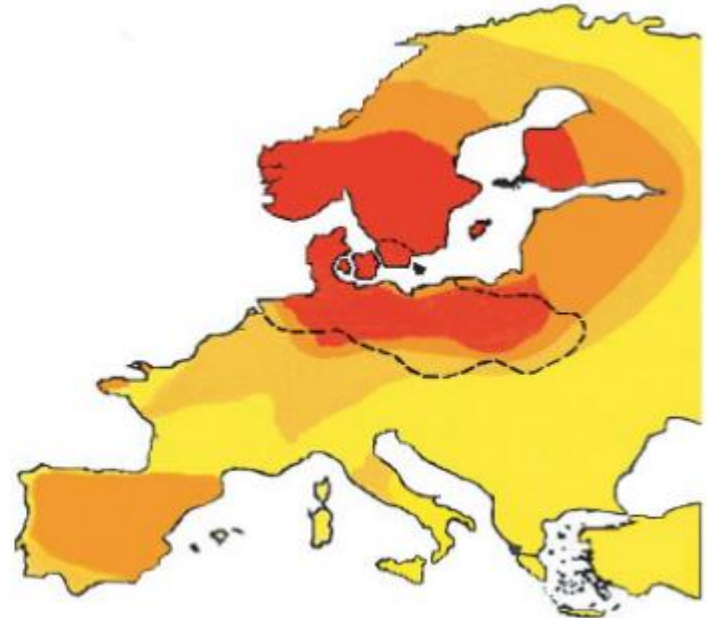


Milk protein variants

Milk protein diversity



Incidence of lactose tolerance



Adapted from Beja-Pereira et al. (2003)

