SMAll RuminanTs breeding for Efficiency and Resilience

# Novel Resilience traits to improve health and welfare (WP 2)

## Highlights

**Final Meeting Toledo**
(21-23 May 2023)

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# Objectives of WP2 - reminder

1. Develop, test and implement new phenotypes for health, resistance and resilience to endemic disease (Task 2.1) Joanne Conington (SRUC)
2. Develop novel traits from automated data capture systems for ante- and post-natal foetus and neonate survival (Task 2.2) Arnaud Delpeuch (Dominique Hazard; INRAE)
3. Quantify new behavioural indicators for adaptation to different farming systems including extensive production systems (Task 2.3) Sotiria Vouraki (AUTH).
4. Identify new traits for lifetime resilience and evaluate their impact in national small ruminant breeding programmes (Task 2.4) Karolina Kaseja (SRUC).

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# Objectives of WP2 Task 2.1

Develop, test and implement new phenotypes for health, resistance and resilience to endemic disease

# TASK 2.1: Health and disease phenotypes

## ➢ New biomarkers for parasite resistance incl. immunological indicators

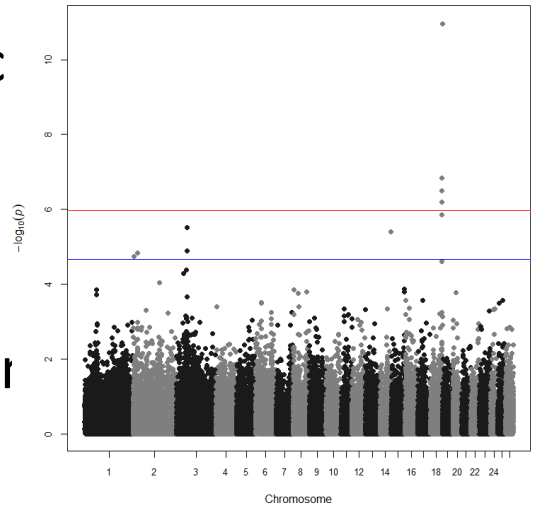
**Objective :** Determine genetic basis and genomic profiles of key immunological indicators (IgA, IL4,IL10, IFN-γ) linked to 3 different parasites (Nematodirus, Strongyles, coccidia) in Scottish Blackface (indigenous) sheep.

**Animal resources** : Experimental sheep n=1766

**Key results:**
- ➢ Host resistance to immunological indicators is heritable (0.14-0.41) - Scope
- ➢ rgs mostly moderate -selection for FEC confers some resistance against others
- ➢ low rg between immunological indicators and disease expression

**Novelty:**
- ➢ New insight for these traits @ gen and Genomic level - polygenic
- ➢ first genetic parameters for immunology and GWAS

**Recommendations for EU**: Cannot substitute metabolic profiling for disease phenotyping (yet!). Polygenic nature of traits – genomic selection



# TASK 2.1: Health and disease phenotypes

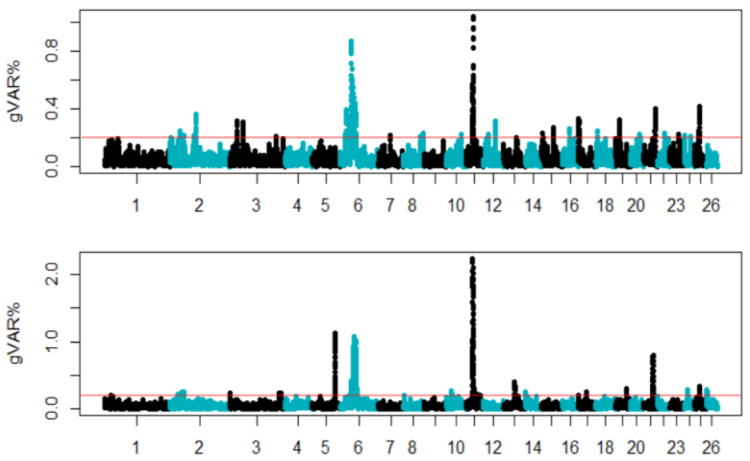
**Objective** To identify genomic regions associated with gastrointestinal nematodes (GIN) resistance in Corriedale and Merino. Use of genomics to determinate genetic level in commercial flocks

