

**REDIVERSE**  
**Biodiversity within and between European Red dairy breeds – conservation through utilisation.**  
( Research and Innovation actions)

Start of the project – April 3, 2017  
End of the project – May 3, 2020  
Budget – 1 790000,00 / 100000,00 EUR

The European Red dairy cattle breeds (ERDB) sustain unique genetic diversity, are well adapted to local diverse farming conditions and are clearly superior in functional and health traits. Nevertheless these breeds are more and more replaced by higher yielding but less adapted and less robust breeds. The irreplaceable genetic diversity of these breeds is underutilized in favour of higher yielding, yet less adapted and robust breeds. So, the main objective of REDIVERSE is to develop and demonstrate economically and corporately sustainable concept to preserve and effectively utilize the unique biodiversity of European Red dairy breeds. REDIVERSE focus on the conservation of genetic diversity and competitiveness of ERDB by development of enhanced methodologies for population management, conservation strategies, characterisation and evaluation of genetic resources and the promotion of an increased demand for diverse, high-quality ERDB products, e.g. with enhanced functionality and health benefits for consumers. Furthermore, the effect of using ERDB are investigated with respect to animal welfare, productivity and economic gains. All in all, REDIVERSE activities increase awareness of the value of genetic resources by end-users and result in a stronger engagement of end-users in the sound management of these resources. REDIVERSE focus on force up the competitiveness of Red dairy breeds by development of enhanced methodologies for management, conservation, characterisation and evaluation of genetic resources and an increased availability of diverse, high quality products, e.g. with enhanced health benefits for consumers.

REDIVERSE will reach this ambitious goal by pursuing these six objectives: 1. Development of a breeding model for ERDB. 2. Development of genome-based future conservation concepts. 3. Identification of beneficial effects of ERDB milk and milk proteins. 4. Demonstration of socio-economic advantages of ERDB: demonstration of beneficial social and economic effects associated with breeding of the locally and culturally anchored ERDB. 5. Development of a comprehensive strategy for ERDB breeding and conservation: combine new precision breeding, selection, and conservation concepts with economic consequences and possibilities for development and marketing of new products considering the socio-economic aspects at farm level; development of cooperation strategies for ERDB across countries. 6. Raise awareness for the value of genetic resources by end-users through dissemination.

**Work packages:**

**WP1: Dissemination and Exploitation** - will be responsible for monitoring the project progress specifically with respect to time-line and milestones as indicated for the work packages; dissemination of results to stakeholders and end-users and managing the exploitation of results as well as use of data after the project has ended -

**WP2: Connectedness and population structure** - will substantially improve our understanding of the population structure and genetic connectedness between different ERDB. Population history in the more distant past, fine-scale responses to migration events (footprints of other breeds) and selection (selection signatures) as well as population differentiation will be analyzed using genomic

data, i.e. genotypes and sequence data. WP 2 will exploit all the pedigree and marker data available at the start of the project and define a best practice for phenotype collection and estimation of inbreeding. WP2 will identify key animals for further genotyping and sequencing. All in all this work package will improve *in situ* conservation of genetic resources by the farming sector, enhance characterisation of genetic diversity within and between breeds, and increase the awareness of the value of present genetic resources in ERDB.

**WP3: Genomic and proteomic tools & resources** - will generate genomic data and validate genomic findings with respect to patterns of milk protein variants at the proteome level and study possible functional implications for human health. This WP will design an SNP chip customized for the ERDB, which provides high-quality genomic information for genomic selection (GS). Characterization of breed differences at the sequence level will support the development and implementation of strategies to exploit this new knowledge to conserve genetic diversity (GD). WP3 will improve understanding of how population admixture is detectable in genomic data.

**WP4: Development of selection methods** - ERDBs and other local breeds are faced with the problem that improving genetic gain by selection proceeded slowly due to the small population sizes. Consequently, genetic gain was largely achieved by introgression of genetics from Holstein and other higher-yielding breeds. These migrant contributions elevated genetic gain for milk yield, but reduced the genetic distinctness of the breeds. Moreover, the heterosis that was exploited by breeders during the first generations of introgression was lost in subsequent generations. Never the less, introgression continued until quite recently. It is likely to continue after introduction of genomic selection. The effects of alleles originating from higher-yielding breeds are estimated more accurately, so selection for yield will favour chromosome segments originating from these higher-yielding breeds. Genetic gain in higher-yielding breeds has been accelerated considerably in recent years due to the introduction of genomic selection. This was not the case for most ERDB due to their smaller population sizes. This has diminished their competitive ability. On the other hand, ERDB are very well suited as crossing partners with higher-yielding breeds in a two or three breed rotational cross breeding scheme designed to exploit heterosis effects and improve functional traits. Therefore, the objectives of the selection methods that will be developed in this WP are twofold. First to increase competitiveness and genetic uniqueness of Red dairy cattle as pure breeds, and, second, to increase competitiveness by using Red dairy cattle as crossing partners for high yielding breeds such as Holsteins.