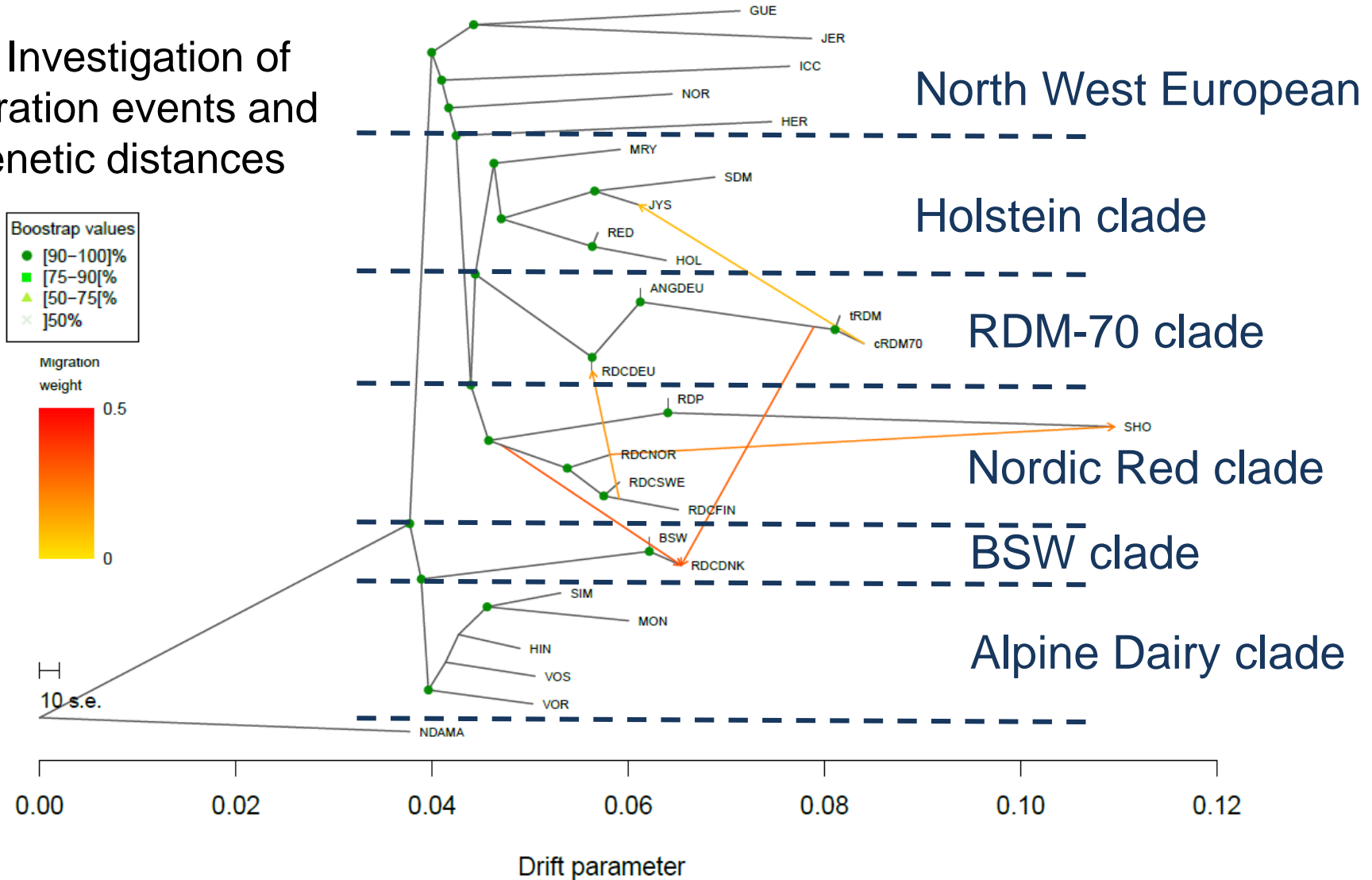


Beja-Pereira et al. (2003) have found coincidence between the milk protein diversity in cattle breeds and the geographic distribution of the lactase persistence allele in humans



TreeMix analysis

→ Investigation of migration events and genetic distances



(Anna Schönherz, 2018)



WP 4 – Development of selection methods

Leader WP4: Jörn Bennewitz, University of Hohenheim



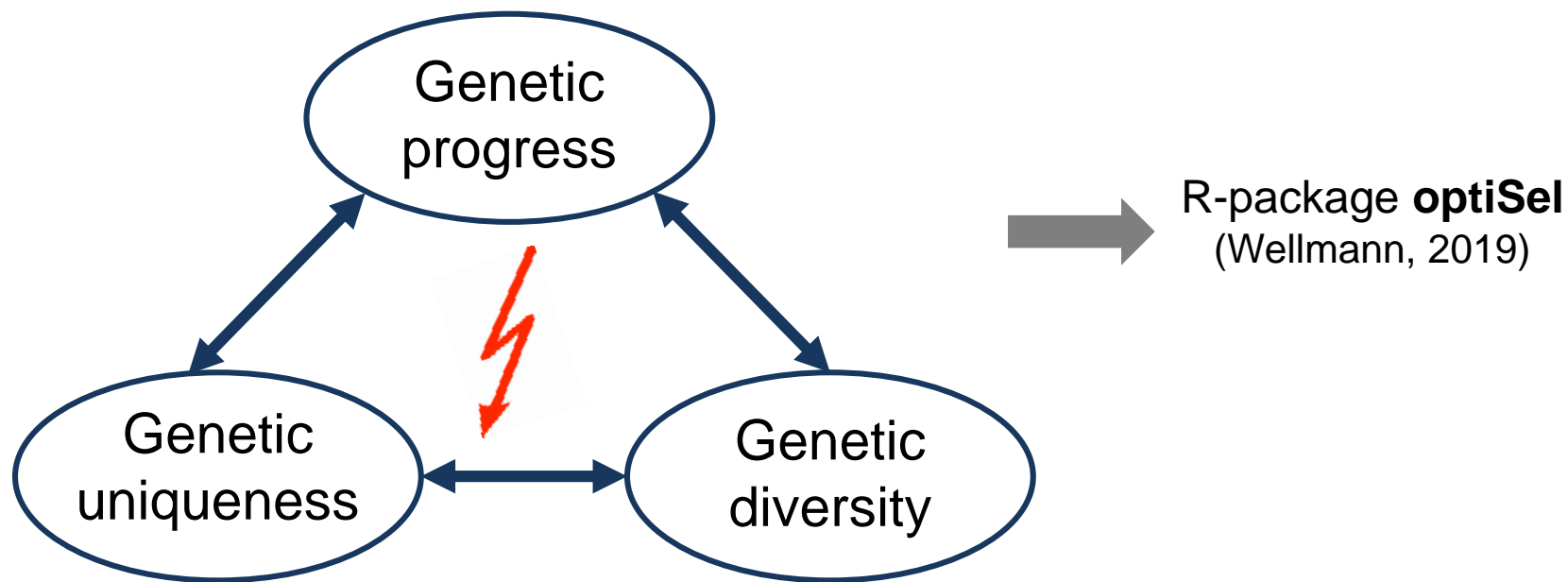
UNIVERSITY OF
HOHENHEIM

- Development and evaluation of selection methods
 - Maximization of purebred and crossbred performance while preserving genetic uniqueness of ERDB
- Development of breeding programs for the genomic prediction of crossbred performance
- Comparison of simulated breeding programs
 - Focussing on genetic gain and genetic uniqueness



