



TOWARDS IMPROVEMENT OF **RUMINANT** BREEDING
THROUGH **GENOMIC** AND EPIGENOMIC APPROACHES

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Guidelines to adapt breeding objectives for future environmental conditions and conservation of genetic diversity in dairy cattle

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1 Summary

1.1 Objectives

Provide practical guidelines for adapting dairy cattle breeding objectives to future environmental conditions (with a focus on heat-stress adaptation and robustness) while conserving genetic diversity within and among breeds.

1.2 Rationale/Methodology

The guideline synthesises technical results from multiple RUMIGEN work packages (e.g., THI-based heat-stress analyses and reaction-norm EBVs; diversity management under genomic selection; biomarkers/epigenetics; gene-editing case studies). Recommendations are paired with a Green/Amber/Red acceptance label using the WP2 Room-of-Acceptance framework. Practical scenarios are drafted using a standard casebox template and will be reviewed by breed associations and AI companies for relevance and feasibility.

1.3 Teams involved

EFFAB (lead), INRAE, ELIANCE, IDELE, WR, WU, AU, INIA-CSIC, IRIAF, UEDIN, NMBU, with inputs from WP2 (Room of Acceptance), WP3 (Heat stress), WP4/WP8 (Diversity & trade-offs), WP5 (Genome Editing), WP6/WP7 (Biomarkers/Epigenetics) and WP9 (Dissemination).

1.4 Methodology

The guidelines were developed through a structured process to ensure they are **evidence-based, implementable**, and aligned with stakeholder expectations.

1.4.1 Evidence gathering from RUMIGEN work packages

Technical results and recommendations were extracted from relevant RUMIGEN deliverables across work packages, with an emphasis on outputs that directly inform breeding objectives under future conditions (e.g., heat-stress modelling, reaction-norm EBVs, genomic selection impacts on diversity, biomarkers/epigenetics, and gene-editing case studies). Each WP provided key messages, data/tool requirements, and references (deliverable codes and figure/table anchors).

1.4.2 Synthesis into operational themes and recommendations

Findings were organised into thematic chapters (animal health & welfare; genetic diversity and long-term resilience; climate/heat-stress adaptation; and cross-cutting gene editing). For each theme, results were translated into **actionable recommendations** describing:

- the trait(s) and indicator(s) to use,
- how to incorporate them into selection indices and mating plans,
- minimum data requirements and quality checks, and
- monitoring indicators (KPIs) for implementation.

1.4.3 Development of practical scenarios (caseboxes)

A standard scenario template was used to translate the recommendations into “how-to” caseboxes. Each scenario includes: context, objective, data/tools, intervention (traits and

weights/constraints), feasibility, acceptance considerations, expected impact, diversity guardrails, risks/mitigation, and KPIs/timeline (12–36 months). Scenarios were designed to reflect real decision points faced by breeding organisations and AI centres.

1.4.4 Feasibility and relevance review with end users

Draft scenarios and key recommendations were reviewed for relevance and feasibility by **breed associations and AI companies** using a short scorecard (feasibility, cost/recording burden, and acceptance implications). Feedback was incorporated through iterative revisions, and final “Ready” scenarios were marked only after this co-review step.

1.4.5 Implementation and dissemination packaging (WP9)

Finally, the guideline content was formatted into user-oriented outputs for dissemination under WP9, with consistent use of the scenario template, acceptance labels, and KPI dashboard.

1.5 Basis

Task 8:10: Guidelines to adapt breeding objectives for future environmental conditions and conservation of genetic diversity within/among dairy cattle breeds.

Inputs: WP technical results (all relevant WPs), **WP2 “room of acceptance”**, workshop scenarios (breed associations, AI companies).

Objective: Produce operational guidelines that (i) update dairy breeding objectives for plausible future environments (climate/market/health constraints), (ii) **embed genetic-diversity safeguards**, and (iii) reflect **stakeholder acceptance** (WP2). The guidelines will be evidence-graded, scenario-tested with **breed associations and AI companies**, and packaged for roll-out under **WP9**.

1.6 Purpose

European dairy cattle breeding is under simultaneous pressure from rising heat stress, tightening animal welfare expectations, and accelerating inbreeding under genomic selection. Left unaddressed, these converging challenges will erode herd health, long-term genetic potential, and sector competitiveness. These guidelines translate evidence from the RUMIGEN research project (Work Packages 2–8) into an operational playbook for breeding organisations, AI centres, recording bodies, breed associations, and regulators.

The central proposition: select animals that perform well and hold up under stress, while keeping genetic diversity intact as a long-term resource. Every recommendation is paired with an evidence grade and a Green / Amber / Red acceptance label derived from the WP2 Room-of-Acceptance framework, so technical choices remain anchored in social and stakeholder context.

