SMARTER

SMAll RuminanTs breeding for Efficiency and Resilience

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Report on Summary of WP7 and recommendations for breeding Simulations of Lacaune sheep and Alpine and Saanen goat breeding programs

AbacusBio

* Deliverable leader – Contact: tbyrne@abacusbio.co.uk

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About the SMARTER research project

SMARTER will develop and deploy innovative strategies to improve Resilience and Efficiency (R&E) related traits in sheep and goats. SMARTER will find these strategies by: i) generating and validating novel R&E related traits at a phenotypic and genetic level ii) improving and developing new genome-based solutions and tools relevant for the data structure and size of small ruminant populations, iii) establishing new breeding and selection strategies for various breeds and environments that consider R&E traits.

SMARTER with help from stakeholders chose several key R&E traits including feed efficiency, health (resistance to disease, survival) and welfare. Experimental populations will be used to identify and dissect new predictors of these R&E traits and the trade-off between animal ability to overcome external challenges. SMARTER will estimate the underlying genetic and genomic variability governing these R&E related traits. This variability will be related to performance in different environments including genotype-by-environment interactions (conventional, agro-ecological and organic systems) in commercial populations. The outcome will be accurate genomic predictions for R&E traits in different environments across different breeds and populations. SMARTER will also create a new cooperative European and international initiative that will use genomic selection across countries. This initiative will make selection for R&E traits faster and more efficient. SMARTER will also characterize the phenotype and genome of traditional and underutilized breeds. Finally, SMARTER will propose new breeding strategies that utilise R&E traits and trade-offs and balance economic, social and environmental challenges.

The overall impact of the multi-actor SMARTER project will be ready-to-use effective and efficient tools to make small ruminant production resilient through improved profitability and efficiency.

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1. Work package 7 summary

The research outputs from SMARTER WP7 are interesting and informative. They demonstrate that there are significant opportunities to create value through genetic improvement for resilience and efficiency (R&E) traits, that there is a clear view from farmers that animal resilience and efficiency is needed for robust future farming systems, and that there is scope to create breeding goals to achieve the desirable balance of selection across production and R&E traits.

Task 7.1

Deliverable 7.3 (task 7.1) provide insights into the scale of opportunity at farm system level to create higher gross margins through genetic improvement in resilience traits. For example, simulations (using Linear Programming as a mathematical procedure for optimum resource allocation at farm level) showed that for Chios sheep farms under semi-intensive systems in Greece, a gross margin per ewe 15.9% greater can be achieved in the absence of mastitis, gastro-intestinal nematode, and lameness when compared to the same system in the presence of mastitis, gastro-intestinal nematode, and lameness. Interestingly, in this and other modelled scenarios (Assafe, Frizarta, Boutsiko, and Lacaune sheep and Skopelos goats across extensive, semi-extensive and intensive farming system for meat, milk, and dual-purpose production), the increase in gross margins achieved was largely driven by increases in productive output and in some cases a reduction in variable cost. It was not driven by reductions in labour or significant changes to the farming system. This suggests that there are significant opportunities to create value through genetic improvement for resilience and efficiency (R&E) traits, at the farm system level and that these benefits and realisable across the range of farm systems for small ruminants in Europe. In the context of balanced breeding goals, this gives some insight into the potential contribution that R&E traits might make to improving profitability, in a balanced breeding goal including R&E traits. Given the improved gross margins were largely driven by increases in productive output, it is important to manage double counting in the development of economic values for R&E traits. The economic value of improvements in productive output due to genetic changes in mastitis, gastro-intestinal nematode, and lameness cannot be attributed to mastitis, gastro-intestinal nematode, and lameness economic values, if production traits are also in the breeding goal.

Task 7.2

For Deliverable 7.1 (task 7.2), a factorial analysis of data from surveys deployed to 272 farmers in 5 countries with milk, meat, and wool production for 15 breeds of sheep & goat in different local condition (extensive, semi-intensive, intensive management) identified 3 distinct groups of breeders/ farmers: Group 1 (n=93) = non genetic farmers seeking robustness and multifunctionality, Group 2 (n=34) = genetic farmers seeking production efficiency, and Group 3 (n=145) = Breeders seeking production efficiency and sustainability. Group 1 don't know of EBV's whereas Group 3 look for new indexes for sustainability, including R&E. An interesting finding from this study is that strategies and views on sustainability and R&E don'tseem to depend on livestock species or system. There is an overlap between groups and countries:

socio-technical elements could explain the differences between the groups. For goats, the more intensive the system is, the more farmers seem to be interested in genetics.For milk or meat sheep, it is more contrasted and so the 3 groups are more mixed regardlessof the level of intensification. In the context of balanced breeding goals, sustainability is a major concern, but the levers are different, and the sociotechnical system is fundamental in explaining farmer choices. The implies that breeding goals need to be targeted or customized so they address the farmer concerns and/ or sociotechnical systems, in which the animals being ranked are to be used.

Task 7.3

Deliverable 7.2 (task 7.3) aimed to better understand the diversity of breeders' preferences with respect to the relative importance of traits related to animal resilience, health, and efficiency (R&E). Data were obtained through preference surveys based on choice experiment that were administered to small ruminant breeders in 4 countries and for 12 breeds (n=520) with the decision-making software 1000Minds®. Note that the total number of survey responses was 681 across Italy, Spain, Urugay, Greece, and France plus 49 other stakeholders, to a total of 730). Results highlight differences in preferences between the proposed traits with a higher degree of importance for R&E traits, as well as production traits. For example, longevity ranked highly for Assaf (average rank = 2nd), Alpine (1st), Manech Tête Rousse (3rd) and to some extent Saanen (4th). Longevity was the top ranked trait on average, by wool breeders. Feed efficiency also ranked highly for Chios (2nd), Frizarta (2nd), Lacaune (3rd), and Assaf (3rd). Mastitis was also ranked highly (e.g., average rank = 1st for Manech Tête Rousse sheep and 2nd for Saanen goats), while milk was ranked highly by most dairy breeds (average rank = 1st for Assaf, Chios, Frizarta, and average rank = 2nd for Lacaune; in Greece. Average rank = 1st for Saanen and average rank = 2nd for Alpine; in Italy). The second part of the study presents a deeper analysis of famers' preferences in the case of French Romane breeders (meat-oriented production). Principal Component Analysis followed by an ascending hierarchical classification on the first 5 axes of the PCA (corresponding to 85% of the variability) was undertaken. Two preference profiles (A and B) were identified and characterized in Romane (n=38). Profile A includes breeders who particularly prioritize ($P < 0.05$) reproductive performance (Mortality at weaning and Prolificacy). Profile B includes breeders who particularly prioritize ($P < 0.05$) traits related to animal health (Resistance to Footrot, and Resistance to Parasitism). These results can inform breeding objectives for more resilient and efficient animals. Different typologies exist within groups of farmers that have the same breed, and breeding goals therefore need to address both economic and farmer typology aspects within a breed.

Within task 7.3, mathematical modelling of income and labour, on a trait-by-trait basis, was undertaken. This focused on adding labour to the relevant traits in OSIRIS: a bio-economic model used to design new economic breeding goals. For Lacaune, a milking sheep breed, labour allocation across the farm was assessed. This showed that 78% of the annual labour on the farm is explained by activities related to feeding, milking, lambing and lamb management, ewe lamb rearing, parasite management and mastitis management. Economic values were calculated with labour included for longevity, young and adult fertility, prolificacy, lamb survival, milk yield, protein and fat yield, somatic cell score (SCS), mastitis (clinical and sub-clinical) and milking persistency traits. When adjusted for trait the genetic standard deviation, the emphasis in the breeding goal on longevity (€8.22 to €8.37 per trait genetic standard deviation), protein yield (€5.10 to €6.40), fat yield (€8.58 to €8.76) and resistance to mastitis (€17.13 to €17.57) increased, while the emphasis on young and adult fertility (€16.60 to €14.58) and milk yield (€0.69 to €0.59) decreased. The other breeding goal traits remained unchanged. This analysis represents useful insight into how labour influences trait economic values and how R&E traits are impacted by the inclusion of labour, i.e., that the R&E traits longevity and mastitis have a significant impact on labour requirements.

Within task 7.3, a multi-criteria assessment study was completed on 7 farms with mixed production systems (beef cattleand sheep) with super fine wool production, in Uruguay. The methodology used for the evaluation of the environmental impact in the farms of this study was the life cycle analysis (LCA). The evaluation was spatially delimited from the cradle to the animal's mouth for the input emissions phase and from the animal's mouth to the gate of each farm for the animal emissions phase. Then, the study integrated from cradle to gate of the farm. Transport, industry, and the consumer were not included. Different scenarios for genetic improvement in sheep and their impact on GHG emissions were simulated. To determine the results of scenarios with genetic improvement of flocks, four variables were considered: dry matter intake, metabolizable energy consumed, methane emissions per animal and greasy fleece weight per animal. The magnitude of improvement in each variable was established as the difference between the median of the data and the upper quartile of the animals in the national genetic evaluation (Uruguay). It was established that: in Scenario 1 the Consumptionof Dry Matter is 13% lower (difference between median and upper quartile), in Scenario 2 theMetabolizable Energy Consumed is 14.4% lower, in Scenario 3 the Methane produced per animal is 17.1% lower and in Scenario 4 the Greasy Fleece Weight is 12.8% higher. It is observed that in all the proposed scenarios, reductions in GHG emissions were obtained. The variable that presented the greatest incidence in GHG emissions was the Metabolizable Energy Consumed (Scenario 2) where, on average, decreases of 17.9% were obtained, with maximum values of 23.4% and minimum values of 11.8%. Scenarios 1 and 3 presented similardecreases with values of 12% and 12.7%, respectively. Finally, Scenario 4 where increased weight of dirty fleece was the variable that presented the least impact, with a 6% decrease inGHG emissions per unit of product. Therefore, genetic improvement for R&E traits can meaningfully contribute to reducing the GHG emissions from small ruminant agriculture. Other environmental factors beyond emissions including carbon stocks in the soil, water quality, and ecosystem level biodiversity analysis were not affected at the level of the modelled genetic gain in the R&E traits of interest, positively or negatively. In a very indirect (theoretical) way, a higher level of efficiency could imply a higher remaining biomass and more possibilities for carbon storage. This was not captured in the study.

On multi-criteria assessment, the CAP'2ER® tool was used to provide two case studies: one in Lacaune dairy sheep and one in one Alpine dairy goat farm In Lacaune dairy ewes, modeling a long-term selection scenario combining longevity and milk production has a benefit on greenhouse gas emissions (2.7% and 3.9% reduction for enteric CH4 and manure compared to the current situation) compared to selection based on milk production alone (2.5% and 3.8%, respectively). Similar trends were found for nitrogen dioxide (NO2) reduction. The new multicriteria assessment was done on a farm of 318 Alpine goats in a mixed farming system using 50% of its surface as temporary grassland (2% permanent grassland) and 50% to sell cereals on a total of 148 hectares. The latter farm was one of the commercial farms involved in WP1. The MCA performed on the Alpine goats in a mixed farming system showed the following environmental impact: emission of 5 549 kg eq. CO_2/ha UAA (Useful agricultural area); loss of 97 kg Nitrogen/ha UAA; consumption of 20 759 Mj/ha UAA; storage of 388 kg eq. CO_2/ha UAA. The study showed that a large proportion of gas emissions came from enteric methane (34%), effluent management (37%) and feed (17%). Consequently, together with effluent management practice, reducing individual enteric emissions and improving feed efficiency appear to be useful levers for reducing the environmental impact of livestock farming.

Integration of WP7 outcomes into task 7.4

Research has been done on economic selection indexes for small ruminants in Europe (e.g., Byrne et al. 2010 Livestock Science, 132(1):135-144; Theodoridis et al. 2018, Animal, 12(7):1508–1515), and there are models that produce economic values (e.g., OSIRIS model from INRAE) but very few small ruminant breeding programs have implemented a structured framework for economic breeding objectives and selection indexes. As such, there are very few selection index tools for small ruminants in Europe that assimilate economic, environmental, and social aspects of trait improvements into selection and breeding decisions. This made it difficult to implement an analysis that reflected breeding goals combining outputs from farm modelling (T7.1) and choice and labour modelling and multi-criteria assessment analyses (T7.3). However, we have built on the results from the WP7 and wider work package outcomes (WP1 and WP2) to define new R&E traits with the potential to provide environmental, labour, and economic benefits (longevity & feed efficiency highlighted throughout WP1-WP7).

The simulations in T7.4 use a general selection index model framework (Dekkers, 2007) to predict the impact of inclusion of R&E traits into 3 breeding programs (Alpine and Saanen goats, and Lacaune sheep, in France) to understand the long-term impact of including R&E traits as new breeding goals in a selection index. The simulations predict the superiority of individuals of each sex selected using an index and the annual response to selection in a breeding program. We use existing desired gains approaches with embedded new breeding goals for longevity and feed efficiency and leverage genetic parameters, which are essential to this approach (h^2 and rg etc.), provided in WP1 and WP2. The balancing of breeding goals, and the understanding of the implications of including R&E traits in different ways, was described by testing a range of scenarios and a range of sensitivity analyses, including sensitivity of the outcomes of different trait weightings (applied to the existing desired gain weights), correlations between R&E traits and productions traits, and with the use of genomics.

The objectives of the simulations are to:

- Assess the long-term impact of breeding for resilience and efficiency traits in Alpine and Saanen goat populations.
- Test how new genomics data and tools can improve breeding programs and populations faster.
- Produce 20-year forecasts of the productivity gains that can be expected when resilience and efficiency traits are included in the breeding programme.

This simulation forms part of Task 7.4 of the H2020 Small Ruminants Breeding for Efficiency and Resilience (SMARTER) project. A summary of the outcomes is provided below, and full details provided in Annex 1: Task 7.4 Balancing breeding goals.

Summary – Alpine and Saanen goats

Adding resilience and efficiency traits to the Alpine and Saanen goat breeding programmes can result in a long-term (20 year) improvement in these traits, depending on several factors: population genetic parameters, the weight given to these traits in the index, and the availability of genomic information to inform breeding values.