WP 4 – Development of selection methods

Conflicting objectives in animal breeding programs



Development and evaluation of selection methods to maximise performance while preserving the genetic diversity and genetic uniqueness provided by ERDB



WP 5 – Economic and social impact

Leader WP5: Uwe Latacz-Lohmann, Kiel University



Christian-Albrechts-Universität zu Kiel

- Assessment of benefits and costs of conserving genetic diversity at the farm level
- Evaluation of farmers' preferences keeping and breeding Red dairy cattles
- Determination of farmers' preferences for the introduction of Red dairy cattles genes in high yielding breeds (e.g. HF)



Applied methods: Quantitative approaches from social sciences, e.g. Discrete Choice Experiments, interviews



WP 5 – Economic and social impact

Which determinants influence farmers' participation in conservation programs for dairy cattle breeds?

➔ Discrete Choice Experiments, 159 German cattle breeders

	Contract 1	Contract 2	Opt-out
Compensation payment	250€/LU/year	250€/LU/year	No contract
Collective Bonus (population increase > 5%)	40€/LU/year	0€/LU/year	
Conservation breeding program (pairing)	No	Yes	
Keeping conditions	No requirements	Access to free-range area or pasture	
Contract duration	5 yrs	1 yrs	
I choose	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

(Julia Schreiner, 2018)



WP 5 – Economic and social impact

	Coefficient	WTA [€/LU/year]
Compensation payment	0.015***	-
Bonus = 40€/LU/year	-0.0689	5
Bonus = 80€/LU/year	0.453***	-30
Conservation breeding program	-0.159	11
Access to free-range area or pasture	0.230	-15
Access to free-range area or pasture+ prohibition of slatted floors	-2.475***	165
Contract duration = 1 year	0.2706	-18
Contract duration = 5 years	0.4674	-31
Contract duration = 10 years	-1.627***	108

(Julia Schreiner, 2018)

- Monetary incentives contribute to farmers' willingness to participate in conservation programs
- Contract duration → short term contracts were more attractive for farmers → flexibility, independence



WP 5 – Economic and social impact

What are motivations for farmers keeping and breeding Red Dairy cattles?

➔ Q-methodology (systematic analysis of subjective attitudes),
carried out with 66 cattle breeders

Some results:

- + ,ERDB are characterized by good health, claws and conformation
→ lower veterinary costs‘
- + ,ERDB show higher values for milk ingredients (fat + protein) → guarantee for income even milk price is low ‘
- + ,we are keeping ERDB due to traditional reasons, we are emotionally attached‘
- + ,we are keeping ERDB because we are concerned about the cultural value of our region ‘



