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

Bernt Gulbrandtsen, Christin Schmidtmann, Georg Thaller and the REDIVERSE Consortium
Project leaders: Dirk Hinrichs and Georg Thaller

ERP F Meeting
Madrid, May 20, 2019
Motivation

Objectives of ReDIVERSE

ReDIVERSE partners

Work packages

Expected outcomes of ReDIVERSE
- Motivation

- Objectives of ReDIVERSE

- ReDIVERSE partners

- Work packages

- Expected outcomes of ReDIVERSE
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 have a reputation for superior functional characteristics

- High fertility
- Outstanding udder health
- Low incidence of stillbirth
- Good conformation of legs and claws
Motivation

- European Red Dairy Breeds (ERDB) represent a unique source of genetic diversity
- ERDB are well known for superior functional characteristics
  - high fertility
  - outstanding udder health
  - low incidence of stillbirth
  - good conformation of legs and claws
  - complex histories of gene flow and connectedness
  - local adaptation to various environments
  - cultural heritage

Despite their qualities, ERDB are increasingly replaced by higher yielding breeds (e.g., Holstein-Friesian)
Importance of genetic diversity

Genetic diversity – a resource deserving protection

- Animal genetic diversity is a unique and irreplaceable heritage
- Potential to adapt to changing environments
- Ensures 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!
Genomic selection

Phenotypes → Reference population → Genotypes

Statistical analysis

\[ y = Xb + \sum Z_i s_i + e_i \]

Estimation of SNP-effects

Selection based on genomic estimated breeding values
Impact of genomic breeding

Genetic gain (NTM) in Nordic Holstein bulls

NTM 2000-2007 = +3.2 per year
NTM 2010-2013 = +4.8 per year

+50% genetic gain
Impact of genomic breeding

Genetic gain (NTM) in Nordic Red bulls

NTM 2007-2011 = +2.5 per year
NTM 2011-2016 = +3.8 per year

+50% genetic gain
Eurogenomics helps Holstein

- Many Holstein bulls are tested
- Holstein populations have large reference populations
- Now Germany, France, Spain, the Netherlands, Poland, Denmark, Finland and Sweden share their reference
  • Shared development of customized Holstein chip
  • Big improvement of gain
  • In Red breeds: testing of huge numbers of females with EG chip expands red breed reference
Dairy breeds in Northern Germany

Development of dairy cows under milk recording in Schleswig-Holstein

No. of animals

Year

German Holstein

Red-and-White Dual Purpose

Red Angler

(LKV, 2017)
## Dairy breeds in Northern Germany

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

<table>
<thead>
<tr>
<th></th>
<th>Red Angler</th>
<th>Red-and-White Dual Purpose</th>
<th>German Holstein</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of animals in milk recording (2017, SH)</td>
<td>10,257</td>
<td>20,730</td>
<td>233,003</td>
</tr>
<tr>
<td>Milk yield (kg)</td>
<td>7,766</td>
<td>6,771</td>
<td>8,804</td>
</tr>
<tr>
<td>Fat %</td>
<td>4.60</td>
<td>4.34</td>
<td>4.09</td>
</tr>
<tr>
<td>Protein %</td>
<td>3.61</td>
<td>3.50</td>
<td>3.41</td>
</tr>
</tbody>
</table>
How to help the ERDB?

• Support cooperation in breeding
• Support cooperation in breeding value prediction
• Protect unique characteristics
• Exploit advantageous characteristics in breeding
• Understand farmers’ needs and priorities
Motivation

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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
- Survey of farmers’ preferences keeping Red Dairy breeds
**Overall Impact:** Raise awareness of the value of genetic resources and demonstrate economically sustainable concepts to conserve and effectively utilise the unique biodiversity of European Red dairy breeds.