When a 10% relative emphasis is given to RE traits in the Total Merit Index (TMI), Alpine goats are predicted to show a 2 day increase in lifespan and a 0.07 UFL unit increase in feed efficiency after 20 years, relative to the current TMI. Saanen goats are predicted to show a 188 day increase in lifespan and a 0.05 UFL unit increase in feed efficiency after 20 years, relative to the current TMI. Including RE traits reduces the rate of progress in other traits, with most noticeable reductions for protein yield and fat yield.

Genomic evaluations increase RE trait responses significantly. Assuming a genomic accuracy of 50%, the Alpine goat breeding program can achieve a 174 day increase in lifespan and a 0.09 UFL unit increase in feed efficiency after 20 years. The Saanen goat breeding program can achieve a 449 day increase in lifespan and a 0.08 UFL unit increase in feed efficiency.

Genetic parameters like heritability, repeatability, genetic and phenotypic correlations affect responses to selection. The Alpine and Saanen goats breeding programmes are currently experimenting with adding RE traits, so these parameters are currently estimated from preliminary data. In future, once more data is available, a more complete picture of the implications of adding RE traits would be available. It would also help refine the desired gain weight to apply to RE traits in the TMI.

Using economic values in the index, instead of desired gains weights, would deliver real world value to breeders and commercial farmers. These economic values result in an index that represents the profit, or cost, to the farmer. This makes index scores easier to interpret and understand. Economic values can be calculated The underlying framework used to calculate economic weights can also be used to calculate CO2e coefficients per trait, and therefore allow the implications of genetic gain on GHG emissions from enteric methane to be estimated.

Summary – Lacaune sheep

Adding Functional Longevity (FL) and Feed Efficiency (FE) to the breeding program results in a significant long-term (20 year) response to selection for both traits, with 0.3 more lactations and an increase of 13.2% in feed efficiency (13.2% less feed). Genomic evaluations increase these responses to 1.3 lactations and 21.3% in feed efficiency.

As expected, when adding more traits to the index, the relative trait emphasis and response to selection in other traits in the index reduces, with most noticeable reductions for protein yield (PY) and fat yield (FY).

The sensitivity analyses showed that outcomes were most sensitive to changes in the accuracy of genomic breeding values for FL and FE. The emphasis of FL and FE in the index increased significantly, from 11.8% to 17.7%, and 12.7% to 15.3%, respectively, when the accuracy of genomic breeding values increased from 50% to 70%. The emphasis on FL and FE in the index decreased significantly, by similar proportions, when the accuracy of genomic breeding values decreased from 50% to 30%. Adjusting these accuracies resulted in, on average, a 5.2% change in response to selection for PY and FY. For most sensitivity analyses, only slight differences were observed in responses to selection and emphasis of other traits in the breeding program.

Genetic parameters like heritability, and genetic and phenotypic correlations affect responses to selection. Considering that for FE a genetic and phenotypic correlation was only estimated with MY, estimation of the correlations between FE and other index traits and re-running of simulations would provide a more complete picture of the implications of adding FE and of the sensitivity of responses to the genetic relationship between FE and other traits.

Simulation outcomes from the current breeding program (base scenario) show that Lactation Somatic Cell Score ($LSCS$), Teat Angle (TA), Udder Depth (UD) and Teat Position (TP) have an unwanted long-term (20 year) response to selection; increasing $LSCS$ and TA, whilst decreasing UD and TP. By changing the FL and FE weights in the index, these unwanted responses to selection are reduced.

Using economic values in the index, instead of desired gains weights, would deliver real world value to breeders and commercial farmers. These economic values result in an index that represents the profit, or cost, to the farmer. This makes index scores easier to interpret and understand. The underlying framework used to calculate economic weights can be built such that it uses trend data, so that economic indexes are stable over time. The framework can also be used to calculate CO2e coefficients per trait, and therefore allow the implications of genetic gain on GHG emissions from enteric methane to be estimated.

2. Recommendations for breeding/ breeders

There are economic and environmental gains to be made by inclusion of R&E traits in breeding objectives, as demonstrated in farm system (task 7.1) and LCA modelling (task 7.3) in WP7. There are also labour implications as a result of genetic improvement in R&E traits, which manifest in farm system economic impacts and potential changes in trait improvement priorities (task 7.3; labour modelling). However, quantifying the scale of the benefits at the breeding objective/ selection level (trait-by-trait with no double counting) requires the development and deployment of a systematic, data-driven, approach to the calculation of breeding objectives and selection using economic values, instead of desired gains weights. This requires the development of methodology to quantitatively account for different inputs that can influence trait improvement priorities (economics, breeder and farmer preferences, emissions from enteric methane, nitrogen emissions, broader ecological impacts), and ultimately alter the direction of selection.

. Currently, the deployment framework and systems for implementation of breeding objectives and selection indexes in small ruminants in Europe is based on a desired gains approach and, as such, R&D outputs (like breeding values for new traits) are not connected to the value realised at the farmer/ end user level. Research flocks/ herds,national breeding programs, and commercial breeding programs in small ruminants in Europeare, except for Ireland and a subset of breeds in the UK, not using data-driven breeding objective and selection index tools.

At the R&D and commercial level, there are very few selection index tools for small ruminants in Europe that can assimilate economic, environmental, and social aspects of trait improvements into selection and breeding decisions. There appears to be different reasons for this. In some cases (e.g., Lacaune sheep in France), there is a perception that an economic index is not needed because the breeders are fully engaged already, and so a desired gains index is sufficient (pers. comm.Jean-Michel Astruc). This reasoning does not consider the increased complexity of accuratelyweighting traits based on economic, environmental, and societal needs in the future. In other cases(e.g., small ruminants in Greece), it is because of a lack of funding and general breedingprogram fragmentation, including the fact that most farmers do not comprehend the strategic importance and the long-term benefits of genetic improvement (pers. comm. Alexandros Theodoridis). This is fundamental issue related to the organisation, funding, and communication of the value of breeding initiatives in Greece. The advent of genomic selection, which is used in several small ruminant breeding programs in Europe, further increases the need for data-driven breeding objective and selection index tools. Genomics has the potential to speed up rates of genetic gain, and a well-structured data-driven breeding objective ensures that genetic gain is going in the optimal direction.

The underlying framework used to calculate economic values can also be used to calculate CO2e coefficients per trait, and therefore allow the implications of genetic gain on GHG emissions from enteric methane to be estimated on a trait-by-trait basis.

Indications are that there are different needs from different farmers and in different farming systems (D7.1/ task 7.2 and D7.2/ task 7.3) and this implies that breeding goals need to be targeted such that they address the farmer typologies and the sociotechnical systems, in which the animals being ranked are to be used.

Recommendations for balancing R&E traits in breeding objective and for developing breeding objective tools for the future:

- Across breeding programs (research, national, or commercial), develop and deploy a systematic, data-driven, approach to the calculation of breeding objectives and selection using economic values, instead of desired gains weights.
- Ensure that the data-driven approach can be used to also calculate CO2e coefficients per trait, so that the implications of genetic gain on GHG emissions from enteric methane to be estimated.
- Ensure that the data-driven approach can also integrate (in quantifiable terms) the preferences of breeders and farmers (typologies) into trait weightings, including for animal welfare and non-market traits that have value to farmers.
- National or research flock/ herds should lead by example in developing and deploying a systematic, data-driven, approach.
- Breeders/ breeding organisations and commercial producers should be engaged to build understanding and get buy-in to the process and the outcomes.

3. Annex 1: Task 7.4 Balancing breeding goals

Alpine and Saanen goats

Introduction

This report describes the outcomes of a breeding program simulation in Alpine and Saanen goats using a general selection index model framework. The objectives of this simulation are to:

- Assess the long-term impact of breeding for resilience and efficiency traits in Alpine and Saanen goat populations.
- Test how new genomics data and tools can improve breeding programs and populations faster.
- Produce 20-year forecasts of the productivity gains that can be expected when resilience and efficiency traits are included in the breeding programme.

This simulation forms part of Task 7.4 of the H2020 Small Ruminants Breeding for Efficiency and Resilience (SMARTER) project.

Materials and methods

The long-term impact of including resilience (R) and efficiency (E) traits, as new breeding goals in a selection index, was assessed using a general selection index theory modelling framework developed by AbacusBio. Selection index theory (Dekkers, 2007) predicts the superiority of individuals of each sex selected using an index and the annual response to selection in a breeding program. The outcomes depend on the breeding program parameters outlined below.

- Traits included in the selection index with:
    - Heritability,
    - Repeatability,
    - Phenotypic variances, and
    - Genetic and phenotypic correlations with other traits.
- Economic weight or other weight assigned to each trait in the index.
- Data available (including genotypes) for each of the selection candidates.
- Breeding program structure.
- Selection pressure.

Required modelling inputs like breeding program characteristics, trait weights, and genetic parameters were obtained through INRAE (pers. comm. Virginie Clement).

Breeding program parameters

Economic weights

Economic weights are not deployed in the Alpine or Saanen breeding program modelled herein. Rather, desired gains weights provided in the index and sub-indexes are presented in the section below.

Traits and data recording

There are currently 11 breeding goal traits included in the Alpine and Saanen selection indexes. Two additional breeding goal traits are added to these indexes in these simulations: Functional Longevity (FL) as a resilience trait and Feed Efficiency (FE) as an efficiency trait. Table 1 below gives an overview of the traits included, while Appendix Tables 5 and 6 provide the full set of information used in the simulation: trait heritabilities, phenotypic variances, repeatabilities, genetic and phenotypic correlations.

Table 1: Breeding goal traits.

TRAIT NAME	ACRONYM	UNITS	MEASURED DURING PARITY			
			1	2	3	4–10
Current index traits						
Milk yield	MY	kg	YES	YES	YES	YES
Protein yield	PY	kg	YES	YES	YES	YES
Fat yield	FY	kg	YES	YES	YES	YES
Protein content	PC	g/kg	YES	YES	YES	YES
Fat content	FC	g/kg	YES	YES	YES	YES
Somatic cell score	LSCS	score	YES	YES	YES	NO
Udder Profile	UP	point	YES	NO	NO	NO
Floor Position	FP	point	YES	NO	NO	NO
Rear Attachment	RA	point	YES	NO	NO	NO
Fore Udder	FU	point	YES	NO	NO	NO
Teat Orientation	TO	point	YES	NO	NO	NO
Resilience and efficiency (R&E) traits						
Functional longevity	FL	days	NO	NO	NO	*YES
Feed efficiency	FE	UFL unit	†YES	†YES	†YES	†YES

** Functional longevity has only 1 record, taken in females that have reached their 6th lactation*
† Feed efficiency has 4 records per females per lactation

The quantity of data available to inform selection decisions increases throughout the buck’s lifecycle. This increase in available data was modelled for three different life stages: young bucks, emerging sires, and proven sires.

- As a **young buck**, trait data is only available for its mother and maternal half-aunts. At this stage, the buck is assumed to be 1 year.
- An **emerging sire** will have additional data available for some, but not all traits, when its female offspring reach their first parity. The buck is assumed to be 2 years old.
- A **proven sire** will have records available for all traits from its female offspring, and a greater number of trait records for each trait. The buck is assumed to be 7 years old.

The number of data records for each trait, for each relative group is shown in Appendix Table 7.

Indexes and index weights

For both milking goat breeds, the current Total Merit Index (TMI) consists of a weighted sub-index for production traits, a weighted sub-index for type traits, and a weight for somatic cell score (LSCS).

The sub-index for production traits (IPC) is calculated as in **both breeds** as:

$$\mathrm{IPC} = 1 \cdot \mathrm{PY} + 0.4 \cdot \mathrm{PC} + 0.2 \cdot \mathrm{FY} + 0.1 \cdot \mathrm{FC}$$

The sub-index for type traits (IMC) is calculated as in **both breeds** as:

$$\mathrm{IMC} = 1 \cdot \mathrm{FU} + 1 \cdot \mathrm{UP} + 1 \cdot \mathrm{FP} + 1 \cdot \mathrm{RA} + 1 \cdot \mathrm{TO}$$

For the **Alpine breed**, the current Total Merit Index (TMI or ICC), is calculated as:

$$\mathrm{ICC} = 0.63 \cdot \mathrm{IPC} + 0.25 \cdot \mathrm{IMC} + 0.12 \cdot \mathrm{LSCS}$$

For the **Saanen breed**, the current Total Merit Index (TMI or ICC), is calculated as:

$$\mathrm{ICC} = 0.55 \cdot \mathrm{IPC} + 0.28 \cdot \mathrm{IMC} + 0.17 \cdot \mathrm{LSCS}$$

This information was used to calculate the weights used for production and type traits in all simulation scenarios, as shown in Table 2 and Table 3 below.

To assess the long-term impact of including RE traits in the TMI, different scenarios were simulated. In the Base scenario, the desired gains weights for RE traits were assumed to be 0. In all other scenarios, the weights for the RE traits were varied to give the desired relative emphasis on RE traits. For example, if the scenario aim was to give 10% emphasis to RE traits, the weights for RE traits were chosen to reach this goal. The weights for all other traits were kept constant across all scenarios. The full list of scenarios is given in section titled Simulation scenarios. The assumed desired gains weights for each scenario are shown in Table 2 for the Alpine breed and Table 3, for the Saanen breed.

Table 2: Desired gains weights for Alpine goats.