WP 6 – Genomic selection strategies



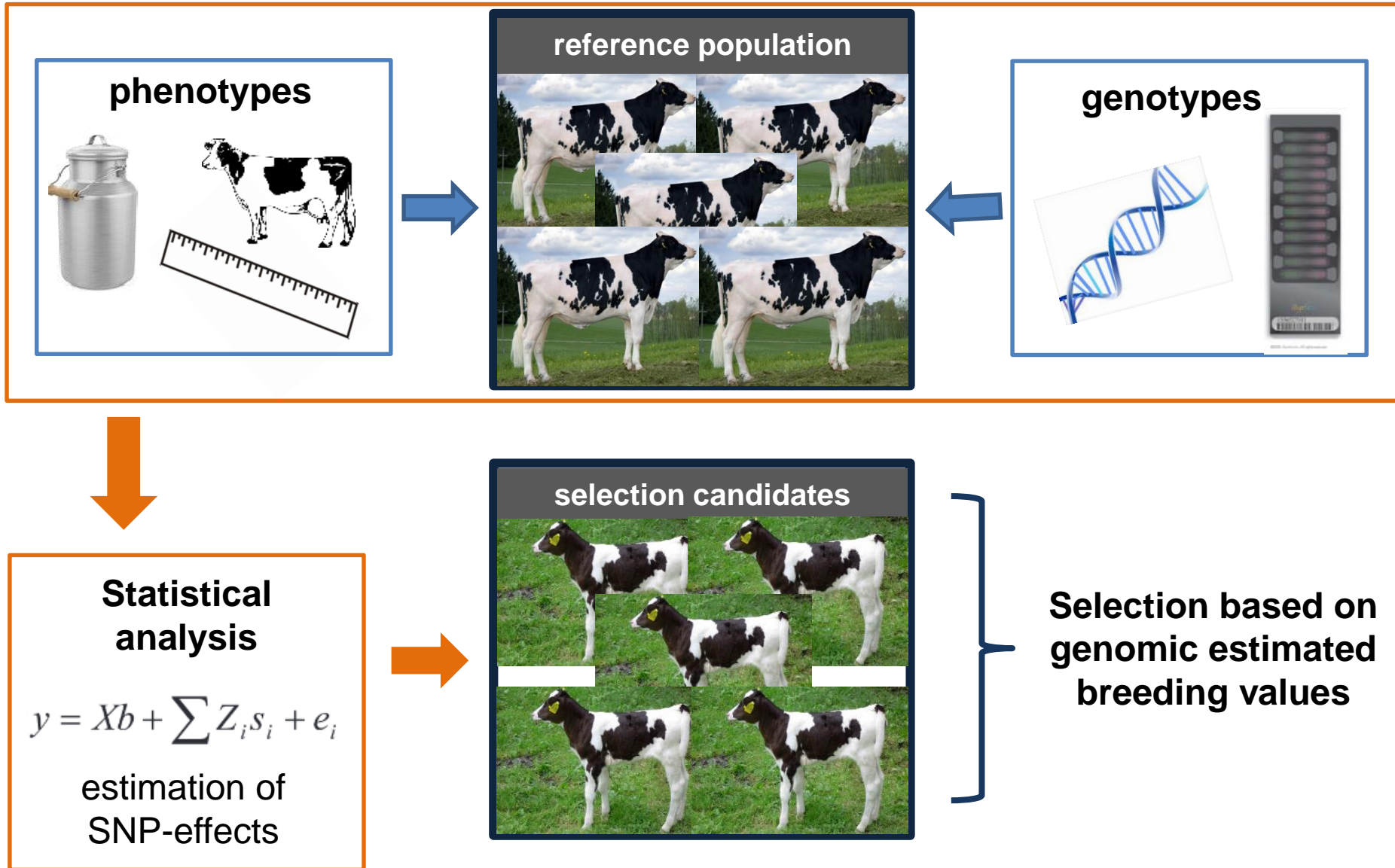
Leader WP6: Mario Calus, Wageningen University

- Improvement of genomic prediction methods for across-breed evaluations and for heterogeneous populations
 - Focussing on maintaining genetic diversity
- Investigation of the potential for implementation of genomic selection in ERDB

Increase competitiveness and create a long-term perspective for European Red Dairy Breeds



Genomic selection





WP 6 – Genomic selection strategies

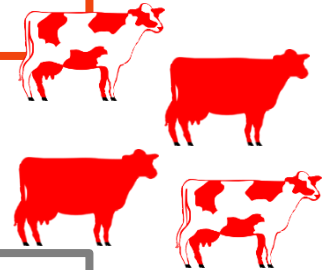
Challenges: European Red Dairy breeds

- are characterized by small population sizes → few progeny tested bulls
- are heterogeneous populations



Possible solution: Multi-breed reference population

- composition of reference population ?
- which breeds are useful to include ?





WP 6 – Genomic selection strategies

Estimation of M_e (effective number of chromosome segments)

- Indicator for relatedness
- Directly predict expected accuracy

Data

- BovineSNP50 data of 5 Dutch Red dairy breeds

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

(Jovana Marjanovic, 2018)



WP 6 – Genomic selection strategies

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

Within M_e

Between M_e

(Jovana Marjanovic, 2018)

- 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



WP 6 – Genomic selection strategies

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

Within M_e

Between M_e

(Jovana Marjanovic, 2018)

- MRV 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 MRV

- M_e shows high variability in relatedness
- Multi-breed RP should be much larger than single-breed RP



WP 7 – Development of breeding goals + conservation strategies

Leader WP7: Morten Kargo, Aarhus University



AARHUS
UNIVERSITY

- Breeding goal setting for European Red Dairy Breeds
 - Development of national + transnational breeding objectives
- Breeding scheme simulations
- Evaluation of breeding schemes with respect to genetic gain, genetic diversity and promotion of breed-specific characteristics
 - With respect to genetic gain, genetic diversity and promotion of breed-specific characteristics