1.7 The Four Themes at a Glance

1.7.1 Theme A — Animal Health & Welfare

Health and robustness traits — mastitis, lameness, metabolic stability, fertility disorders, and calf vitality — are elevated from secondary considerations to core breeding goals. Reaction-norm Estimated Breeding Values (EBVs) score each animal on two dimensions: typical performance under normal conditions and performance under stress. Optimal Contribution Selection (OCS) ensures welfare gains do not come at the cost of genetic diversity.

1.7.2 Theme B — Genetic Diversity & Long-Term Resilience

Diversity is treated as a hard constraint, not a trade-off. OCS with genomic (ROH/IBD-aware) relationship matrices caps inbreeding at $\Delta F \leq 0.5\%$ per generation for large breeds, with stricter limits for small and local breeds. Sire usage caps and allele-reweighting protect rare, favourable variants from drift. Public-facing diversity dashboards are recommended to accompany genetic trend reports.

1.7.3 Theme C — Climate & Heat-Stress Adaptation

Reaction-norm evaluations generate two numbers per trait: a level (performance under thermoneutral conditions, THI ≈ 50) and a slope (rate of decline under heat load, THI ≈ 70). RUMIGEN analyses across five populations (French and Spanish Holsteins, Dutch Holstein, French Montbéliarde, Dutch Meuse-Rhine-Yssel) show that high-producing animals are systematically more heat-susceptible in both fertility and production. Robustness-oriented selection is therefore a strategic priority, not an optional add-on.

1.7.4 Theme D — Gene Editing (Cross-Cutting)

Gene editing (GE) is positioned as a last-resort, case-by-case tool within a 'select → manage → (if justified) edit' decision hierarchy. No GE application is recommended without a Green or conditional Amber acceptance label and explicit diversity guardrails. The current EU regulatory gap (post-ECJ 2018 ruling, pending animal NGT regulation) means most applications remain in the R&D or pre-commercial phase. Stakeholders are encouraged to engage with ongoing policy processes and ensure evidence and traceability frameworks are ready.

1.8 Implementation

A phased three-stage implementation framework assigns clear actions, KPIs, and responsibilities to six stakeholder groups: breeding organisations, breed societies, AI centres, recording organisations, regulators, and researchers. FAIR data pipelines (Findable, Accessible, Interoperable, Reusable), standardised THI linkage windows (3-day for milk/SCC; 8-day for conception rate), and model cards are required infrastructure.

1.9 Tracking Progress

Table 1 KPIs for tracking progress

KPI	Target / Signal
Inbreeding rate (ΔF)	$\leq 0.5\%$ per generation for large breeds; tighter for small/local breeds (OCS-controlled)
Conception rate at high THI	Stable or improving trend at THI ≥ 70 ; no systematic re-ranking toward heat-susceptible sires
Mastitis / SCC trend	Declining mastitis incidence and SCC under stress conditions; welfare sub-index score maintained

1.10 How to Use This Document

- Breeding organisations & AI centres: start with Themes A–C for trait definitions and tool specifications, then use the Implementation Playbook for phased rollout.
- Breed societies & associations: focus on the Practical Scenarios, the Room-of-Acceptance labels, and the Key Takeaways boxes at the end of each Theme.

- Recording organisations & data hubs: the FAIR data section of the Implementation Playbook and Theme C's THI linkage specifications are your primary reference.
- Regulators & policymakers: the Acceptance labels (Green/Amber/Red) and the Gene Editing theme (Theme D) cover governance and traceability requirements.
- Researchers: Themes A–C provide validated model specifications; the Annexes contain trait definitions, THI protocols, and the Room-of-Acceptance scoring template.

2 Introduction

European dairy breeding is entering a period of hotter summers, tighter welfare expectations, and the need to safeguard genetic resources. This guideline turns RUMIGEN evidence into practical direction on adapting breeding objectives for future environments while preserving diversity within and among breeds. It sets out clear trait definitions (including heat tolerance and other functional traits), selection and mating tools (reaction-norm EBVs, optimal contribution selection), diversity guardrails, and one-page scenarios co-designed with breed associations and AI companies. These guidelines synthesize technical findings from WPs 2–8 (heat-stress modelling, diversity-aware selection, biomarkers/epigenetics, GE pilots) and apply the WP2 Room-of-Acceptance framework to every recommendation.

Every recommendation carries an evidence grade and a Green/Amber/Red acceptance label from the WP2 “Room of Acceptance,” keeping technical choices anchored in social context. In short: a concise, operational playbook to sustain performance under stress today and protect adaptability for tomorrow.