ALPINE GOATS	**DESIRED GAINS WEIGHTS**					
SCENARIO:	**BASE**	**+ 5% RE**	**+ 10% RE**	**+ 10% RE (R Focus)**	**+ 10% RE (E Focus)**	**+ 20% RE**
Milk yield	0	0	0	0	0	0
Protein yield	0.63	0.63	0.63	0.63	0.63	0.63
Fat yield	0.126	0.126	0.126	0.126	0.126	0.126
Protein content	0.252	0.252	0.252	0.252	0.252	0.252
Fat content	0.063	0.063	0.063	0.063	0.063	0.063
Somatic cell score	0.12	0.12	0.12	0.12	0.12	0.12
Udder Profile	0.25	0.25	0.25	0.25	0.25	0.25
Floor Position	0.25	0.25	0.25	0.25	0.25	0.25
Rear Attachment	0.25	0.25	0.25	0.25	0.25	0.25
Fore Udder	0.25	0.25	0.25	0.25	0.25	0.25
Teat Orientation	0.25	0.25	0.25	0.25	0.25	0.25
Functional longevity	0	0.00225	0.004	0.0055	0.003	0.00725
Feed efficiency	0	6.5	9	6.5	10.5	13.5

Table 3: Desired gains weights for Saanen goats

SAANEN GOATS	DESIRED GAINS WEIGHTS					
SCENARIO:	**BASE**	**+ 5% RE**	**+ 10% RE**	**+ 10% RE (R Focus)**	**+ 10% RE (E Focus)**	**+ 20% RE**
Milk yield	0	0	0	0	0	0
Protein yield	0.55	0.55	0.55	0.55	0.55	0.55
Fat yield	0.11	0.11	0.11	0.11	0.11	0.11
Protein content	0.22	0.22	0.22	0.22	0.22	0.22
Fat content	0.055	0.055	0.055	0.055	0.055	0.055
Somatic cell score	0.17	0.17	0.17	0.17	0.17	0.17
Udder Profile	0.28	0.28	0.28	0.28	0.28	0.28
Floor Position	0.28	0.28	0.28	0.28	0.28	0.28
Rear Attachment	0.28	0.28	0.28	0.28	0.28	0.28
Fore Udder	0.28	0.28	0.28	0.28	0.28	0.28
Teat Orientation	0.28	0.28	0.28	0.28	0.28	0.28
Functional longevity	0	0.005	0.0065	0.008	0.005	0.01
Feed efficiency	0	6	8.5	10	8.5	13

Selection pressure

In the current milking goat breeding programme, the selection nucleus is 170,000 goats in 600 farms (60% Alpine, 40% Saanen). There are 1,300 matings planned to produce 400 bucks for both breeds, genotyped at 3-4 months. Based on these early genomic indexes, 70% of bucks are selected to become AI bucks. Once progeny data is available, a further 30% of these bucks are selected.

For the simulations, the selection proportion assumptions presented in Table 4.

Table 4: Selection proportions by buck lifecycle.

SELECTION PROPORTIONS:	YOUNG	EMERGING	PROVEN
Age	1	2	7
Selection proportion (at each stage)	0.70	0.30	0.70
Selection proportion (of initial population)	0.70	0.21	0.15

Genetic parameters

Genetic parameters required for the simulations are provided in Appendix 1.

Simulation scenarios and sensitivity analyses

Main scenarios

The modelling framework consisted of three main scenarios:

- **Base scenario**: The breeding programme was simulated using the current TMI index.
- **Base scenario + 10% RE**: The breeding programme was simulated using the TMI index, plus a 10% emphasis on resilience and efficiency traits, shared equally between FL and FE. It was assumed only phenotypic data was available for estimating EBVs.
- **Base scenario + 10% RE + Genomics**: The breeding programme was simulated using the same approach as the previous scenario, except with genomic data now available for estimating EBVs, with a genomic accuracy of 50%.

Sensitivity analysis: Changing trait weights

A sensitivity analysis was therefore performed, varying the desired gains weight allocated to FL and to FE. Outcomes were assessed for sensitivity under the following simulations:

- **Base scenario + 5% RE**: The breeding programme using the TMI index, plus a 5% emphasis on resilience and efficiency traits, shared equally between FL and FE.

- **Base scenario + 10% RE:** The breeding programme using the TMI index, plus a 10% emphasis on resilience and efficiency traits, shared equally between FL and FE.

- **Base scenario + 20% RE**: The breeding programme using the TMI index, plus a 20% emphasis on resilience and efficiency traits, shared equally between FL and FE.

An additional sensitivity analysis was performed to understand how changing the balance of emphasis between the two RE traits would affect the results:

- **Base scenario + 10% RE (Balanced)**: The breeding programme using the TMI index, plus a 10% emphasis on resilience and efficiency traits, shared equally between FL and FE.

- **Base scenario + 10% RE (R Focus)**: The breeding programme using the TMI index, plus a 10% emphasis on resilience and efficiency traits, but with a greater share of emphasis (7%) on resilience (FL) and a reduced emphasis (3%) on efficiency (FE)

- **Base scenario + 10% RE (E Focus)**: The breeding programme using the TMI index, plus a 10% emphasis on resilience and efficiency traits, but with a greater share of emphasis (7%) on efficiency (FE) and a reduced emphasis (3%) on resilience (FL)

The assumed desired gains weights for all scenarios are shown in Table 2 for the Alpine breed and Table 3, for the Saanen breed.

Sensitivity analysis: Changing genomic accuracy

Currently, FL and FE are not included in the genomic evaluation programme for milking goats, so the genomic accuracies for these traits are unknown. A sensitivity analysis was carried out to understand how the results would vary with a genomics accuracy of 30%, 50% and 70%:

- **Base + 10% RE + 30% Genomics accuracy**
- **Base + 10% RE + 50% Genomics accuracy**
- **Base + 10% RE + 70% Genomics accuracy**

Sensitivity analysis: Changing genetic correlations

Finally, the results are sensitive to the correlations between traits included in the index. A sensitivity analysis was performed to understand how the genetic correlation between the resilience traits (FL) and protein yield (PY) can affect the index response. PY was chosen as it is the trait with the highest percent emphasis in the index. FE was not included in this sensitivity analysis since it is a measure of residual feed intake, so it is assumed to have a correlation of 0 with PY. The scenarios simulated were:

- **Base scenario + 10% RE – 20% r_g PY-FL:** The breeding programme using the TMI index, plus a 10% emphasis on resilience and efficiency traits, but with the current correlation between FL and PY by reduced 20%.

- **Base scenario + 10% RE + 20% r_g PY-FL**: The breeding programme using the TMI index, plus a 10% emphasis on resilience and efficiency traits, but with the current correlation between FL and PY by reduced 20%.

Analysis

The following diagnostics were used to analyse and summarise the results from all simulation scenarios.

Percent emphasis

The percent emphasis for each scenario was calculated as described in (Zhang & Amer, 2021).

Annualised response to selection

The annual response to selection was calculated by calculating a weighted average of response to selection obtained in young, emerging, and proven sires. The distribution of sires in the population was based on the ages and selection proportions given in Table 4. The annualised response to was multiplied by 20 years to predict the long-term progress obtained in goal traits.

Results

Alpine goats

Main scenarios

Figure 1 summarises the relative emphasis on traits under the three main scenarios.

The Base scenario gives the relative emphasis on traits in the current breeding program; there is a 0% relative emphasis on RE traits. As expected, the relative emphasis on RE traits increases to 10% in the Base + 10% RE scenario. Adding in genomics data increases the emphasis to 17% in total, 10% emphasis on FL and 7% on FE. If genomic data is available, lessdesired gain weight needs to be placed on RE traits to get the desired emphasis.

Adding RE traits also reduces the relative emphasis of the other traits in the index. The most noticeable reductions in trait emphases are observed for PY and FY, with a 7% and 2%

reduction in emphasis respectively, compared with the current breeding program. When genomics is added as an additional information source to evaluate RE traits, the relative trait emphasis of PY and FY decreases by 9% and 3% respectively, relative to the current breeding program.

Figure 2 summarises the long-term (20 years) impact of including RE traits in the Alpine goat breeding programme.

In the Base scenario, there is progress in FL, but not in FE. This is because FL has positive genetic correlations with the production traits, particularly with MY, so progress in these traits results in a small amount of progress in FL. In the Base + 10% RE scenario, FL increases by an additional 2.1 days (0.07 months) and FE increases by 0.07 UFL units, relative to the Base scenario. When there are genomic evaluations available for both traits, FL increases by an additional 174 days (5.8 months) and FE increases by 0.09 UFL units, relative to the Base scenario.

There is a notable increase in the trait response for FL when a genomic EBV is available for this trait. FL is measured once in females that have reached their 6th lactation. This means there is little phenotypic information available for making selection decisions and the buck is 7 years before the first records on its female progeny are available. There may records available from its other female relatives (mother and maternal half-aunts), but the buck may still be as old as 5 years before these are available. Adding a genomic EBV for FL means there is an alternative data source available for making decisions on young and emerging bucks. In contrast, for FE, there are 4 records per female, per lactation. Bucks will have multiple records from its older female relatives (mother and maternal half-aunts) from birth, plus multiple records on its female progeny from 2 years of age. This means there is much greater phenotypic information available for making selection decisions.

Adding RE traits to the index reduces the response to selection for the other traits. Progress is made in MY, PY, FY, and PC, but it is reduced on average by 4% in the Base + 10% RE scenario and by 7% Base + 10% RE + Genomics scenario, both relative to Base.

There is a desirable response to selection for LSCS. Progress in LSCS is reduced on average by 97% in the Base + 10% RE scenario and by 90% Base + 10% RE + Genomics scenario, both relative to Base.

Three type traits (UP, FP, TO) show a long-term decrease when RE traits are included. Two type traits (RA, FU) show a long-term decrease when RE traits are included.

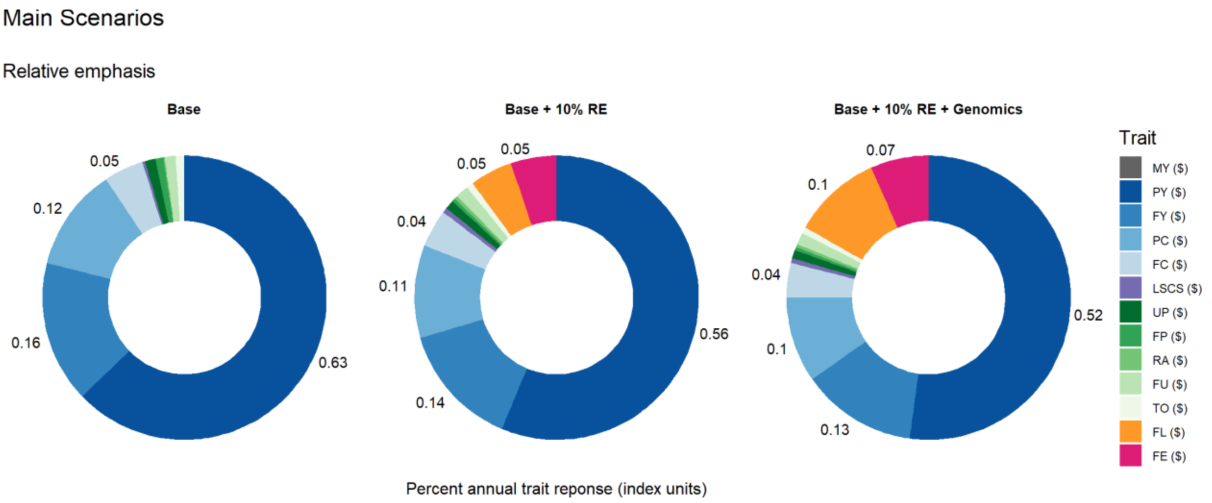


Figure 1: Relative emphasis in the three main scenarios for Alpine goats.

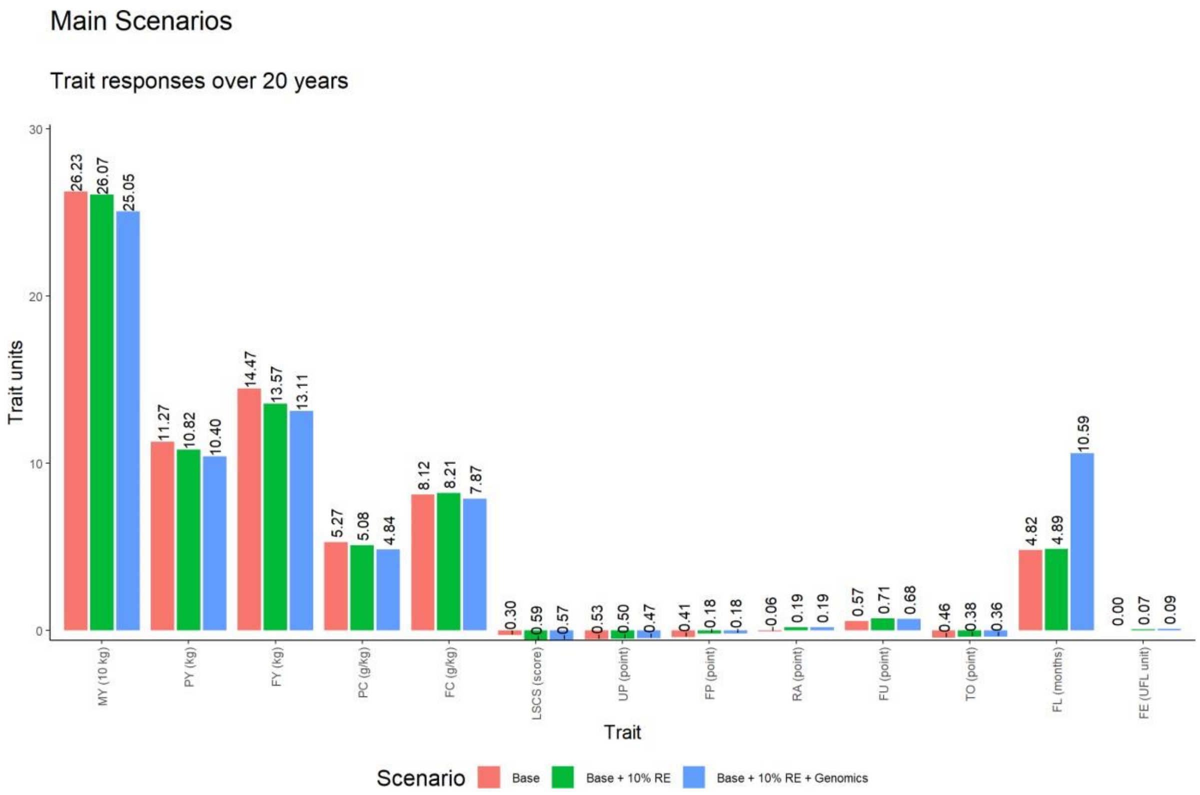


Figure 2: Long-term trait responses for the three main scenarios in Alpine goats.

Sensitivity analysis: Changing desired gain weights

In the first part of this sensitivity analysis, the desired gain weights on RE traits were varied to give a 5%, 10%, and 20% relative emphasis on RE traits, as shown in Figure 3. Figure 4 summarises the long-term (20 years) impact in trait units for each scenario. This shows increased weight on FL does not result in a substantial increase in FL response. This suggests that adding a genomics EBV for FL results would be a more effective way to increase longevity than increasing the desired gain weight on FL (compare with Figure 2) – see commentary in the previous section on the limited phenotype records for FL. In contrast, increasing the desired weight on FE results in a substantial response, comparable to adding genomics.