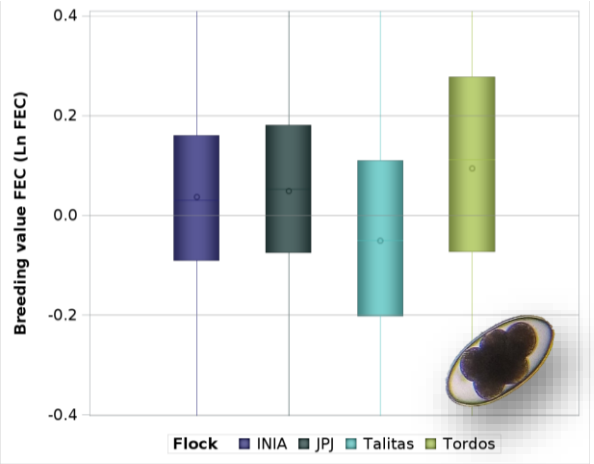
**Animal resources** **Corriedale (C):** 19,547 records and 400 genotyped animals (50k); **Merino (M):** 26,638 records, 1,697 genotyped

**Traits investigated** **Faecal egg count - FEC** 1 & 2 (post-weaning 7-9 and 10-14 months-old lambs)

**Key results**

- Merino: heritability 0.20±0.01, genetic correlation FEC 1 and 2: **0.88**±0.03
- Significant genomic regions were identified in chromosomes **C:** 1, 3, 7, 12, 19 and 24 and **M:** 2, 6, 11, 17, 25
- Good average accuracy (0.41) for genomic prediction of FEC genetic level in commercial flocks




## Recommendations for EU

The development of traning populations with FEC (and other valuable) information allows estimating the genetic level in commercial flock. This tool can be used in agroecological transitions or in certifications

# TASK 2.1: Health and disease phenotypes

## > Auxiliary traits for parasite resistance in dairy sheep

**Objective** : Quantification of new disease biomarkers linked to production.

Animal resources: 1250 phenotyped Lacaune dairy ewes including pedigree information

**Key results:**

- Heritabilities: FEC = 0.33 (0.08), FAMACHA = 0.30 (0.08), packed cell volume = 0.36 (0.08), milk yield = 0.34 (0.08)
- genetic correlations: FEC and FAMACHA = 0.03 (0.22): not suitable as a auxiliary trait, FEC and milk yield = 0.07 (0.22), slightly unfavourable

**Novelty:**

- FAMCHA was tested as auxiliary trait in a European dairy sheep breed
- genetic correlation of potential auxiliary trait and production was estimated

Recommendations for EU: **FAMACHA as auxiliary trait not feasible (Switzerland), Selection according to FEC feasible without production impairment**

# TASK 2.1: Novel resilience traits to improve health and welfare

## ➢ Footrot (FRT) and mastitis (California Mastitis Test, CMT) in Texel sheep

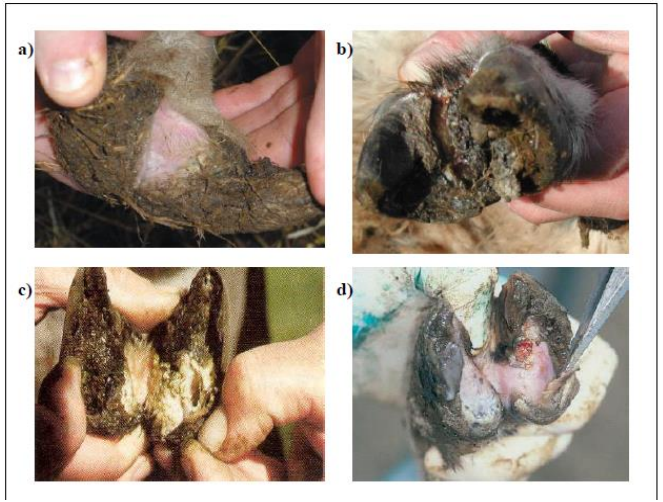
**Objective:** Develop, test and implement new phenotypes for health, resistance and resilience to endemic disease

**Animal resources**: data collected on Texel sheep across the UK: >9,000 FRT records and >4,700 CMT records; >10,000 genotypes

**Key results:**
- ➢ Both traits are heritable: 0.12 FRT and 0.07 CMT
- ➢ GWAS shown no genome-wise significant SNPs for FRT and CMT
  - ➢ Three chromosome-wise significant SNPs for FRT on chromosomes 19, 23 and 26
  - ➢ Two chromosome-wise significant SNPs for CMT on chromosomes 14 and 17

**Novelty:**
- ➢ Results give a good overview about footrot and mastitis in UK Texel sheep population
- ➢ Both traits are polygenic
- ➢ Genetic selection can be performed against both diseases