Table 2 Audience and how the guidelines is used

Audience	How they use this guideline
Breeding organisations & breed societies	Update goals, index weights, and mating policies while capping ΔF and tracking ROH
AI centres & breeding companies	Select and disseminate sires/embryos using level+slope EBVs; apply OCS and usage caps
Recording organisations & data hubs	Standardise trait definitions and THI windows; ensure FAIR pipelines and QA/QC
Regulators & competent authorities	Check alignment with welfare/diversity aims; note GE context and labelling/traceability needs
Researchers & service providers	Develop/validate models, biomarkers, epigenetic pilots, and decision tools

2.1 Scope — what this guideline covers

- Dairy cattle (transferable methods for other ruminants with calibration).
- Adapting breeding objectives to future environments while conserving genetic diversity within/among breeds.
- Outputs: trait definitions, selection/mating tools (reaction-norm EBVs, OCS), diversity guardrails (ΔF /ROH), acceptance labels, and practical scenarios co-designed with breed associations & AI centres.
- Not legal/regulatory advice; not a replacement for national economic weighting. For navigation guidance by role, see the “How to Use This Document” section in the Executive Summary.

2.2 Guiding Principles

- Animal welfare by design: prioritise resilience, robustness, health, fitness; avoid unintended welfare trade-offs.

- Genetic diversity as a constraint: explicit guardrails (e.g., ΔF targets, ROH, OCS) alongside gain.
- Transparency & accountability: publish trait choices, weights, assumptions, and expected trade-offs.
- FAIR data stewardship: data are Findable, Accessible, Interoperable, Reusable with QC and privacy (see Implementation Playbook for data standards and ready-to-adopt defaults).
- Evidence-graded, acceptance-aware: each recommendation carries an evidence grade and G/A/R label.
- Proportional risk management: safeguards match the magnitude/reversibility of potential impacts.

2.3 Foundations

2.3.1 Definitions

- **Epigenetics:** heritable changes in gene activity without DNA sequence change (e.g., DNA methylation, histone marks, small RNAs) that can reflect environment/management and contribute to intergenerational effects.
- **Resilience** is the ability to **recover quickly and return to normal** after a challenge (e.g., heat, disease, feed change). *Typical measures:* recovery time and size/duration of deviations from baseline (milk, activity, health).
- **Robustness** is the ability to **stay stable and avoid big losses** when conditions are challenging. *Typical measures:* smaller performance drop under stress (flatter slope), fewer disease events, stable fertility/SCC
- **New/functional traits:** sustainability-oriented traits added or refined (e.g., heat-tolerance slope, disease resistance, longevity, methane proxies, robustness indicators, fertility quality). Validation path: discovery → pilot → routine.

Temperature-Humidity Index (THI): a combined measure of air temperature and relative humidity used to quantify heat load on livestock. $THI = (1.8 \times T + 32) - (0.55 - 0.0055 \times RH) \times (1.8 \times T - 26)$, where T = temperature (°C) and RH = relative humidity (%). Values above 68 indicate onset of heat stress in dairy cattle. Used throughout this guideline with standardised linkage windows: 3-day window around test date for milk/SCC; 8-day window around AI for conception rate.

- **Gene editing modalities:**
 - SDN1: small indels via error-prone repair (no template).
 - SDN2: precise small edits using a short template.
 - SDN3: targeted larger insertions/replacements.
Programme choices must reflect current legal/market context.

2.3.2 Acceptance labels (Green / Amber / Red)

Purpose: Pair technical recommendations with a quick, comparable acceptance signal.

How to assign: Score the Room of Acceptance dimensions (welfare, intrusiveness vs conventional, ownership, naturalness, benefits/risks, responsibility, trust, economic effects). Then assign:

- Green — broadly acceptable: clear welfare/benefit, manageable risks, transparent governance.
- Amber — conditional: proceed with mitigations (e.g., stricter ΔF cap, traceability, phased pilot, extra engagement).
- Red — not acceptable now: do not implement; redesign or gather further evidence.

3 Theme A: Animal Health & Welfare

Welfare-by-Design: Breeding for healthy, robust cows that thrive

3.1 Introduction / The Problem

The challenge

Health and welfare traits (mastitis, lameness, metabolic stress, fertility disorders, calf vitality) are under-recorded, heterogeneous across countries, and often **underweighted** in breeding goals. Many evaluations still emphasise output (milk volume/components) over **robustness and resilience**, and environmental stress (e.g., heat, feed variability) can turn small trade-offs into large welfare costs.

Why it matters

- **Sustainability:** healthier cows live longer, waste less, and use inputs more efficiently.
- **Welfare & ethics:** proactive selection reduces pain, disease and interventions (antibiotics, culling).
- **Competitiveness:** robust herds maintain production during stress, lowering vet costs/downtime.
- **Policy & market:** aligns with EU welfare ambitions, antimicrobial reduction, and public expectations.

3.2 Solution

A **welfare-by-design** approach to breeding objectives:

- Elevate **health and robustness traits** to core goals, not add-ons.
- Use **reaction-norm EBVs (EBVs that estimate both typical performance and how that performance changes under stress)** (level+slope) so health performance is valued **under stress** (e.g., heat, negative energy balance).
- Integrate **early-warning phenotypes** (activity, rumination, temperature, SCC dynamics, metabolic indicators) and **composite welfare indices**.
- Apply **optimal contribution selection (OCS — a mathematical framework that maximises genetic gain while capping the rate of inbreeding per generation)** so health gains don't erode genetic diversity.
- Pair each recommendation with a **Green/Amber/Red acceptance label** and an **evidence grade**.