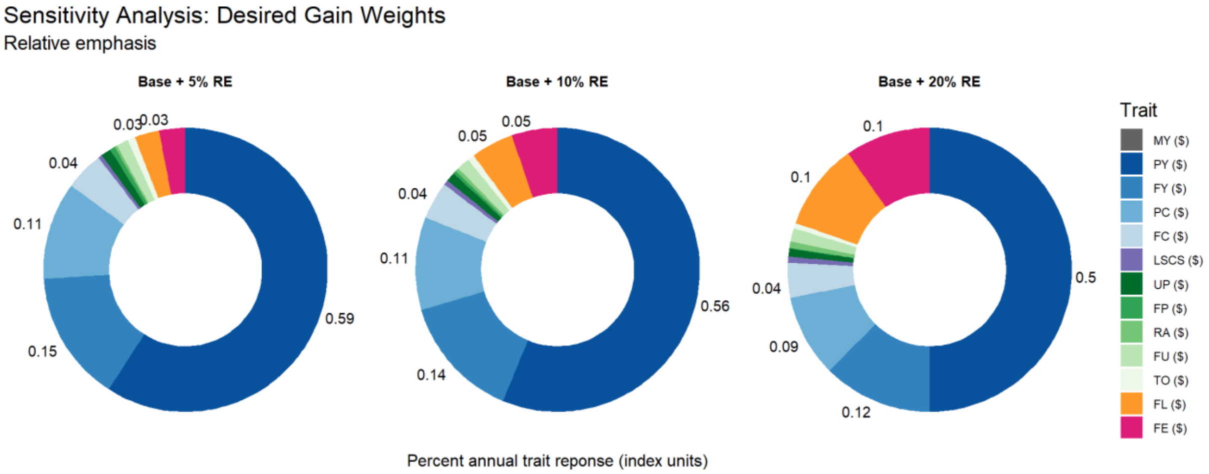


Figure 3: Relative emphasis when changing the desired gain weights assigned to RE traits in Alpine goats.

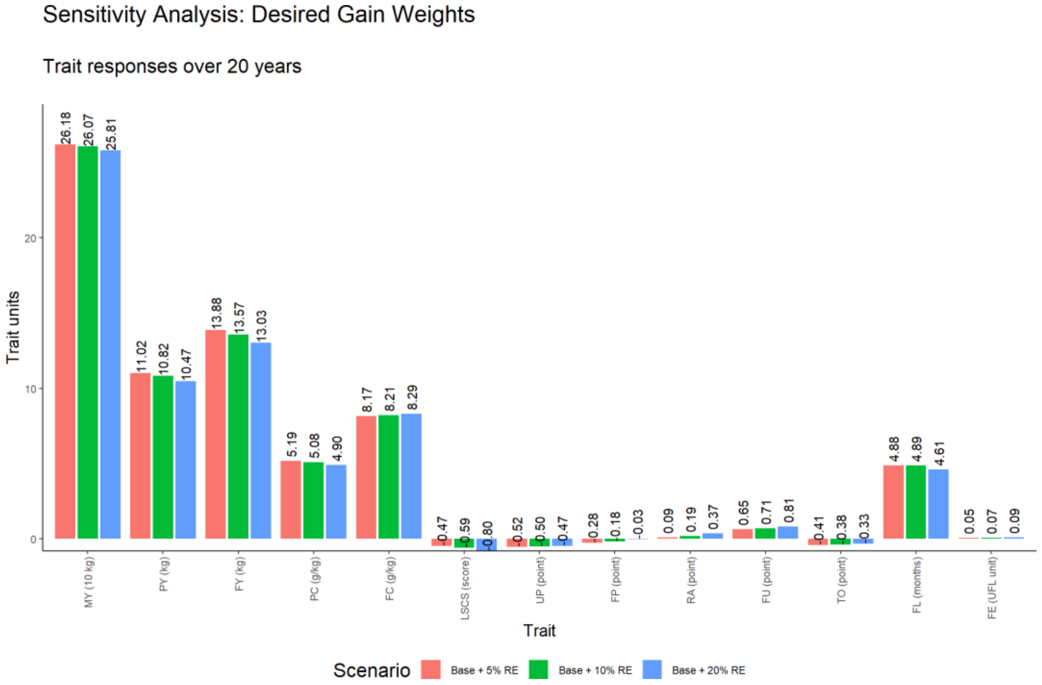


Figure 4: Long-term trait responses when changing the desired gain weights assigned to RE traits in Alpine goats.

In the second part of this sensitivity analysis, the desired weights on RE traits were varied to achieve a 10% relative emphasis on RE traits but split differently between the two traits in the different scenarios, as shown in Figure 5. Figure 6 summarises the long-term (20 years) impact in trait units for each scenario. Varying the focus on FL has little impact on FL response,when compared with adding a genomics EBV (compare with Figure 2). In contrast, increasingthe focus on FE results in a response that is comparable to adding genomics.

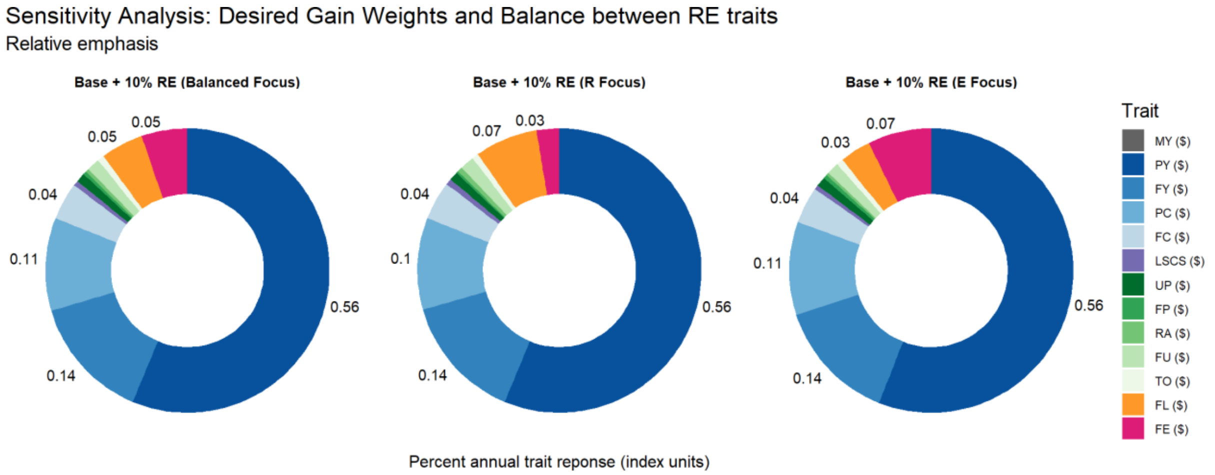


Figure 5: Relative emphasis when changing the balance of weights assigned to RE traits in Alpine goats.

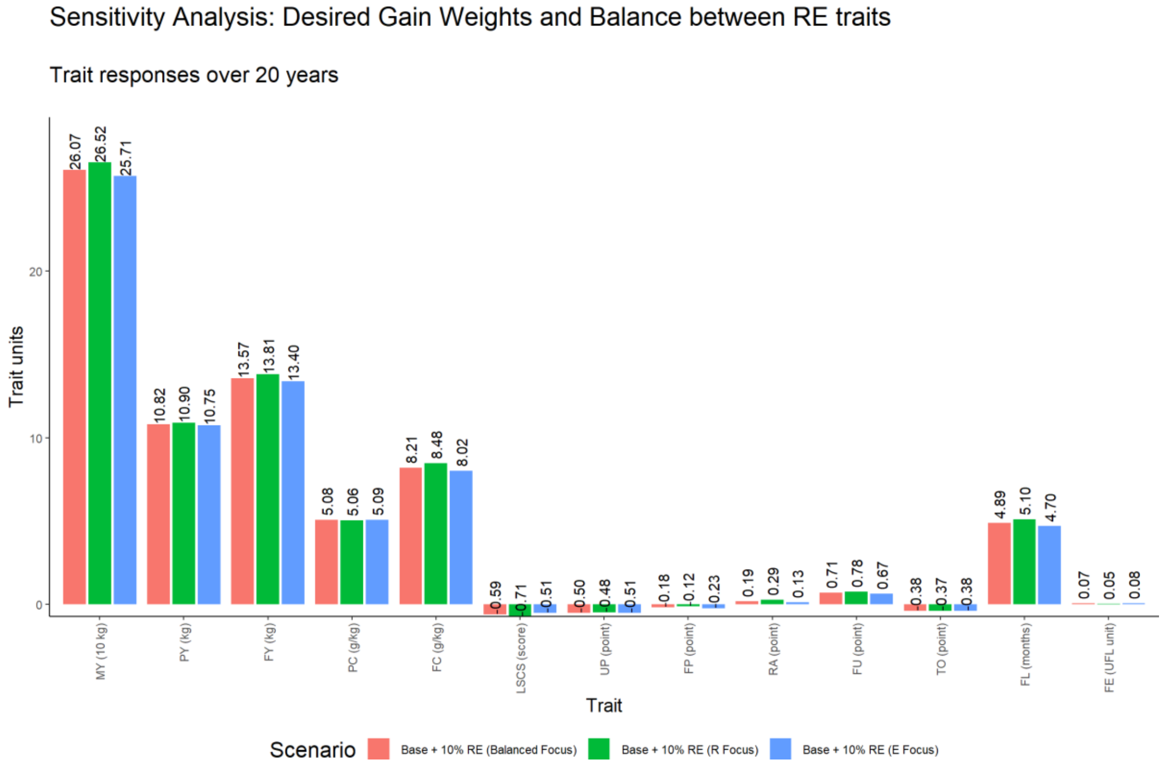


Figure 6: Long-term trait responses when changing the balance of weights assigned to RE traits in Alpine goats.

Sensitivity analysis: Changing genomic accuracy

In this sensitivity analysis, the assumed genomic accuracy was varied from 30%, 50%, to 70%, and the impact on RE traits was assessed.

Figure 7 summarises the impact of different accuracies on trait relative emphasis. Even at 30% accuracy, having genomics data increases the emphasis on RE traits to 13% in total, rising to 17% and 22% at the higher accuracies. If genomic data is available, less desired gain weight needs to be placed on RE traits to get the desired emphasis, even at lower accuracy.

Figure 8 summarises the long-term (20 years) impact in trait units for each scenario. In the 30% accuracy scenario, FL increases by an additional 212 days (7.1 months), increasing to 318 days (10.6 months) and 462 days (15.4 months) respectively in the higher accuracy scenarios. FE increases by 0.08 UFL units, increasing to 0.09 and 0.11 UFL units respectively in the higher accuracy scenarios. Having genomics data for FL results in a substantial increase in FLresponse relative having only phenotypic data, even at 30% accuracy. This suggests that adding a genomics EBV for FL results would be a most effective way to increase longevity (compare with Figure 2 – see commentary in the previous section on the limited phenotype records for FL).

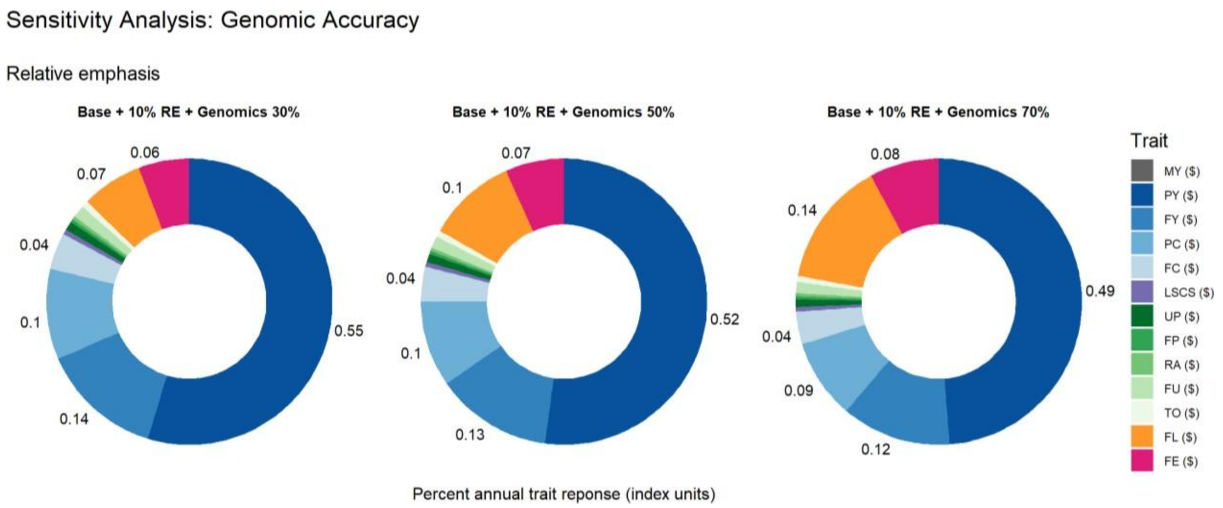


Figure 7: Relative emphasis when varying genomic accuracy in Alpine goats.