**WP5: Economic and social impact** - the overarching objective of WP 5 is to highlight the economic value of red breeds diversity and to establish the costs of conserving that diversity.

Specific objectives: for red dairy breeds that are still used in milk production and that are potentially competitive, the key objective is to establish the reasons why farmers prefer red breeds to specialized modern dairy breeds. For red dairy breeds that are threatened by marginalization and extinction, the key objective is to identify the conditions under which farmers would be willing to conserve the animal genetic resources of local red breeds on their farms by participating in appropriate conservation schemes. Such policy schemes offer farmers incentive payments to keep breeds that would otherwise be unprofitable at the farm level but carry high non-market value for society. For red dairy breeds that serve as a potential gene pool for reintroducing specific traits into modern, high-yielding dairy breeds, the primary objective is to elicit farmers' preferences for specific functional traits from red breeds for reintroduction into modern breeds.

**WP6: Genomic selection strategies** - the overall objective is to improve genomic prediction (GP) methods for across breed evaluation and for heterogeneous populations, while maintaining genetic diversity (GD). This is important because not all breeds involved in REDIVERSE are numerically large enough or lack the financial resources to establish a sufficiently large breed-specific reference

population that enables GP with a competitive level of prediction accuracy. Especially for small breeds the number of bulls with daughter based breeding values to be included in the reference population is often limiting. This limitation can be relaxed by adding cows of the same breed to the reference population, or by adding bulls and cows from a different but related breed. Both solutions increase the heterogeneity of the phenotypes and genotypes used in the analyses. This WP will develop procedures and tools to design reference populations that optimally use this kind of heterogeneous data in GP. The developed tools will also be useful for breeds which are not involved in REDIVERSE.

**WP7: Breeding goals & conservation strategies** - the goal of this project is to maintain and conserve genetic diversity in the ERDB improvement programs by generating one or several commercially competitive breeds and promoting this/these on the basis of superior performance. Furthermore, breeding schemes for smaller to medium sized national breeding programs (< 30.000 animals) with specific breeding goals, including traits for niche production, will be optimized. In order to do so breeding goals will be derived and breeding schemes for both large across countries improvement programs and the smaller national breeding programs will be optimized through stochastic simulation. The optimization will be judged on rate of long-term genetic gain for the aggregate genotypes and rate of inbreeding. Use of genomic enhanced breeding values based on different types of reference populations will be used in all simulations. Optimised gene-flow between the large across countries breeding programs and the national breeding programs will facilitate the balance between genetic progress in the ERDB improvement programs and preserving the uniqueness of specific breeds in the national breeding programs. The overall goal is to generate a decision tool to advise industry partners and farmers how to exploit the advantages of ERDB. Further, discrete choice modelling will be undertaken to describe, explain, and predict motives of farmers for keeping ERDB, to ease transmission of results to the industry. All results of the WP will be collated and presented to the industry partners, so that consequences of the various alternatives on genetic gain and diversity are made clear. Finally, a set of recommended action points will be provided to enable efficient uptake of results.

**Partners:**

Kiel University (CAU) Kiel, Germany; University Hohenheim (UH,) Stuttgart, Germany; Wageningen UR Livestock Research (DLO), Wageningen, The Netherlands; Aarhus University (AU) Tjele, Denmark; Swedish University of Agricultural Sciences (SLU) Uppsala, Sweden; Norwegian University of Life Sciences (NMBU) Ås, Norway; Lithuanian University of Health Sciences (LUHS), Kaunas, Lithuania; Wrocław University of Environmental and Life Sciences (WUELS) Wrocław, Poland; CRV BV Wassenaarweg, Arnhem; VikingGenetics (VG) Skara, Sweden; Animal Breeders Association of Latvia (ABAL) Riga, Latvia; Rinderzucht Schleswig-Holstein eG (RSH) Neumünster, Germany; Lietuvos žaliųjų galvijų gerintojų asociacija Šiauliai d., Lithuania.