3.3 Impact / Benefits

For scientific knowledge

- Better genotype-to-phenotype links via richer health phenotypes, longitudinal sensors, and (where available) biomarker/epigenetic signals.
- Validated models for **robustness** (resilience indices, health reaction norms).

For stakeholders (breeding orgs, AI centres, farmers)

- Fewer disease events (mastitis, lameness), improved **fertility under heat**, longer productive life.
- Clear KPIs (e.g., mastitis incidence trend, cull risk, resilience score) to steer selection and on-farm decisions.

Broader societal/environmental

- Reduced antibiotics use and treatment emissions; improved animal wellbeing and consumer trust.
- More stable supply with fewer “shock” losses in heat waves or feed disruptions.

3.4 How it Works

3.4.1 Key features

- **Trait set & definitions:** clinical/subclinical mastitis (event-based & SCC dynamics), lameness/locomotion, metabolic stability (NEFA/BHBA proxies), fertility quality (non-return rate, conception under high THI, interval traits), calf vitality, temperament/handling ease.
- **Models:** multi-trait with **reaction norms** (health level + slope under stressors); genomic predictions augmented by routine data; optional biomarker/epi pilots for hard-to-measure traits.
- **Indices:** increase a **Health & Welfare sub-index** with minimum weights and **guardrails** (e.g., no net loss of welfare score when reweighting for production).
- **Diversity:** run **OCS** with ΔF targets; monitor **FROH** and sire usage to avoid bottlenecks while pushing health gain.

3.4.2 Examples

- **Mastitis-aware selection:** combine SCC dynamics + mastitis events; penalise sires with steep “worse-under-heat” slopes.
- **Fertility-under-heat:** select on conception-rate level at moderate THI **and** on slope near high THI; publish both in sire proofs.
- **Robustness and resilience index:** integrate activity, rumination, and milk perturbation recovery as a composite “bounce-back” score.

3.4.3 Access

- **Data & tools:** national health recording, sensor streams, THI feeds; standard APIs to data hubs; reference pipelines for QC.
- **Transnational collaboration:** shared trait definitions/metadata; cross-country evaluations where feasible; case-exchange of welfare indices.
- **Standards, ethics, QA:** FAIR metadata, farmer consent for health data, transparent model cards (assumptions, limits), periodic bias checks.

3.5 What’s Next / Future Outlook

- Scale **sensor-derived** health indicators into routine evaluations.
- Pilot **biomarker/epigenetic** augmentation on fertility/robustness where cost-effective; report Δ -accuracy and calibration.

- Add **behaviour/temperament** and **calf vitality** more consistently to indices.
- Publish **acceptance labels** with each release; co-design communication with farmers and vets.
- Annual review of **welfare weights and guardrails** as evidence and markets evolve.

3.6 Key Takeaways / For Non-Experts

- Health and welfare are **built into** breeding—not bolted on.
- We select animals that **stay healthy and fertile under stress**, not just those that perform in perfect conditions.
- Diversity matters: we use tools that **limit inbreeding** while improving welfare.
- You'll see **simple labels** (Green/Amber/Red) alongside recommendations, so you know where society stands and what mitigations are in place.
- Expect clearer proofs: **two numbers per trait** (typical performance and performance under stress) to make practical choices easier.

4 Theme B: Genetic Diversity & Long-Term Resilience

Diversity-as-Design: Keeping options open while making progress

4.1 Introduction / The Problem

4.1.1 The challenge

Genomic selection and market pressure can concentrate sire usage and accelerate inbreeding, shrinking effective population size (N_e) and fixing long runs of homozygosity (ROH). Small/local breeds are especially vulnerable; even large breeds risk losing rare, favourable alleles and adaptive potential (e.g., heat tolerance, disease resistance).

4.1.2 Why it matters

Sustainability & welfare: genetic variety underpins robustness to heat, disease, feed shocks.

Competitiveness: programmes with higher N_e keep response possible over decades (less plateauing).

Policy & society: aligns with EU genetic resources targets and public expectations to safeguard biodiversity.

4.2 Solution

Make diversity a hard constraint in breeding objectives and day-to-day decisions:

- Use Optimal Contribution Selection (OCS) to cap ΔF per generation while maximising gain.
- Track and manage genomic diversity (FROH, segment-level IBD) — not just pedigree.
- Balance short- vs long-term response with allele-reweighted selection where drift threatens valuable variants.
- Design usage policies (caps, minimum sire numbers) and mating plans that spread risk without sacrificing too much gain.