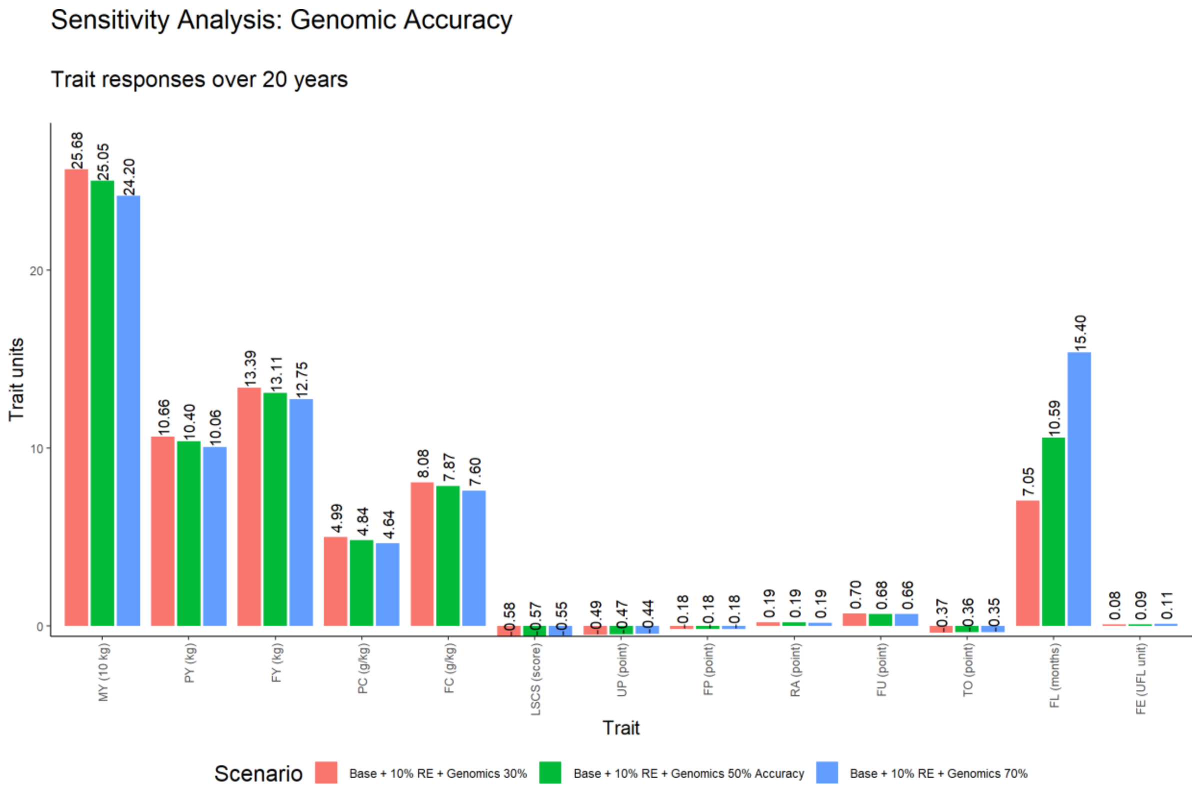


Figure 8: Long-term trait responses when varying genomic accuracy in Alpine goats.

Sensitivity analysis: Changing genetic correlations

Genetic and phenotypic correlations between traits can affect responses to selection. As the Alpine goats breeding programmes are currently experimenting with adding RE traits, so these parameters are currently estimated from preliminary data. In this sensitivity analysis, the current genetic correlation (0.14) between PY and FL was increased by 20% (to 0.17) and decreased by 20% (to 0.11).

Figure 9 summarises the impact of different accuracies on trait relative emphasis. Changing the genetic correlations has a negligible impact on the percent emphasis.

Figure 10 summarises the long-term (20 years) impact in trait units for each scenario. When the correlation is reduced by 20%, FL response decreases by 66 days (2.2 months) relative to the scenario using the currently estimated correlation. When the correlation is increased by 20%, FL response increases by 50 days (1.7 months), compared to the scenario using the current correlation.

In future, once more data is available to accurate estimate the genetic correlations between RE and other traits, a more complete picture of the implications of adding RE traits would be available. It would also help refine the appropriate desired gain weight to apply to RE traits in the TMI.

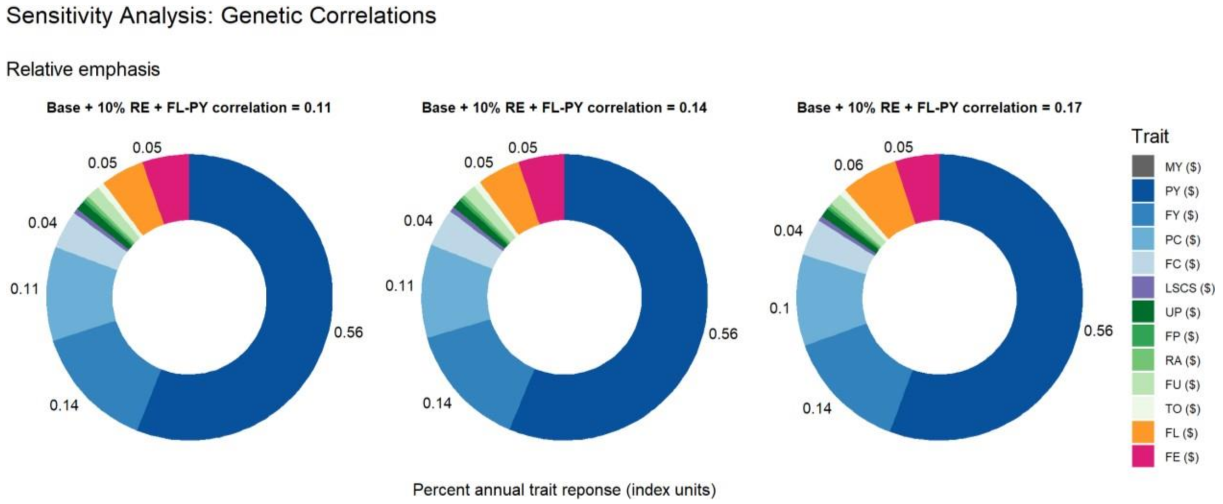


Figure 9: Relative emphasis when varying genomic correlation between PY and FL in Alpine goats.

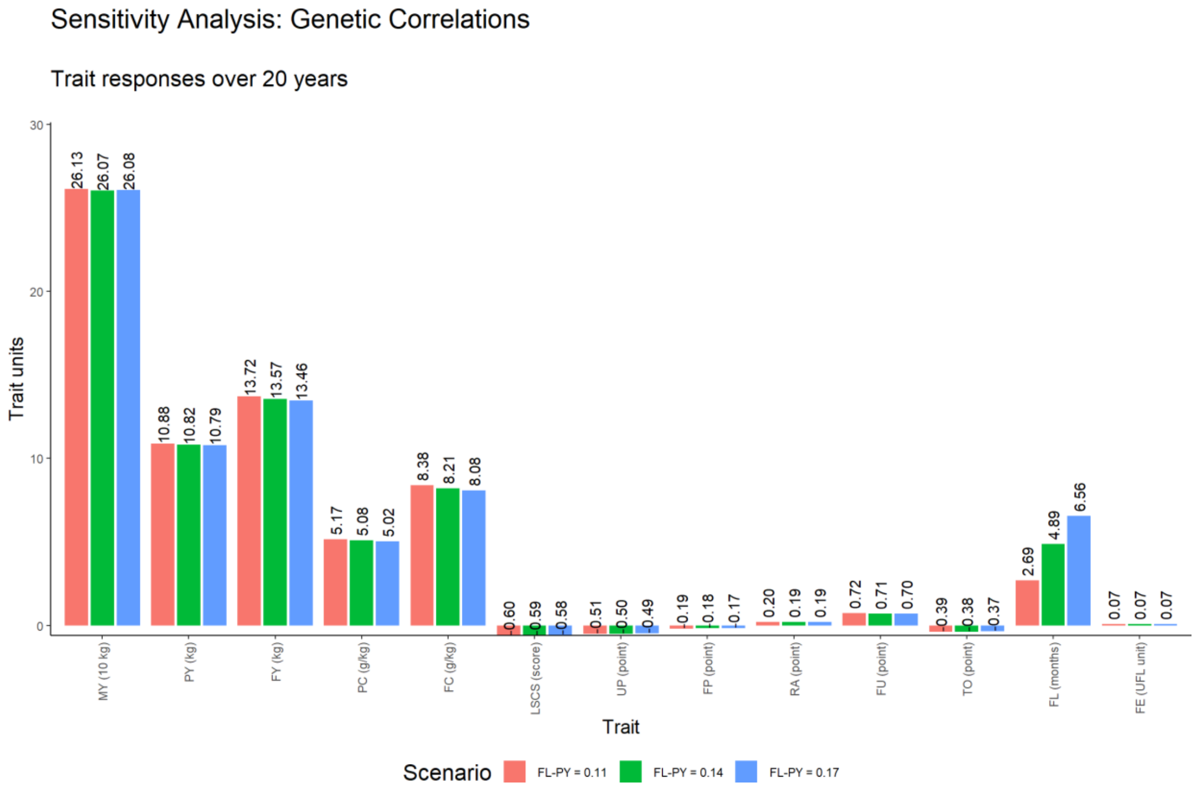


Figure 10: Long-term trait responses when varying genomic correlation between PY and FL in Alpine goats.

Saanen goats

Main scenarios

Figure 11 summarises the relative emphasis on traits under the three main scenarios.

The Base scenario gives the relative emphasis on traits in the current breeding program; there is a 0% relative emphasis on RE traits. As expected, the relative emphasis on RE traits increases to 10% in the Base + 10% RE scenario. Adding in genomics data increases the emphasis slightly to 25% in total, 19% emphasis on FL and 6% on FE. If genomic data is available, less desired gain weight needs to be placed on RE traits to get the desired emphasis.

Adding RE traits also reduces the relative emphasis of the other traits in the index. The most noticeable reductions in trait emphases are observed for PY and FY, with a 7% and 1% reduction in emphasis respectively, compared with the current breeding program. When genomics is added as an additional information source to evaluate RE traits, the relative trait emphasis of these traits decreases by 18% and 4% respectively, relative to the current breeding program.

Figure 12 summarises the long-term (20 years) impact of including RE traits in the Saanen goat breeding programme.

In the Base scenario, there is an unfavourable response in FL, which is predicted to decrease by 144 days (4.8 months) in the simulation. In Saanen goats, FL has much weaker genetic correlations with the production traits compared to Alpine goats, and even has a weak negative correlation with FY, unlike in Alpine goats, progress in production traits does not result in a progress in FL. In the Base scenario, there is no response in FE which, as a measurement of residual feed intake, is assumed to have no genetic correlations with the other traits. In the Base + 10% RE scenario, FL increases by an additional 188 days (6.27 months) and FE increases by 0.05 UFL units, relative to the Base scenario. When there are genomic evaluations available for both traits, FL increases by an additional 449 days (15 months) and FE increases by 0.08 UFL units, relative to the Base scenario.

There is a notable increase in the trait response for FL when a genomic EBV is available for this trait. As in Alpine goats, FL is measured once in females that have reached their 6th lactation, so there are limited phenotype records for FL for making selection decisions. Adding a genomic EBV for FL means there is an alternative data source available for making decisions on young and emerging bucks. In contrast, FE has greater phenotypic information available for making selection decisions.

Adding RE traits to the index reduces the responses to selection for the some of the production traits. Progress is still made in MY, PY, and FY but it is reduced on average by 8% in the Base + 10% RE scenario and by 16% Base + 10% RE + Genomics scenario, both relative to Base. Although, there is a desirable response to selection for PC, which increases by 26%

in the Base + 10% RE scenario and by 18% Base + 10% RE + Genomics scenario, both relative to Base.

There is also a desirable response to selection for LSCS. Progress in LSCS is reduced on average by 33% in the Base + 10% RE scenario and by 33% Base + 10% RE + Genomics scenario, both relative to Base.

All type traits (UP, FP, RA, FU and TO) show a long-term increase when RE traits are included, although the rate of increase slows.

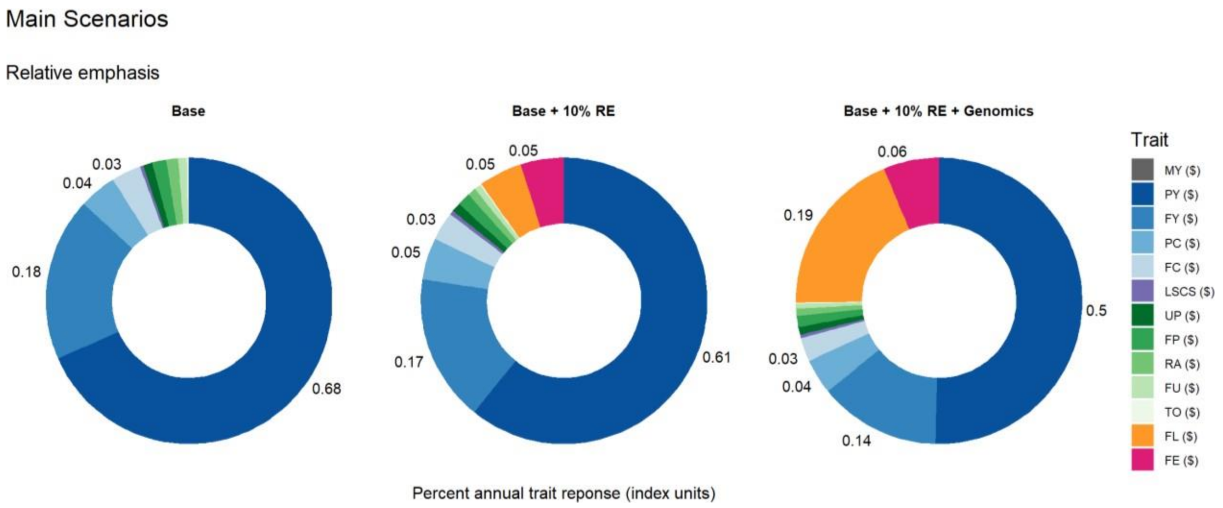


Figure 11: Relative emphasis in the three main scenarios for Saanen goats.