Recommendations for EU: **genetic selection for these health traits may be a potential strategy to improve health and welfare in the meat sheep**



# TASK 2.1: Health and Disease phenotypes

**Objective** Quantify the genetic variation present in three key health-related traits in the Irish sheep population

**Animal resources** 39,315 animals records on a multi-breed population (measured by trained technicians)

**Traits investigated** Lameness, mastitis and dag score


Texel (100%), Birth Notified, 26-JAN-2023, R5 (73%) T5 (74%), Et

Current EuroStars *(Published On: 17-MAY-2023)*

| Index | Across breed Value | Accuracy | Within breed Rank | Stars |
|---|---|---|---|---|
| Replacement | €3.29 | 73% | Top 2% | ★★★★★ |
| Terminal | €2.86 | 74% | Top 3% | ★★★★★ |
| No. Lambs Born | 0.00 | 72% | Top 4% | ★★★★★ |
| Daughter Milk | 0.3 kg | 77% | Top 6% | ★★★★★ |
| Survivability | 1.27% | 69% | Top 5% | ★★★★★ |
| Days to Slaughter | -19.4 days | 79% | Top 5% | ★★★★★ |
| Barrenness | -1.00% | 68% | Top 35% | ★★★★ |
| Lambing Difficulty (% difficult) | 11.77% | 77% | Top 3% | ★★★★★ |
| Lamb Vigour (% vigorous) | 78.54% | 77% | Top 38% | ★★★★ |
| Ewe Mothering Ability (% good mothering) | 88.18% | 70% | Top 6% | ★★★★★ |
| Ewe Lameness | 0.70% | 70% | Bottom 44% | ★★★ |
| Lamb Lameness | -0.20% | 72% | Top 11% | ★★★★★ |
| Daginess (% dirty) | 23.09% | 72% | Bottom 16% | ★ |
| Ewe Mature Weight | 3.4 kg | 75% | Bottom 6% | ★ |
| Carcass Conformation | 0.28 | 72% | Top 19% | ★★★★★ |
| Carcass Fat (higher = fatter) | -0.03 | 63% | *No stars apply for this trait* | |

Details

| | |
|---|---|
| NSIS | IE043743107344G |
| Pedigree ID | HUI2307344 |
| Flock Name | GREENHILL |
| Animal Name | GUCCI |
| Birth Date | 26-JAN-2023 |
| Birth Rank | ET |
| Breed | Texel (100%) |
| Sex | Male |
| Pedigree Status | Birth Notified |
| Genotyped? | Yes |
| Genomic Evaluation? | Yes |
| Scrapie Status | ARR/ARR |
| Scrapie Type | 1 |

## Key results

Prevalence:

- Lameness ewes **10%** and lambs **16%**, mastitis **3%**

Heritability:

- Dagginess 15%, lameness 6% (ewes) and lambs (12%), mastitis (4%)
- Breeding values for health traits included in the Irish national genetic evaluations

**Recommendations for EU** Health traits are heritable → can be improved through genetic selection
Consider including such traits in sheep breeding objectives.

# TASK 2.1: Health and disease phenotypes

## ➢ D2.1: Report on new immunological and physiological profiles linked to disease phenotypes in locally-adapted breeds

**Objective:** To assess the potential use of **new udder health phenotypes** as predictors of **subclinical mastitis** in three semi-extensively reared dairy goat breeds (Eghoria, Skopelos, Damascus) in Greece

**Animal resources**: 531 dairy goats (Eghoria n=189, Skopelos n=151, Damascus n=191) from 7 semi-extensive farms

**Key results:**
- Significant positive correlations (0.30 – 0.59) of udder health phenotypes based on thresholds for SCC >$10^6$ cells/ml and TVC >$2\times10^4$ cfu/ml with subclinical mastitis in all goat breeds

**Novelty:**
- First study to associate udder health phenotypes based on thresholds for SCC and TVC with milk microbiological cultures
- Studied udder health phenotypes could be used as indicators of subclinical mastitis in Eghoria, Skopelos and Damascus goats

**Recommendations for EU**: Selection to improve udder health in dairy goats could be based on thresholds for **SCC >$10^6$ cells/ml and TVC >$2\times10^4$ cfu/ml**

# TASK 2.1: Health and disease phenotypes

## ➢ D2.3: Paper on quantification of (genetic and phenotypic parameters) of new diseases biomarkers linked to production

**Objective**: To estimate the **repeatability of health and welfare traits** and their **correlation with performance traits** in three semi-extensively reared dairy goat breeds (Eghoria, Skopelos, Damascus) in Greece