4.3 Impact / Benefits

4.3.1 For scientific knowledge

- Routine, segment-aware metrics (FROH by length class; IBD segment tracking) enable research on linkage drag, heterozygosity–fitness links, and long-horizon response.
- Validation of OCS/allele-reweighting strategies across breeds and trait architectures.

4.3.2 For stakeholders

- Breeding orgs/AI centres: predictable gain with tighter inbreeding control; fewer “genetic dead-ends.”
- Farmers: steadier performance across years; reduced recessive disorder risk; more resilient calves and cows.

4.3.3 Broader societal/environmental

- Preservation of within- and among-breed diversity; options to respond to future climate/market change.
- Credible alignment with conservation policy and consumer trust.

4.4 How it Works (Mechanism / Key Features / Examples)

4.4.1 Key features

Targets & guardrails:

- set $\Delta F \leq 0.5\%/gen$ for large breeds (tighter for small/local); monitor N_e , FROH, and top-N sire share.
- OCS engine: optimise contributions using A (pedigree) and G/IBD (genomic, segment-aware) relationship matrices.

Mating & usage policies:

- Minimum sire numbers per cohort; caps on top-10 sire contribution.
- Mate allocation to avoid long ROH in offspring; penalise mating pairs that stack identical long segments.
- Allele-reweighting: when key favourable alleles are drifting downward, add a mild weight to their frequency in sire ranking (bounded to avoid distortion).

Breed-portfolio measures:

- For small/local breeds (e.g. Montbéliarde, Meuse-Rhine-Yssel, and other regional breeds), combine index variants (e.g., welfare/robustness emphasis) with cryo-recovery or targeted introgression from related stocks.

4.4.2 Examples

Large breed (Holstein):

- OCS + IBD matrices; publish FROH>8Mb prevalence quarterly; rank sires with a small penalty on long shared segments with the female pool.

Local breed:

- Enforce minimum S sires/year; OCS under tighter ΔF ; periodic cryobank inflow; allele-reweighting on 2–3 rare, favourable variants (with sunset dates).

Diversity-aware GE/introgression:

- If a welfare allele is validated via GE elsewhere, consider introgression path for acceptance; when GE is used in R&D, parallel OCS to avoid founder bottlenecks.

4.4.3 Access

- Data & tools: routine genotypes; phased haplotypes; ROH/IBD callers; OCS solver integrated with evaluation outputs.
- Transnational collaboration: share segment panels, diversity dashboards, and cryobank catalogues; coordinate cross-border use to avoid correlated bottlenecks.

- Standards, ethics, QA: transparent diversity dashboards (definitions, targets, methods); report model assumptions; farmer consent and governance for data reuse.

4.5 What's Next / Future Outlook

- Move from average F to segment-aware diversity control as standard (IBD/ROH-guided OCS and mating).
- Publish public-facing diversity reports (simple trend charts, glossary) alongside genetic trend reports.
- Develop early-warning indicators (e.g., rapid rise in long ROH or top-sire share) with automatic policy triggers.
- Tie financial or label incentives to programmes meeting diversity targets (ΔF , N_e , ROH thresholds).
- Expand among-breed strategies: structured crossbreeding/introgression for resilience traits while preserving breed identity.

4.6 Key Takeaways / For Non-Experts

- Diversity isn't a "nice-to-have"; it's the fuel for future progress.
- We control inbreeding on purpose (OCS, usage caps) while still making gain.
- New diversity metrics (like ROH length) help avoid hidden bottlenecks.
- Small/local breeds (e.g. Montbéliarde, Meuse-Rhine-Yssel) need tighter guardrails and more sires per year.
- When special alleles are at risk, we can nudge selection or draw on cryobanks / introgression to keep them alive.

5 Theme C: Climate / Heat-Stress Adaptation

5.1 Introduction / The Problem

Climate change is already affecting dairy production: hotter, more humid summers are reducing milk components, raising SCC, and depressing fertility across European breeds. The core challenge is how to define and measure heat tolerance traits within existing genetic evaluation systems, and how these traits interact with the traits already included in breeding goals.

The challenge: Hotter, more humid summers are already reducing milk components, raising somatic cell counts (SCC), and depressing fertility. Traditional breeding goals emphasise production under “normal” conditions, but don’t fully capture how animals **perform under heat** or **how fast they deteriorate** as heat load rises.

Why it matters: Without heat-tolerance measures in routine evaluations, selection may favour high-output animals that are **less resilient** to heat, risking more mastitis, poorer conception rate (CR), and compromised welfare—ultimately affecting farm profitability and sector sustainability.

5.2 Solution

The combination of daily temperature and relative humidity (Temperature Humidity Index or THI) provided by the national weather agencies can describe the outside weather conditions of each farm and indicate the heat load that animals endure. Based on this indicator and the data used in the current national genetic evaluations, it is possible to measure heat load's impact on the performances at the population and cow levels. In RUMIGEN, such studies were conducted on five populations (French, Spanish and Dutch Holsteins, French Montbéliarde and Dutch Meuse-Rhine-Yssel) and a large panel of abilities, i.e., milk production, udder health (milk somatic cell counts) and fertility.