**WP7: Breeding goals and conservation strategies for the European Red Dairy Breeds**

- **Functional concepts**
- **Breeding concepts**
- **Conservation concepts**

**WP1: Dissemination and exploitation**

**WP5: Economic and social impact**

**WP2: Connectedness and population structure**

**WP3: Genomic and proteomic tools and resources**

**WP4: Development of selection models**

**WP6: Genomic selection strategies**
European Red Dairy Breeds

<table>
<thead>
<tr>
<th>Breed</th>
<th>Herdbook animals</th>
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</thead>
<tbody>
<tr>
<td>Meuse–Rhine-Yssel</td>
<td>17,771</td>
</tr>
<tr>
<td>Groningen White Headed</td>
<td>2,488</td>
</tr>
<tr>
<td>Deep Red</td>
<td>1,563</td>
</tr>
<tr>
<td>Dutch Red Friesian</td>
<td>700</td>
</tr>
<tr>
<td>Modern Angeln Cattle</td>
<td>10,257</td>
</tr>
<tr>
<td>Red and White Dual Purpose</td>
<td>2,846</td>
</tr>
<tr>
<td>Vorderwald Cattle</td>
<td>6,050</td>
</tr>
<tr>
<td>Hinterwald Cattle</td>
<td>600</td>
</tr>
<tr>
<td>Finnish Ayrshire</td>
<td>190,000</td>
</tr>
<tr>
<td>Swedish Red and White Cattle</td>
<td>130,000</td>
</tr>
<tr>
<td>Modern Red Danish Cattle</td>
<td>40,000</td>
</tr>
<tr>
<td>Latvian Brown</td>
<td>44,280</td>
</tr>
<tr>
<td>Lithuanian Red</td>
<td>30,295</td>
</tr>
<tr>
<td>Estonian Red</td>
<td>18,000</td>
</tr>
</tbody>
</table>
- Motivation
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REDIVERSE partners

Academic partners

- Germany (Kiel, Kassel, Hohenheim)
- The Netherlands (Wageningen)
- Denmark (Aarhus)
- Sweden (Uppsala) w. Interbull
- Norway (Ås)
- Lithuania (Vilnius)
- Poland (Wroclaw)
Industrial partners

- CRV
- Rinderzucht Schleswig-Holstein eG
- Viking Genetics
- Lithuanian Red Cattle Improvement Association
- Animal Breeders Association of Latvia
- Geno
- Motivation
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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 to 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 and population structure

Numbers of pedigree information per sex and reporting country

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

(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 by trait/country

<table>
<thead>
<tr>
<th>Trait/Country</th>
<th>Production</th>
<th>Udder health</th>
<th>Conformation</th>
<th>Longevity</th>
<th>Calving ease</th>
<th>Female fertility</th>
<th>Workability</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lithuania</td>
<td>X</td>
<td>X</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Denmark, Sweden, Finland</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
</tr>
<tr>
<td>Netherlands</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
</tr>
<tr>
<td>Germany</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
</tr>
<tr>
<td>Latvia</td>
<td>X</td>
<td>X</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Poland</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Norway</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
</tr>
</tbody>
</table>

(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
- 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
- Detect admixture in genomic data
ERDB chip add-on

• Design a customization of chips suitable for Red Dairy Breeds

• To include:
  • QTL-associate SNP
  • Breed private SNP
   • Imputation support SNP for Red Dairy Breeds
  • Red Dairy Breed milk protein variants

• Will include findings from whole-genome sequencing in Red Dairy Breeds

• Deploy chip in Red Dairy populations with too small reference populations
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

North West European clade
Holstein clade
RDM-70 clade
Nordic Red clade
BSW clade
Alpine Dairy clade

(Anna Schönherz et al., 2018)
WP 4 – Development of selection methods

Leader WP4: Jörn Bennewitz, 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
  - Focusing 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 maximize 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

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

Applied methods: Quantitative approaches from social sciences, e.g., discrete choice experiments, interviews
Which determinants influence farmers’ participation in conservation programs for dairy cattle breeds?

Discrete Choice Experiments, 159 German cattle breeders

<table>
<thead>
<tr>
<th></th>
<th>Contract 1</th>
<th>Contract 2</th>
<th>Opt-out</th>
</tr>
</thead>
<tbody>
<tr>
<td>Compensation payment</td>
<td>250€/LU/year</td>
<td>250€/LU/year</td>
<td></td>
</tr>
<tr>
<td>Collective Bonus (population increase &gt; 5%)</td>
<td>40€/LU/year</td>
<td>0€/LU/year</td>
<td>No contract</td>
</tr>
<tr>
<td>Conservation breeding program (pairing)</td>
<td>No</td>
<td>Yes</td>
<td></td>
</tr>
<tr>
<td>Keeping conditions</td>
<td>No requirements</td>
<td>Access to free-range area or pasture</td>
<td></td>
</tr>
<tr>
<td>Contract duration</td>
<td>5 yrs</td>
<td>1 yrs</td>
<td></td>
</tr>
<tr>
<td>I choose</td>
<td>☑</td>
<td>☐</td>
<td>☐</td>
</tr>
</tbody>
</table>