**Animal resources**: 1,210 dairy goats (Eghoria n=418, Skopelos n=429, Damascus n=363) from 7 semi-extensive farms

**Key results:**
- ➢ Significant repeatability for all udder health (0.08 – 0.59) and most of welfare traits (0.16 – 0.99) in all breeds, GIN and cestode FEC and GIN and lungworm infection in Eghoria (0.09 – 0.32) and myiasis (0.34) in Skopelos goats
- ➢ Correlations of health and most of welfare traits with performance → non-significant or favourable (-0.12 to -039)

**Novelty:**
- ➢ First study to investigate the repeatability of a wide range of health and welfare traits and their association with performance traits in semi-extensively reared dairy goats
- ➢ Selection to reduce subclinical mastitis, GIN infections, and myiasis and improve welfare status of animals can be applied based on records early in life for timely and informed culling decisions
- ➢ Potential to improve health and welfare without compromising milk production and BCS

**Recommendations for EU**: **Health, welfare and overall performance** of semi-extensively reared dairy goats can be improved with appropriate **management and selection practices**

# TASK 2.1: Health and disease phenotypes

## ➢ Welfare in Dairy Goats

**Objective :** investigate the phenotypic and genetic variability of 11 health and welfare traits in French dairy goats

Animal resources : 1,977 Alpine and Saanen primiparous goats [from 14 farms, same in task 1.2)

**Key results:**
- ➢ among the 11 traits, frequency of disorders ranged between 0.5% and 23%
- ➢ the total number of disorders per animal was low (=0.94)
- ➢ some of the traits had a genetic determinism ($h^2$ from 4% to 26%)

**Novelty:**
- ➢ Results give a good overview about health and welfare traits in dairy goat in France (done in other countries: Greece…)
- ➢ Health and welfare assessment at the animal and/or farm level can be done quite easily
- ➢ first genetic parameters for welfare

Recommendations for EU: **genetic selection for welfare may be a potential strategy to improve health and welfare traits in dairy goats**

# TASK 2.1: Health and disease phenotypes

## > Blood beta-hydroxybutyrate concentration

**Objective** : estimate the factors of variation and the genetic parameters of blood beta-hydroxybutyrate concentration (GWAS (Deliverable 2.5) → not done yet)

Animal resources : 534 Alpine and Saanen primiparous goats [from 5 farms (same in task 1.2), measured 3 or 4 times during their lactation (1,836 records)]

**Key results:**

- a large phenotypic variability exists (mean=0.48 mmol/L, SD=0.18, CV=38%)
- the factors of variation are: the farm (breeding and feeding system), lactation stage, kidding month, breed, year, milk yield
- heritability = 11%, repeatability = 28%

**Novelty:**

- large dataset of blood beta-hydroxybutyrate concentration, measured in different farming systems and breeds
- a genetic determinism exists

Recommendations for EU: **blood beta-hydroxybutyrate concentration is a key metabolite used as a proxy**

- to better understand the energy metabolism in dairy goats
- to select dairy goats for resilience

# TASK 2.1: Health and disease phenotypes

## > Automatic scoring of ruminal temperature (ruminal bolus)

**Objective** : estimate the genetic parameters of rumen temperature in Alpine goats

Animal resources : 120 Alpine goats [from an INRAE experimental farm, measured during 1 or 2 years
12 millions of records = 5-minute temperature measurements]

Key results:
- Characterization of kinetics for ruminal temperature during the day was characterized
- the phenotypic variability was low (mean=39.68, SD=0.51, CV=1%)
- heritability ranged from 3% to 12% and repeatability ranged from 20% to 32%, depending on the time of the day

Novelty:
- description of the kinetics of ruminal temperature during the day
- identification of factors of variation
- estimation of genetic parameters

Recommendations for EU: **ruminal temperature could be used to assess basal metabolism or response to various stressors (heat stress, infection…)**

## SMARTER PARTNERS

*Thank you for your attention*

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| Traits | $h^2$ (s.e.) |
|---|---|
| IFN-$\gamma_{(PWM)}$ | 0.33 (0.10) |
| IL-$4_{(PWM)}$ | 0.77 (0.09) |
| IL-$10_{(PWM)}$ | 0.16 (0.07) |
| IFN-$\gamma_{(T\text{-}ci)}$ | 0.27 (0.08) |
| IL-$4_{(T\text{-}ci)}$ | 0.14 (0.06) |
| IL-$10_{(T\text{-}ci)}$ | 0.22 (0.08) |
| IgA | 0.41 (0.09) |