Adopt **reaction-norm evaluations** that produce **two numbers per trait**:

- **Level at a reference THI (~50)** — typical performance under thermoneutral conditions (e.g., milk solids, CR).
- **Slope near heat (~THI 70)** — **rate of decline** in performance as heat load increases (susceptibility).

These paired metrics let programmes value both baseline performance **and** resilience to heat.

5.3 Impact / Benefits

5.3.1 For scientific knowledge:

At the breed level, a negative impact of increasing THI was observed on all traits. The patterns were consistent across breeds and countries but different across traits. The decline was more pronounced in milk components and fertility than in udder health traits.

At the individual level, genetic evaluations can provide breeding values for different traits:

- The level of performance at a given THI, for instance, milk yield or conception rate under thermoneutral or heat stress conditions. The level of the traits under heat stress measures the capacity of a cow to produce, reproduce or be healthy in future weather conditions for countries.

- The decline in performance of cows or slope of decay under heat stress due to an increase in THI: this trait measures the susceptibility to increasing heat load of a cow under heat-stress.

These parameters give important information to assess the impact of the present selection (based on levels under thermoneutral conditions) on the ability to adapt animals to heat stress.

Key results:

- As the temperature (or THI) increases, all cows will likely show lower fertility, increased risk of mastitis, and produce less.
- Generally, the best sires selected on the level of a given trait are the same, even under warmer conditions. However, some re-rankings are expected, especially for fertility traits.
- The currently observed trade-offs between milk production and fertility are expected to remain almost stable under heat-stress conditions.
- High production levels are genetically associated with lower heat stress tolerance. Thus, animals with the best breeding values today would be the most affected by increasing THI in terms of both fertility and production.

5.3.2 For stakeholders:

RUMIGEN Recommendation R-C1: A single trait (production, fertility, or udder health separately) cannot summarise the complexity of heat tolerance, and it is important to consider a cow's physiological abilities together to define the best compromise. Today, the selection of dairy cattle should emphasise traits related to robustness to prepare future generations of cows able to face warmer conditions.

5.3.3 Broader societal or environmental implications:

- More heat-tolerant herds mean fewer health events, lower antimicrobial use, and more stable supply during heat waves—supporting welfare goals and climate resilience.

5.4 How it Works (Mechanism / Key Features / Examples)

5.4.1 Access:

- Link farm records to THI (e.g., 3-day window around test date for milk/SCC; 8-day window spanning AI for CR).
- Use reaction-norm models to output Level@THI $\approx$ 50 and Slope@THI $\approx$ 70 per trait.
- Publish dual proofs; provide simple farmer guidance on reading level vs slope.

5.4.2 Transnational collaboration

Share **harmonised THI windows**, trait definitions, and pipelines so results are comparable; co-develop case studies across breeds/regions.

5.4.3 Standards, ethics, quality assurance

- FAIR data: consistent IDs, standardised event codes, documented THI computation.
- Model “cards” (assumptions, validation, limits), bias checks by THI class and parity; farmer consent and transparent communication of use.

5.5 What's Next / Future Outlook

- Scale **THI-aware proofs** nationally; add **fertility-under-heat** and **SCC dynamics** to indices.
- Monitor **slope distributions** to avoid drifting toward heat-sensitive sires.
- Explore **biomarker/epigenetic** augmentation for robustness traits (pilot, report Δ -accuracy).
- Use **practical scenarios** with breed associations and AI centres to validate feasibility, costs, and acceptance; label recommendations **Green/Amber/Red** via WP2.

5.6 Key Takeaways / For Non-Expert

- You'll see **two numbers** per trait: how a cow performs in normal conditions **and** how well she holds up in heat.
- Select for **robustness**, not just output: keep solids high **and** improve **fertility under hot spells**.
- Expect a simple **diversity guardrail** (e.g., $\Delta F \leq 0.5\%/gen$ with OCS) so resilience doesn't come at the cost of long-term adaptability.
- Watch three KPIs: **CR at high THI**, **mastitis/SCC trend**, and **top-sire usage/ ΔF** —they show if the plan is working.

6 Theme D: Cross-Cutting: Gene Editing (GE)

6.1 Introduction / The Problem

Gene editing (GE) technologies — in particular CRISPR-based tools — offer the potential to introduce or accelerate beneficial genetic changes in ruminant populations with greater precision and speed than conventional selection. Potential applications relevant to dairy breeding include enhanced disease resistance (e.g. mastitis, BVDV), improved heat tolerance, and reduced methane output. In R&D contexts, GE is already being used to validate causal variants and study genotype-to-phenotype relationships in ways that are complementary to — not a replacement for — conventional breeding programmes.