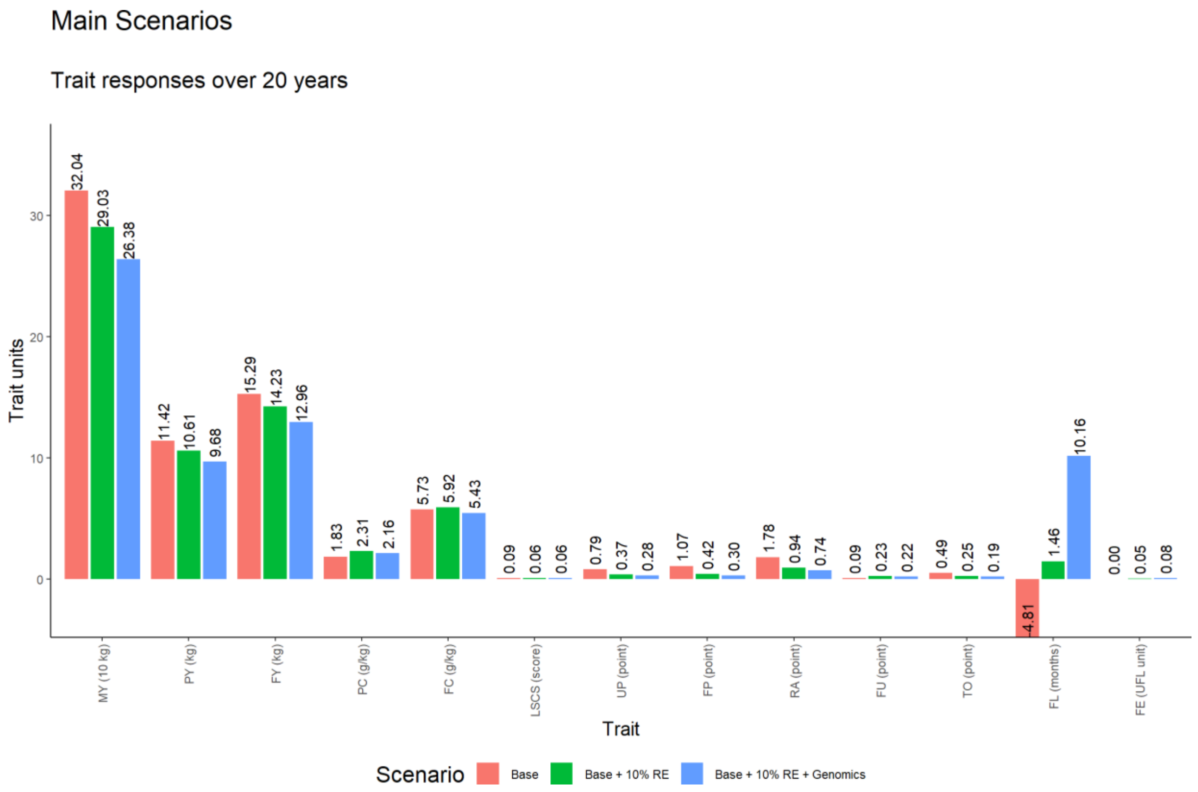


Figure 12: Long-term trait responses for the three main scenarios in Saanen goats.

Sensitivity analysis: Changing desired gain weights

In the first part of this sensitivity analysis, the desired gain weights on RE traits were varied to give a 5%, 10%, and 20% relative emphasis on RE traits, as shown in Figure 13. Figure 14 summarises the long-term (20 years) impact in trait units for each scenario. This shows increased weight on FL results in small increases in FL response, but not as significantly as a genomics EBV. This suggests that adding a genomics EBV for FL results would be a more effective way to increase longevity than increasing the desired gain weight on FL (compare with Figure 12 – see commentary in the previous section on the limited phenotype records for FL). In contrast, increasing the desired weight on FE results in a response that is comparable to adding genomics.

In the second part of this sensitivity analysis, the desired weights on RE traits were varied to achieve a 10% relative emphasis on RE traits but split differently between the two traits in the different scenarios, as shown in Figure 15. Figure 16 summarises the long-term (20 years) impact in trait units for each scenario. Varying the focus on FL has a small impact on FL and FE responses, when compared with adding a genomics EBV (compare with Figure 12).

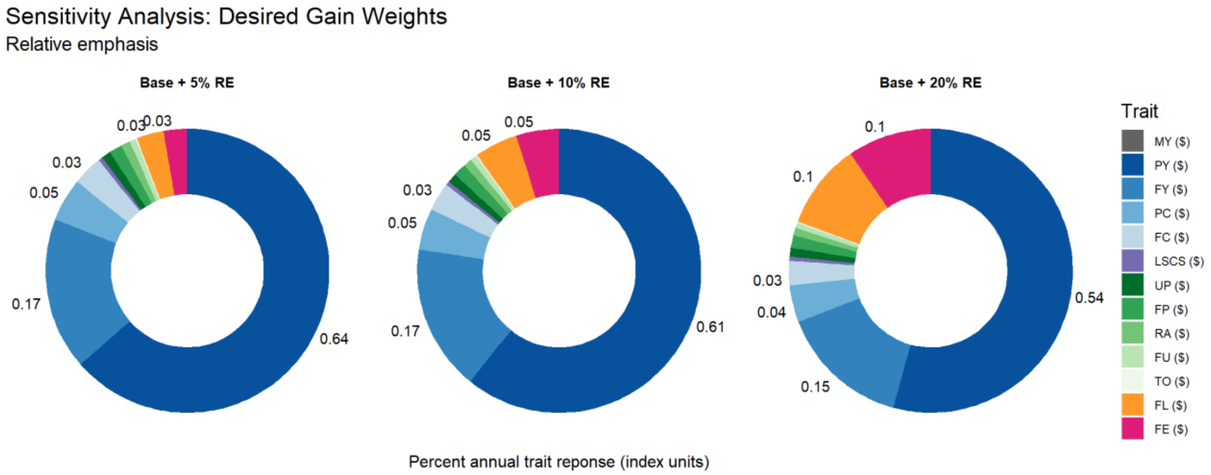
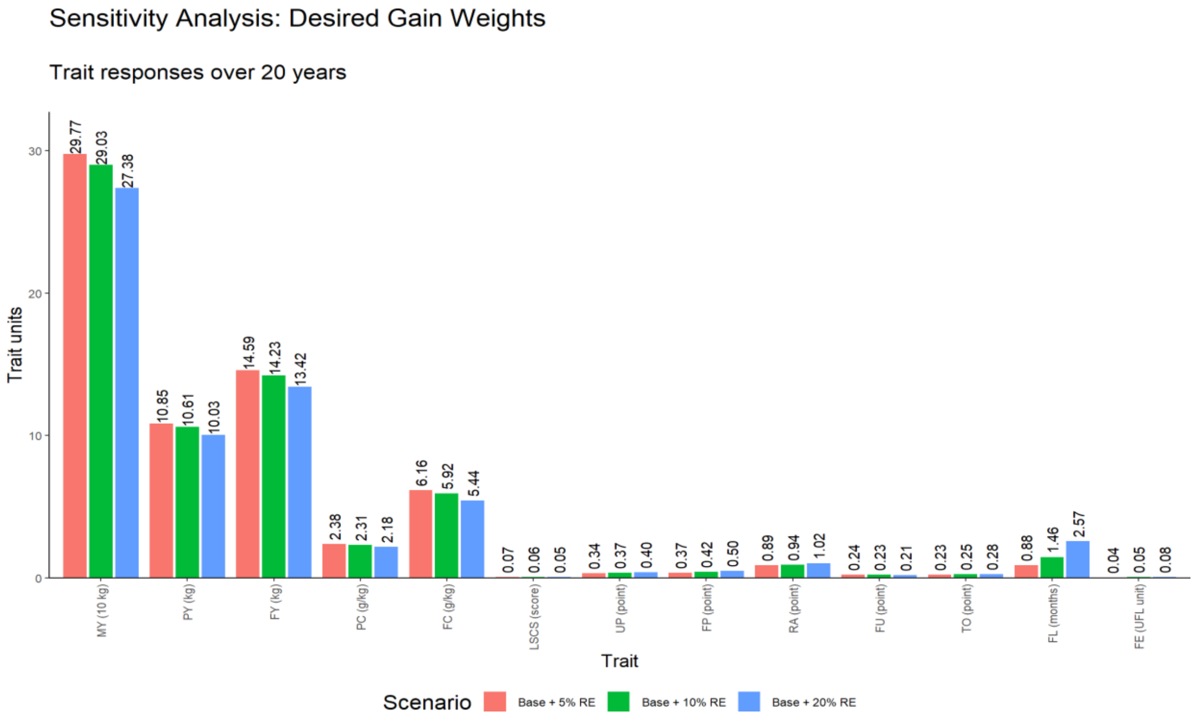


Figure 13: Relative emphasis when changing the desired gain weights assigned to RE traits in Saanen goats.e 14: Long-term trait responses when changing the desired gain weights assigned to RE traits in Saanen goats.



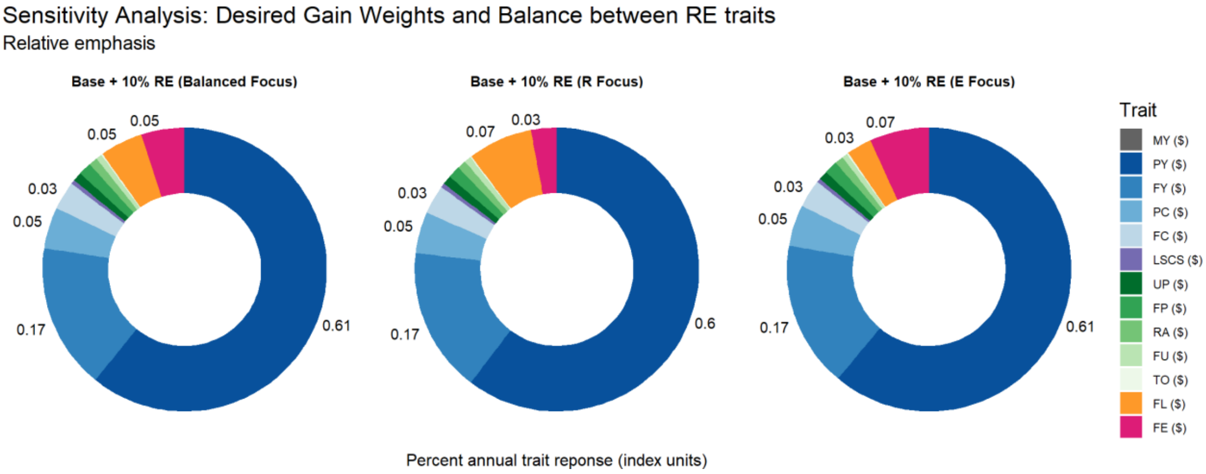


Figure 15: Relative emphasis when changing the balance of desired gain weights assigned to RE traits in Saanen goats.

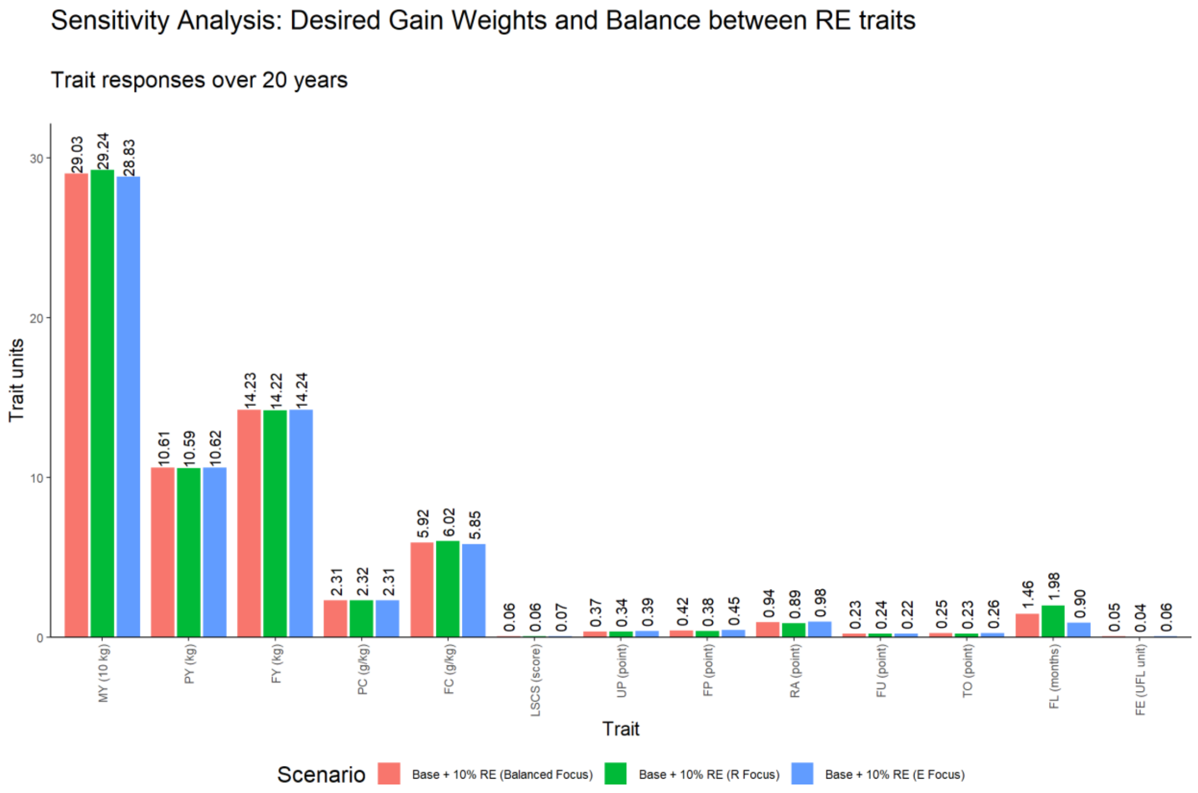


Figure 16: Long-term trait responses when changing the balance of desired gain weights assigned to RE traits in Saanen goats.

Sensitivity analysis: Changing genomic accuracy

In this sensitivity analysis, the assumed genomic accuracy was varied from 30%, 50%, to 70%, and the impact on RE traits was assessed.

Figure 17 summarises the impact of different accuracies on trait relative emphasis. Even at 30% accuracy, having genomics data increases the emphasis on RE traits to 17% in total, rising to 25% and 34% at the higher accuracies. If genomic data is available, less desired gain weight needs to be placed on RE traits to get the desired emphasis, even at lower accuracy.

Figure 18 summarises the long-term (20 years) impact in trait units for each scenario. In the 30% accuracy scenario, FL increases by 151 days (5 months), increasing to 306 days (10.2 months) and 492 days (16.4 months) respectively in the higher accuracy scenarios. FE increases by an additional 0.06 UFL units, increasing to 0.08 and 0.10 UFL units respectively in the higher accuracy scenarios. Having genomics data for FL results in a substantial increase in FL response relative having only phenotypic data, even at 30% accuracy. This suggests that adding genomics to FL would be a most effective way to increase longevity (compare with Figure 12 – see commentary in the previous section on the limited phenotype records for FL). In contrast, increasing the desired weight on FE results in a substantial response, comparable to adding genomics.