Calculation of economic weights

Calculation of economic values for Red Dairy breeds

- Determination of optimal economic selection indices for regional production conditions
- Economic values were already calculated for 3 German dairy breeds (Holstein Friesian (HOL), Angler (ANG), Red-and-White Dual Purpose (RDN))

Applied methods:

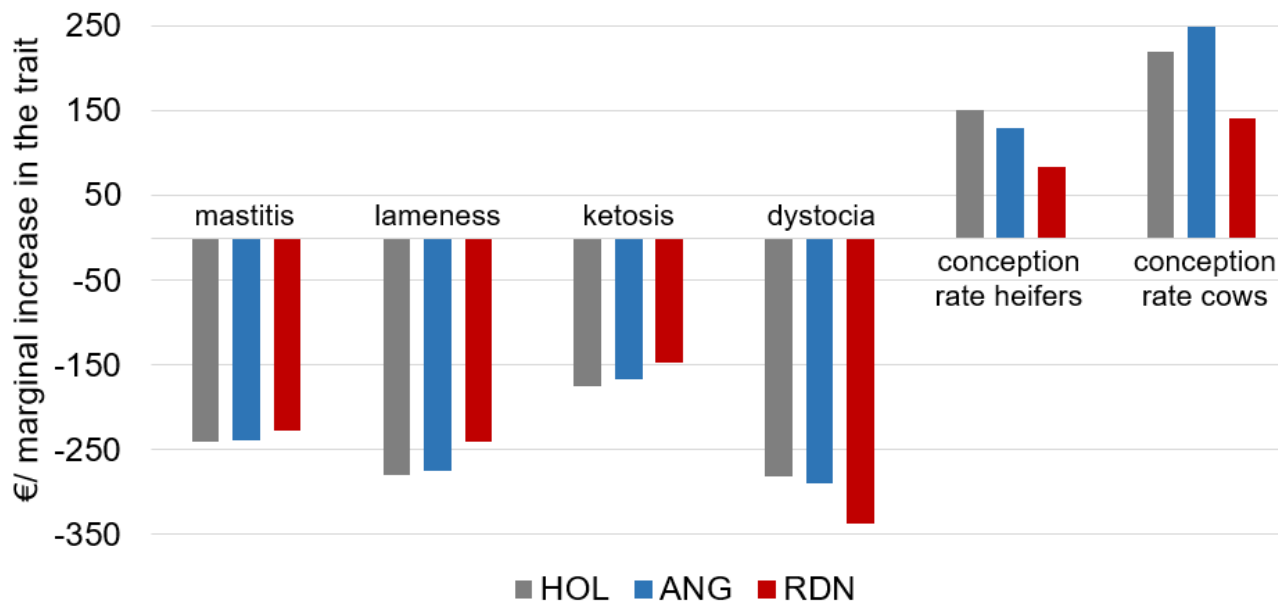


- Bio-economic model SimHerd (Østergaard et al., 2005)
 - Simulation of typical structures in dairy herds
 - Input: phenotypic records (performance, health, reproduction)
- Multiple regression with mediator variables (Østergaard et al., 2016)
 - Prevention of 'double counting' of effects



Calculation of economic weights

Calculated EVs for selected breeding traits



Differences in EV's are due to different assumptions for:

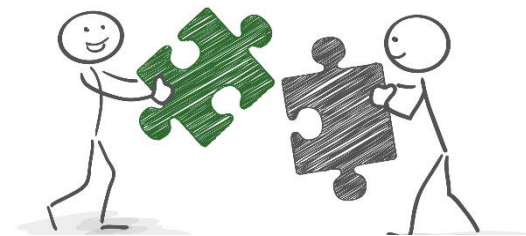
- Performance levels
- Incidence rates
- Reproduction levels
- Market prices

➤ Calculation of economic values for other European Red Dairy Breeds should follow



Breeding scheme simulations

- Heterogeneous conditions regarding Red breeds in Europe
 - Environmental and production conditions
 - Market circumstances (prices, costs, political regulations)
 - Different priorities of farmers (production, health, robustness)
- Enhancing cooperation between breeding organizations
 - Planned workshop → to identify the needs and perceptions of industrial partners regarding the future of Red dairy cattle
- Simulation of breeding scheme scenarios with software ADAM
 - To show the genetic and economic effects of different breeding scheme scenarios