The European Court of Justice's 2018 ruling classified animals modified with gene editing tools as genetically modified organisms (GMOs), subjecting them to stringent GMO regulations. While EU Regulation 2024/1517 introduced a proportionate framework for plants derived from new genomic techniques, an equivalent framework for animals remains under discussion at EU level as of 2025. This regulatory uncertainty presents a significant and ongoing challenge. For European ruminant farmers and breeders, this means potential improvements in livestock health and productivity are currently out of reach. The strict regulations could also limit their access to animals bred using these techniques, potentially putting them at a competitive disadvantage compared to farmers in countries where such techniques are permitted.

The delay in research and innovation due to this uncertainty also means that European farmers and breeders might miss out on the benefits of these advancements. This not only affects the ruminant production sector but also has broader implications for consumers and society in general. Society at large could also lose out on the potential environmental benefits of more sustainable farming practices.

In conclusion, the absence of a clear political ambition and legal framework for New Animal Genomic techniques in the EU is causing disruption and missed opportunities in the sector, affecting not just farmers and breeders but also consumers and society as a whole.

6.2 Solution

Treat GE as a **case-by-case, evidence-graded option** within breeding programmes:

- **Default path:** selection + management; consider GE only when it **clearly advances welfare/health** or solves problems **selection struggles with** (e.g., precise allele introduction).
- **Decision tree:** *select* → *manage* → (*if justified*) *edit* — with an **Acceptance label (G/A/R)** and **diversity guardrails** attached.
- **Transparency by design:** document the **benefit**, the **edit**, how it's **measured**, and how **diversity and welfare** are protected

6.3 Impact / Benefits

6.3.1 For scientific knowledge

- Faster **causal-variant testing**; cleaner comparisons of “edit vs introgression”; better understanding of correlated responses and welfare outcomes

6.3.2 For stakeholders

- Potential for fewer disease events, less medication, and clearer trait outcomes when a specific variant is known.
- Option to validate a solution in R&D even when market use must wait.

6.3.3 Broader societal or environmental implications

- Welfare gains (e.g., resistance to painful conditions) can align with public values when communicated well.
- Targeted edits may reduce resource use (healthier, more robust animals) and environmental pressure.

6.3.4 Potential benefits:

- **Improved animal health and welfare**

The technology can enhance the health and welfare of farmed animals, benefiting both farmers and animals and citizens.

- **Preservation of local breeds**

Gene editing can help in preserving local breeds, which play a crucial social and environmental role. This not only helps to preserve and improve local breeds, but also to use their genetic originality for the benefit of other breed.

- **Biodiversity control**

The technology allows for more efficient and rapid generation of new targeted genetic variants, aiding in the preservation of biodiversity at different levels.

- **Competitive advantage**

Adopting these technologies could prevent the weakening of the EU' s livestock sector compared to countries with less restrictive legislation.

- **Medical advancements**

The technology could also have applications beyond farming, particularly in medical advancements.

6.3.5 Recommendations:

- **Advocate initiatives participate in research:**
 - Engage with local farmer associations and community groups to collectively advocate for a clear roadmap from the European Commission.
 - Collaborate with farming organisations in Member States to amplify the voice of farmers at higher policy levels. Encourage open dialogue with policymakers to ensure that the concerns and needs of the farming community are considered in the decision-making process.
- **Participate in research initiatives:**
 - Actively participate in research projects such as RUMIGEN and other ongoing initiatives within the EU. Collaborate with local research institutions to contribute practical insights and experiences to the ongoing scientific discourse.

- Advocate for increased funding and support for research focused on the safety, welfare, and practical implications of gene editing techniques. Ensure that research findings are communicated transparently to the farming community.
- **Encourage open dialogue and local collaboration:**
 - Organise community forums to discuss and address societal and ethical concerns related to gene editing in ruminant production. Encourage open dialogue between farmers, scientists, and the public to ensure transparency and constructive discussions.
 - Establish and strengthen local networks involving farmers, researchers, and agricultural experts. Promote knowledge exchange and collaborative problem-solving to address challenges specific to the region.
 - Participate in national and European platforms that bring together stakeholders from the ruminant farming sector. Emphasise the importance of collaboration with different sectors and actors in local areas

6.4 How it Works (Mechanism / Key Features/Examples)

Modalities:

- *SDN1*: tiny “typo-like” changes (small insertions/deletions).
- *SDN2*: precise **small** edits using a short template.
- *SDN3*: insertion or replacement of a **larger** sequence.

Programme fit: GE is a **tool**, not a goal—used only where it **beats selection/management** on welfare or feasibility.

Diversity guardrails: avoid founder bottlenecks; pair GE founders with **OCS/mate allocation** and minimum sire numbers.

“Edit vs introgression” complementarity:

- *Introgression* preserves acceptance but can take many generations and drags linked DNA.
- *GE* is faster/precise for validation; use OCS and other developed genomic approaches in WP8 to spread edits without narrowing the base

6.5 What’s Next / Future Outlook

- **Welfare-first pilots** in controlled settings (research or pre-commercial), with transparent endpoints and independent oversight.
- Side-by-side comparisons of **edit vs introgression** for the same allele to guide future choices.
- Evolving **policy** may enable proportionate routes; be ready with **evidence** and **engagement** materials.