(Julia Schreiner, 2018)
WP 5 – Economic and social impact

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

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

(Julia Schreiner, 2018)
WP 5 – Economic and social impact

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

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
Genomic selection strategies

Leader WP6: Mario Calus, Wageningen University

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

Improve competitiveness and create a long-term perspective for European Red Dairy Breeds
WP 6 – Genomic selection strategies

**Challenges:** European Red Dairy breeds
- Small population sizes
- Few progeny tested bulls
- Heterogeneous populations

**Possible solution:**
- Multi-breed reference population
- Composition of reference population ?
- Which breeds are useful to include ?
- Connectedness
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

<table>
<thead>
<tr>
<th>Breed</th>
<th>N</th>
</tr>
</thead>
<tbody>
<tr>
<td>MRY</td>
<td>423</td>
</tr>
<tr>
<td>Groningen White Headed (GWH)</td>
<td>129</td>
</tr>
<tr>
<td>Dutch Belted (DB)</td>
<td>41</td>
</tr>
<tr>
<td>Dutch Friesian (DF)</td>
<td>352</td>
</tr>
<tr>
<td>Deep Red (DR)</td>
<td>44</td>
</tr>
</tbody>
</table>

(Jovana Marjanovic, 2018)
WP 6 – Genomic selection strategies

## Results

<table>
<thead>
<tr>
<th></th>
<th>MRY</th>
<th>GWH</th>
<th>DB</th>
<th>DF</th>
<th>DR</th>
</tr>
</thead>
<tbody>
<tr>
<td>MRY</td>
<td>293</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GWH</td>
<td>17906</td>
<td>151</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>DB</td>
<td>14883</td>
<td>16315</td>
<td>104</td>
<td></td>
<td></td>
</tr>
<tr>
<td>DF</td>
<td>16452</td>
<td>10890</td>
<td>7625</td>
<td>212</td>
<td></td>
</tr>
<tr>
<td>DR</td>
<td>3662</td>
<td>17516</td>
<td>17047</td>
<td>14560</td>
<td>149</td>
</tr>
</tbody>
</table>

(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
Genomic selection strategies

Results

<table>
<thead>
<tr>
<th></th>
<th>MRY</th>
<th>GWH</th>
<th>DB</th>
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(Jovana Marjanovic, 2018)

Within $M_e$

Between $M_e$

- $M_e$ 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

- Breeding goal setting for European Red Dairy Breeds
  - Development of national and transnational breeding objective and improvement programs
  - Conservation of genetic diversity
- Evaluation of breeding schemes with respect to genetic gain, genetic diversity and promotion of breed-specific characteristics
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 (heifers+lactating cows)
  - Input: phenotypic records (performance, health, reproduction)

- Multiple regression with mediator variables (Østergaard et al., 2016)
  - Prevention of “double counting” of effects
WP 7 – Development of breeding goals + conservation strategies

Economic values for selected 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 next
Implications on genetic gain and genetic diversity

**Dairy type**
- Finnish Ayrshire
- Swedish Red
- Danish Red
- Angler

**Dual purpose**
- Norwegian Red
- MRY
- RDN

**Eastern Europe**
- Lithuanian Red
- Latvian Brown
- Polish Red

Stochastic simulations:
- Implications on genetic gain and genetic diversity
- Motivation
- Objectives of ReDIVERSE
- ReDIVERSE partners
- Tasks of the work packages
- Expected outcomes of ReDIVERSE
Expected outcomes

- Sustainable management of genetic diversity provided by European Red Dairy Breeds
- Formation of aligned breeding objectives
- Collaboration in evaluation
- Shared genomic resources

Ultimately: \textit{preservation} of European Red Dairy Breeds by improved breeding \textit{utilizing} their \textit{unique} characteristics
Thank you for your attention!

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