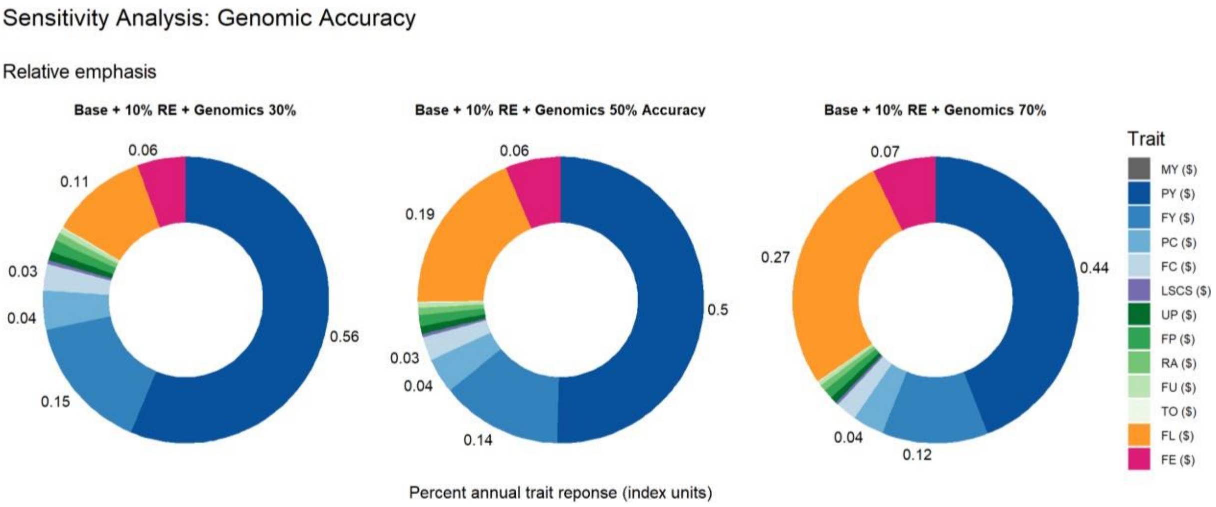


Figure 17: Relative emphasis when varying genomic accuracy in Saanen goats.

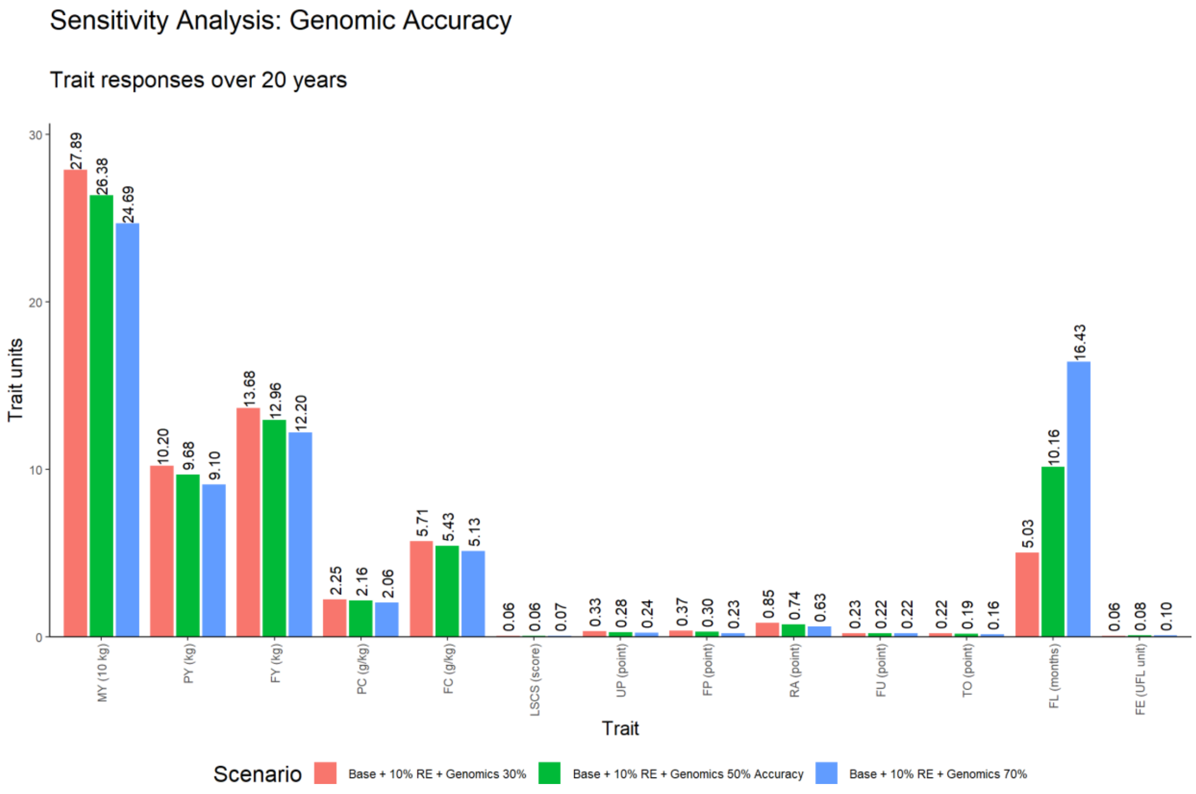


Figure 18: Long-term trait responses when varying genomic accuracy in Saanen goats.

Sensitivity analysis: Changing genetic correlations

As the Saanen goats breeding programmes are currently experimenting with adding RE traits, so these parameters are currently estimated from preliminary data. In this sensitivity analysis, the current genetic correlation (0.02) between PY and FL was increased by 20% (to 0.016) and decreased by 20% (to 0.024).

Figure 19 summarises the impact of different accuracies on trait relative emphasis. Changing the genetic correlations has a negligible impact on the precent emphasis.

Figure 20 summarises the long-term (20 years) impact in trait units for this sensitivity analysis. When the correlation is reduced by 20%, FL response decreases by 7 days (0.24 months) relative to the scenario using the currently estimated correlation. When the correlation is increased by 20%, FL response also increases by 7 days (0.23 months), compared to the scenario using the current correlation.

Even though the current correlation between PY and FL is weak, it does change the expected FL response. In future, updated correlation data can help outline the implications of adding RE traits to the current TMI and refine the appropriate desired gain weight to apply to these traits.

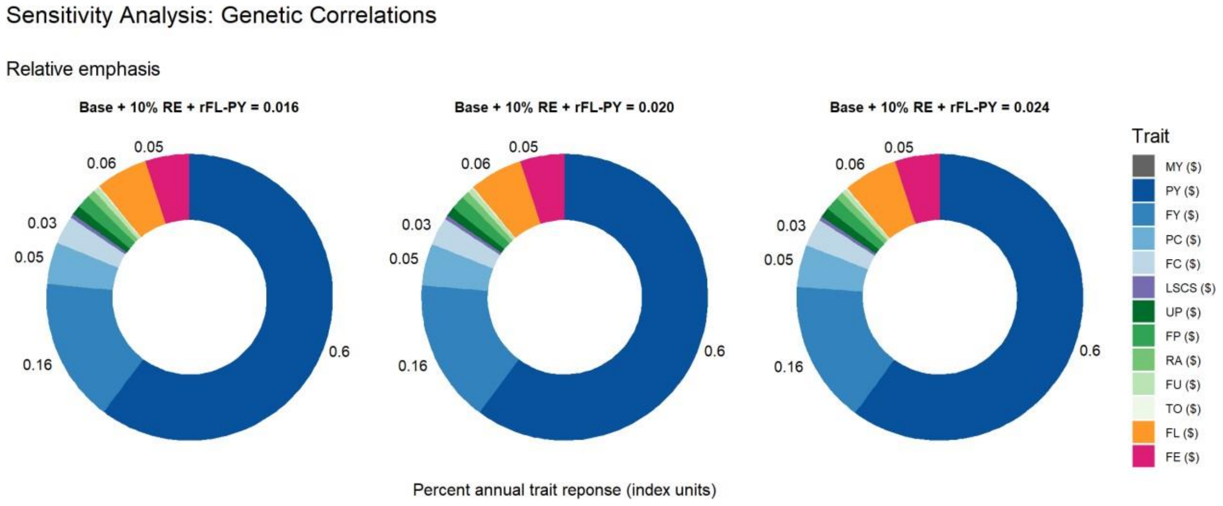


Figure 19: Relative emphasis when varying genomic correlation between PY and FL in Saanen goats.

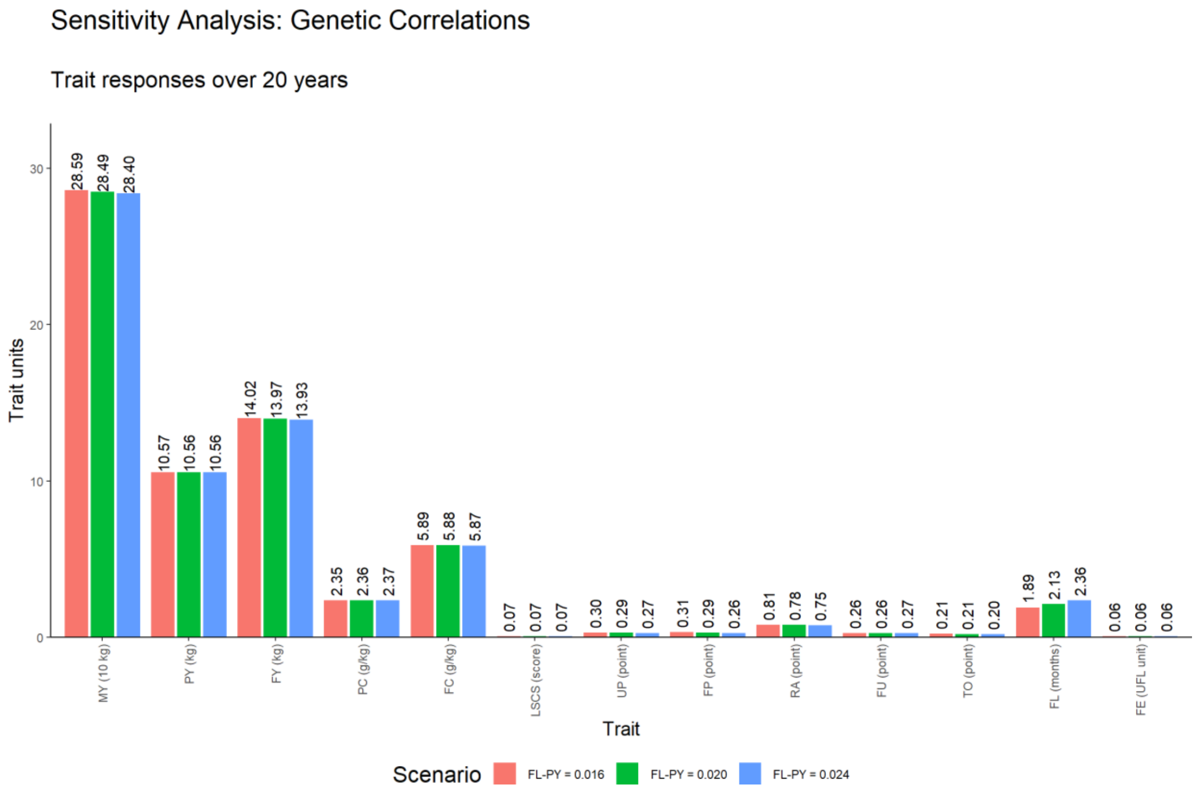


Figure 20: Long-term trait responses when varying genomic correlation between PY and FL in Saanen goats.

Lacaune sheep

Introduction

This report describes the outcomes of a breeding program simulation in Lacaune sheep using a general selection index model framework. The objectives of this simulation are to:

- Assess the long-term impact of breeding for resilience and efficiency traits in Lacaune sheep populations.
- Test how new genomics data and tools can improve breeding programs and populations faster.
- Produce 20-year forecasts of the productivity gains that can be expected when resilience and efficiency traits are included in the breeding programme.

This simulation forms part of Task 7.4 of the H2020 Small Ruminants Breeding for Efficiency and Resilience (SMARTER) project.

Materials and methods

The long-term impact of including resilience (R) and efficiency (E) traits, as new breeding goals in a selection index, was assessed using a general selection index theory modelling framework developed by AbacusBio. Selection index theory (Dekkers, *J Anim Breed Genet*, **124**:331-341, 2007) predicts the superiority of individuals of each sex selected using an index and the annual response to selection in a breeding program. The outcomes depend on the breeding program parameters outlined below.

- Traits included in the selection index with:
    - Heritability,
    - Repeatability,
    - Phenotypic variances, and
    - Genetic and phenotypic correlations with other traits.
- Economic weight or other weight assigned to each trait in the index.
- Data available (including genotypes) for each of the selection candidates.
- Breeding program structure.
- Selection pressure.

Required modelling inputs like breeding program characteristics, trait weights, and genetic parameters were obtained through INRAE (pers. comm. Jean-Michel Astruc).

Breeding program parameters

The breeding program parameters are described in more detail in the sections below.

Economic weights

Economic weights are not deployed in the Lacuane breeding program modelled herein. Rather, desired gains weights provided in the index and sub-indexes are presented in the section below.

Traits and data recording

There are currently 8 breeding goal traits included in the Lacaune selection index. Details on the breeding goal traits (those being part of the index) and recorded traits (not included in the index) available in the breeding program are provided in Table 5. Two additional breeding goal traits are added to these indexes in these simulations: Functional Longevity (FL) as a resilience trait and Feed Efficiency (FE) as an efficiency trait.

Table 5: Details on breeding goal and recorded traits in the Lacaune sheep breeding program.

			MEASURED DURING PARITY		
TRAIT NAME	ACRONYM	WEIGHT	1	2	3
Current index traits					
Milk yield	MY	Not a goal trait	YES	YES	YES
Fat yield	FY	0.5	YES	YES	NO
Protein yield	PY	0.925	YES	YES	NO
Fat content	FC	1/25	YES	YES	NO
Protein content	PC	1/64	YES	YES	NO
Somatic cell score	LSCS	-0.5	YES	YES	NO
Teat angle	TA	0.5 x -0.25 = -0.125	YES	NO	NO
Udder cleft	UC	Not a goal trait	YES	NO	NO
Udder depth	UD	0.5 x 0.5 = 0.25	YES	NO	NO
Teat position	TP	0.5 x 0.25 = 0.125	YES	NO	NO
Resilience and efficiency (R&E) traits					
Functional longevity	FL				
Feed efficiency	FE				

The modelled information sources available for young rams, emerging sires, and proven sires were defined to represent the situation as best as possible using the provided breeding program characteristics. In general, as rams become older, more information becomes available to estimate their breeding values and therefore TMI. For more details on the available information sources and underlying assumptions, see Relative groups and assumptions on available information sources.