6.6 Key Takeaways / For Non-Experts

- GE is a tool, not a shortcut. We still use selection and management first.
- Only where it helps welfare or solves a stubborn problem do we consider editing—and we attach safeguards.

- Diversity stays protected (usage caps, OCS, minimum sires).
- Simple labels (Green/Amber/Red) show where acceptance stands and what's being done about concerns.
- Clear information and traceability are part of any GE discussion or pilot.

7 Implementation Playbook

Outcome. Enable **two-number proofs** (Level @ THI≈50; Slope @ THI≈70), safe **OCS/ΔF** control, and a reliable KPI feed—without heavy IT.

FAIR

- **Findable** — one ID per thing: AnimalID, HerdID, GenotypeID, EvalRunID; a versioned **Trait/Event dictionary**; searchable metadata (breed, parity, **THI window**).
- **Accessible** — role-based access; a single API or file-drop to the data hub; signed data-sharing agreements.
- **Interoperable** — same trait units and event codes across partners; shared **THI windows** (milk/SCC: **3-day** around test; CR: **8-day** around AI); standard schemas (CSV/Parquet + JSON metadata).
- **Reusable** — light QC (missingness/outliers/sensor drift), documented preprocessing, **model cards** (assumptions, validation), consent/privacy logs. FAIR compliance status should be recorded in each evaluation run's model card, linking data stewardship to the model card concept introduced in the Guiding Principles.

Ready-to-adopt defaults

- Data completeness for key fields **≥95%**; THI coverage **≥90%** of relevant records; evaluation data latency **≤48h** from file drop; change-log per evaluation.

Table 3 Implementation by stakeholder (meets T8.10)

Stakeholder	Phase 1	Phase 2	Phase 3	KPIs
Breeding organisations	Aim; lock trait defs & THI windows ; draft weights (Level+Slope, mastitis/robustness); OCS ON + ΔF cap; add G/A/R tags	Simulate; pilot dual proofs on 10–20% matings; co-review scenarios with breed assoc. & AI centre; adjust	Adopt index; 100% matings under guardrails; publish Diversity/Heat dashboards; annual review & labels	ΔF , Ne, FROH>8Mb, top-10 share; CR @ high THI; SCC trend; % Green/Amber; % matings via OCS; % herds using dual-proofs
Breed societies / associations	Define scenarios; run farmer panels; apply Room-of-Acceptance checklist	Score pilots (Feasibility/Cost/Acceptance) via scorecard ; agree Amber mitigations	Endorse “Ready” scenarios; promote member uptake; feed outcomes to reviews	# scenarios reviewed; mitigations closed; member uptake; trust/understanding
AI centres & breeding companies	Enable OCS /usage caps; set mate allocation to avoid long ROH; prep comms for Level vs Slope	Pilot matings with dual proofs; keep top-sire share within cap; staff training	Scale OCS/mating rules; maintain min sires; feed usage & performance to dashboards	% matings via OCS; top-10 share; calves/sire; CR @ high THI; farmer comprehension
Recording orgs & data hubs	Implement THI linkage (3-day/8-day); harmonise codes; FAIR mini-QC; host scenario scorecard feed	Deliver THI features to evaluations; KPI feeds; routine QC	Maintain FAIR pipelines; expand sensor coverage; support X-country comparability	THI coverage; valid codes%; latency; QC pass; # scorecards logged
Regulators & competent authorities	Map to welfare/diversity aims; clarify consent/traceability expectations; observe acceptance panel	Review pilot safeguards; provide proportionate guidance	Monitor outcomes; refine guidance; support WP9 outputs	Issues resolved; time-to-approve pilots; stakeholder satisfaction
Researchers & service providers	Build reaction-norm models; model cards; simulation set-up	Validate dual proofs; bias/stability checks; (opt.) epi/biomarker pilots with Δ -accuracy	Maintain models; support annual updates; publish tools	Accuracy & calibration; Δ -accuracy; reproducibility

8 Annex

8.1 Article Template for each theme

Title

A concise, engaging title reflecting the content

1. Introduction / The Problem

What is the specific challenge it addresses (e.g. gaps in understanding genotype-to-phenotype relationships in farmed animals, limited access to standardised data or biobanks, etc.).

Why it matters: for sustainability, animal health & welfare, industry competitiveness, policy, etc.

2. Solution

3. Impact / Benefits

For scientific knowledge:

For stakeholders

Broader societal or environmental implications

4. How it Works (Mechanism / Key Features/Examples)

Access:

Transnational collaboration

Standards, ethics, quality assurance

5. What's Next / Future Outlook

6. Key Takeaways / For Non-Experts