Breeding scheme simulations - Example

Dual purpose

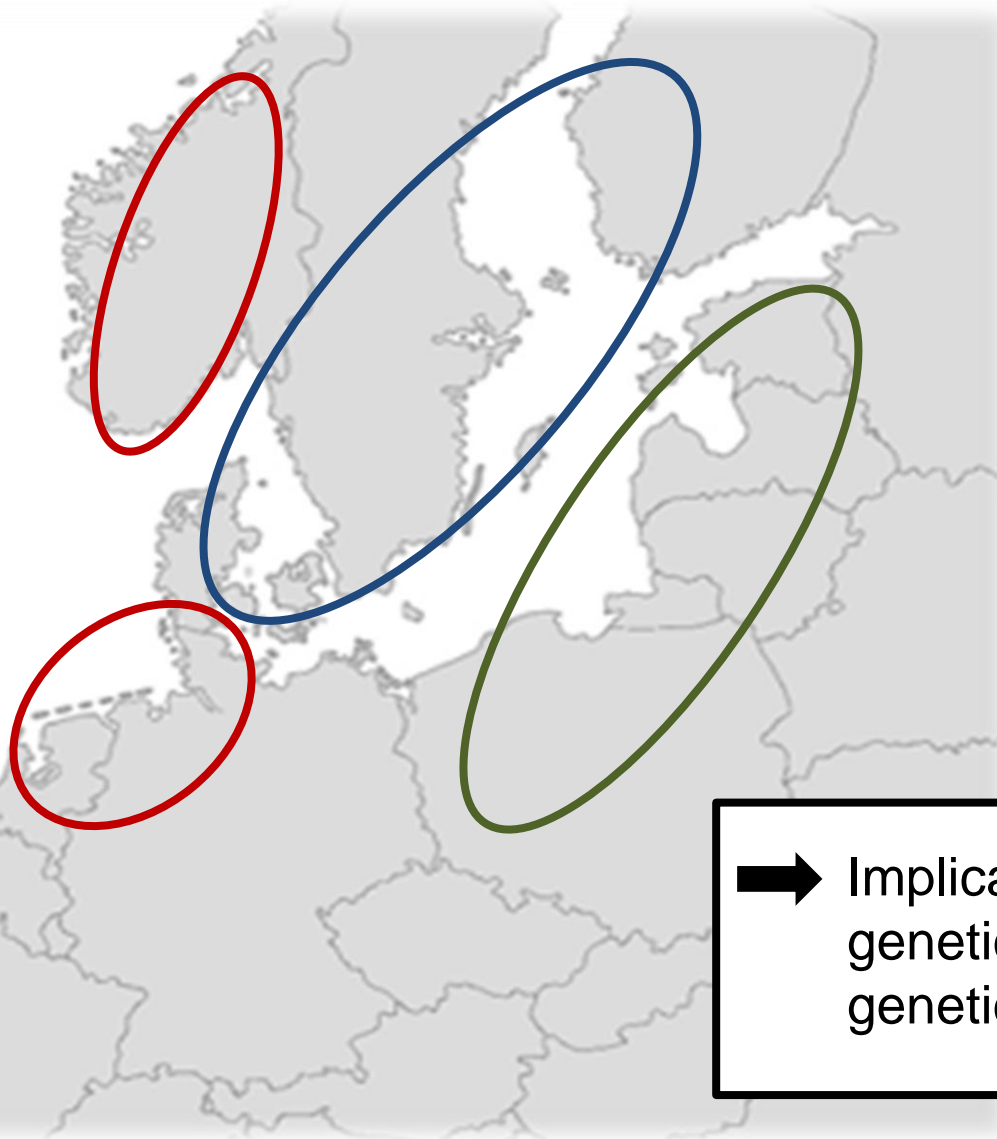
Norwegian Red
MRY
RDN

Dairy type

Finnish Ayrshire
Swedish Red
Danish Red
Angler

Eastern Europe

Lithuanian Red
Latvian Brown
Polish Red



Implications on
genetic gain and
genetic diversity



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Expected outcomes

- Sustainable management of genetic diversity provided by European Red Dairy Breeds
- Formation of joint breeding programs
- Shared genomic resources



**Ultimately: preservation of European Red Dairy Breeds
by improved breeding utilizing their unique
characteristics**



Thank you for your attention!



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