The availability of information within a scenario remained constant, such that traits are always measured on the same animals, with the same proportions of animals being selected as candidates (e.g., the selection proportion in the proven sire scenario is always 0.01 (see the section on Selection pressure) with 3 records on MY, 1 record on UD, etc. from the mother contributing towards the sire's EBVs). The breeding goal remained the same across the modelled scenarios, but with FL and FE added when the breeding goal was expanded with these resilience and efficiency traits, using phenotypic data only, or both phenotypic and genomic data.

Indexes and index weights

Traits in the current Lacaune sheep Total Merit Index (TMI) are measured on ewes only and selection of males is done on the TMI. Rams are selected on additional traits like functional traits, and semen quality, but none of these traits are recorded, so cannot be considered in the modelling framework other than through general selection intensity parameters.

The TMI consists of sub-indexes for production ($PROD$) and udder ($UDDER$), with a weight on somatic cell score ($LSCS$), and is calculated as follows:

$$TMI = 1 \times PROD - 0.5 \times LSCS + 0.5 \times UDDER.$$

The production sub-index ($PROD$) is

$$PROD = 0.5 \times FY + 0.925 \times PY + {}^{1}/_{25} \times FC + {}^{1}/_{64} \times PC,$$

with all values in units of the traits (for trait names see Table 5), without any rescaling takingplace.

The udder sub-index ($UDDER$) is calculated as

$$UDDER = -0.25 \times TA + 0.5 \times UD + 0.25 \times TP.$$

Considering individual traits, the aim is to decrease $LSCS$ and TA, while increasing the other traits. This means that the genetic correlation (+0.19; Appendix 1) between MY and $LSCS$ is unfavourable.

Selection pressure

About 3,000 rams are chosen each year within the Lacaune breeding program based on pedigree and are those that descend from the best artificial inseminations (AI) matings of dams of rams, and sires of rams. These rams are genotyped and 300 are chosen for AI (based on GEBVs). These 300 AI rams are used for 1 year and produce about 35 ewes each.

The best 10% of AI rams (based on TMI) are selected as sires of rams and about 70-80% of the 300 AI rams will continue breeding each year, based on daughter information. Selected proportion of rams or sires used in the simulations reflect the breeding program and are provided in Table 6.

Table 6: Selection proportion and information sources for the 3 modelled scenarios.

SCENARIO	Age	SELECTION PROPORTION
Young ram	1	0.10
Emerging sire	2	0.075
Proven sire	4	0.01

Genetic parameters

Genetic parameters required for the simulations are provided in Appendix 1.

Simulation scenarios and sensitivity

To assess the impact on genetic progress by adding FL and FE, the following scenarios were simulated, with details provided in Table 7.

1. This scenario simulated the progress obtained using the current TMI index, based on desired gains weights. This base Lacaune sheep breeding program is used as comparison with other (extended) scenarios.

2. In the base plus R&E traits scenario the breeding goal is expanded with FL and FE (phenotypes only) with a weight of X allocated to FL and Y to FE, being the desired gains for these traits:

$$TMI = 1 \times PROD - 0.5 \times LSCS + 0.5 \times UDDER + X \times FL + Y \times FE.$$

3. The last scenario includes the base plus R&E trait and genomics data with an assumed accuracy of 50% for FL and FE genomic EBVs.

Within scenarios 1 and 2 above, several sensitivity analyses were performed (Table 7) to determine how much the outcomes are affected by changing X and Y. Additionally, the genetic correlations between FL and FE with MY were changed ± 20%. A sensitivity analysis was performed, by changing the accuracy of genomic EBVs by +/- 20%.

Table 7: Simulated scenarios and parameters altered in sensitivity analysis.

SCENARIO	SENSITIVITY ANALYSIS X and Y values and r_g between $MY\text{-}FL$, $MY\text{-}FE$
Base (TMI)	
Base + R&E	$X, Y = 0.005, 0.125$ $r_g = -0.18, 0.80$
+20% more weight	$X, Y = 0.006, 0.15$ $r_g = -0.18, 0.80$
-20% less weight	$X, Y = 0.004, 0.1$ $r_g = -0.18, 0.80$
FL focus	$X, Y = 0.006, 0.125$ $r_g = -0.18, 0.80$
FE focus	$X, Y = 0.005, 0.15$ $r_g = -0.18, 0.80$
+20% r_g $MY\text{-}FL$	$X, Y = 0.005, 0.125$ $r_g = -0.216$
-20% r_g $MY\text{-}FL$	$X, Y = 0.005, 0.125$ $r_g = -0.144$
+20% r_g $MY\text{-}FE$	$X, Y = 0.005, 0.125$ $r_g = 0.96$
-20% r_g $MY\text{-}FE$	$X, Y = 0.005, 0.125$ $r_g = 0.64$
Base + R&E + G	Accuracy of 50%
+20% accuracy	Accuracy of 70%
-20% accuracy	Accuracy of 30%

Percent emphasis

The percent emphasis for each scenario was calculated as described in (Zhang & Amer, 2021).

Annualised response to selection

The annual response to selection was calculated by calculating a weighted average of response to selection obtained in young, emerging, and proven sires. The distribution of sires in the population was based on the ages and selection proportions given in Table 6. The annualised response to was multiplied by 20 years to predict the long-term progress obtained in goal traits.

Results

Annual and long-term response to selection

The annual response to selection was calculated by calculating a weighted average of response to selection obtained in young ram, emerging sire, and proven sire. For that, the distribution of rams/sires in the population based on selection proportions (Table 6) was used as well as their respective ages, being 1, 2, and 4 years-of-age. The population consisted of 54% young rams (300 out of 555), 41% emerging sires (225 out of 555), and 5% proven sires (30 out of 555).

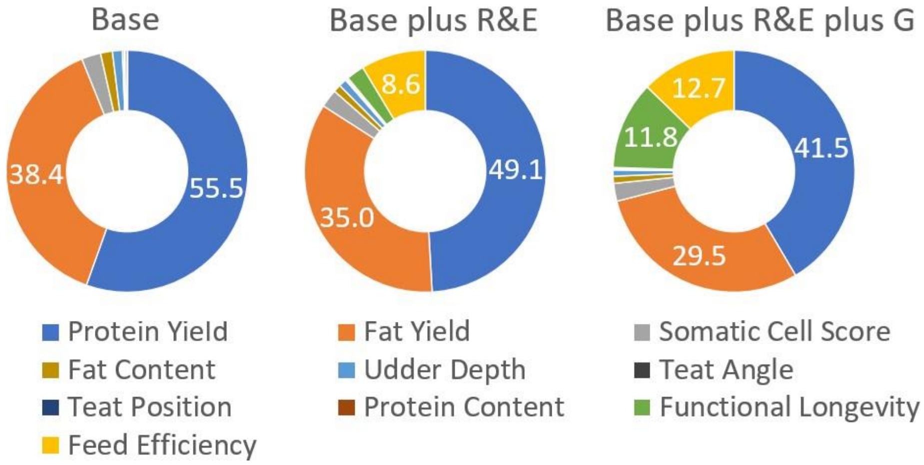
The annual response to selection (when selecting on the index) was multiplied by 20 years to predict the long-term progress obtained in goal traits, as well as MY.*

Comparing the relative trait emphasis on goal traits in the index (Table 8 and Figure 21) across the various scenarios indicates that adding the resilience & efficiency traits FL and FE reduces the relative emphasis of the other traits in the index. The most noticeable reductions in trait emphases are observed for PY and FY, with a 25.2% (from 55.5% to 41.5%) and 23.2% reduction in emphasis (from 38.4% to 29.5%), respectively, comparing the current breeding program (base scenario) with the scenario where resilience & efficiency traits FL and FE are included in the index and genomically evaluated (base + R&E + G scenario). When genomics is added as an additional information source to evaluate FL and FE, the relative trait emphasis of these traits increases from 2.4% and 8.6% and 11.8% and 12.7%, respectively.

Table 8: Relative goal trait emphasis, based on response.

	RELATIVE TRAIT EMPHASIS IN THE INDEX		
TRAITS* (UNIT)	BASE	BASE + R&E	BASE + R&E + G
$FY\ (kg)$	38.4%	35.0%	29.5%
$PY\ (kg)$	55.5%	49.1%	41.5%
$FC\ (g/l)$	1.6%	1.0%	0.9%
$PC\ (g/l)$	0.3%	0.2%	0.2%
$LSCS\ (score)$	2.6%	2.4%	2.4%
$TA\ (point)$	0.2%	0.1%	0.1%
$UD\ (point)$	1.3%	1.1%	0.8%
$TP\ (point)$	0.1%	0.1%	0.1%
$FL\ (lactation)$	-	2.4%	11.8%
$FE\ (\%)$	-	8.6%	12.7%

*FY = fat yield, PY = protein yield, FC = fat content, PC = protein content, LSCS = somatic cell score, T = teat angle, UD = udder de pth, TP = teat position, FE = feed efficiency, and FL =



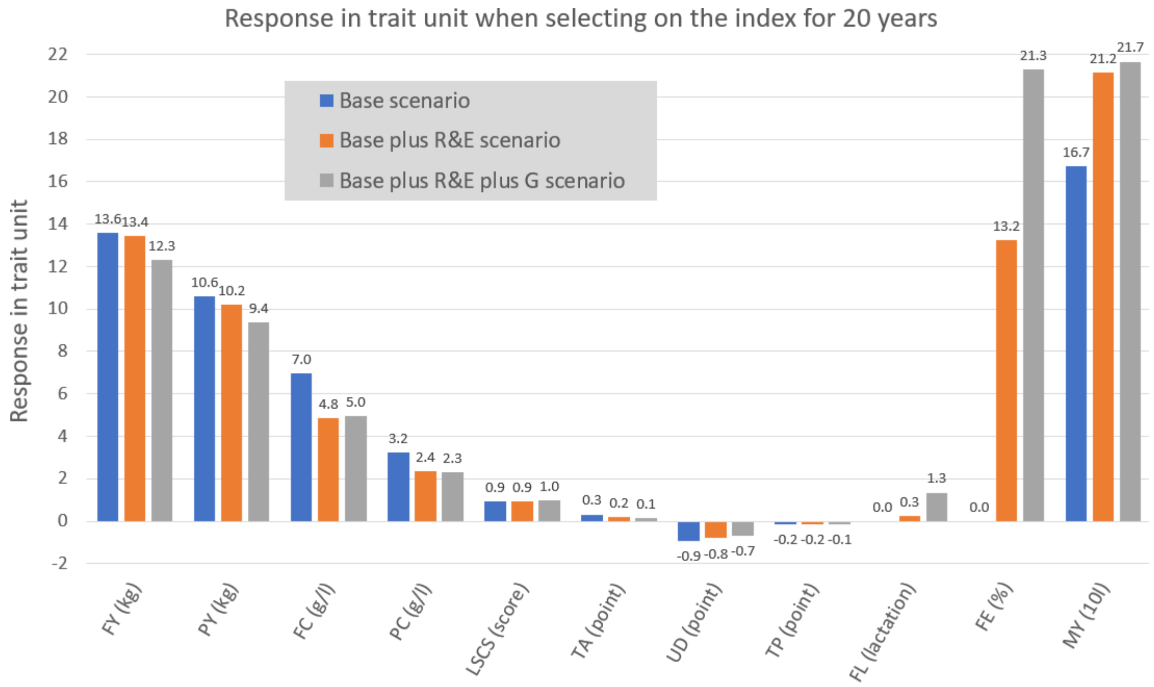
In the long-term (20 years), adding FL and FE to the breeding goal results in 0.3 more lactations and an increase of 13.2% in FE (base plus R&E scenario) (Figure 22). When these traits are genomically evaluated the response to selection is 1.3 more lactations and an increase of 21.3% in FE (base plus R&E plus G scenario).

The response to selection for FY, PY, FC, and PC reduces on average by 15.5% when FL and FE are added to the breeding goal (comparing base scenario with base plus R&E scenario) and on average by 19.6% when FL and FE are genomically evaluated (comparing base scenario with base plus R&E plus G scenario). The biggest reductions in response to selection are observed for FC and PC, with almost 30% less response compared to the current breeding program (base scenario).

Interpreting the long-term (20 year) response to selection (in trait units) across the scenarios suggests that the current breeding program (base scenario) obtains undesired responses to selection for $LSCS$, TA, UD, and TP; a decrease in $LSCS$ and TA is the aim and an increase in all other traits.

A genomic evaluation of the resilience & efficiency traits FL and FE (base plus R&E plus G scenario) reduces the undesired response to selection for TA, UD, and TP (e.g., from 0.3 to 0.1 for TA, and from -0.9 to -0.7 for UD). However, the undesired response to selection increases from a 0.9 score to a 1.0 score for $LSCS$ when FL and FE are added to the breeding goal and genomically evaluated (comparing base scenario with base plus R&E plus G scenario).

Compared to the current breeding program (base scenario), the response to selection for MY increases by 26.4% when FL and FE are added to the breeding goal (base plus R&E scenario), and by 29.4% when genomics is added as an information source to evaluate FL and FE (base plus R&E plus G scenario).



MY = milk yield; despite not being a profit trait (milk yield is not included in the index), response to selection is reported as the only available genetic correlation for FE was between MY and FE.

Figure 22: Long-term response to selection (trait change after 20 years) for index traits and milk yield, across scenarios.

Sensitivity analyses

Changing R&E trait weights

Testing the sensitivity of outcomes to the weights applied to FL and FE in the index (+/ - 20% on X and Y, respectively) indicated that:

1. As expected, the relative emphasis of FL and FE in the index changed significantly (on average, by 36.6%) as well as their response to selection (an average change of 18.9%) when their weights were increased or decreased by 20%.
2. The emphasis of other traits in the index were only slightly affected by the 20% change in weight applied to FL and FE, with the maximum change in response to selection being 3.0% (for MY).

Detailed outcomes of sensitivity analyses are provided in Appendix IIII – Sensitivity outcomes.

Changing focus on FL or FE

Changing the focus on either FL or FE in the index (increasing either X or Y by 20%) showed that:

1. The relative trait emphasis increased by 34.8% and 33.0% when the weight applied to FL or FE, respectively, was increased by 20%. Also, the response to selection increased by 12.9% for FL and by 12.7% for FE.

2. Only slight differences in relative traits emphasis and response to selection in other traits in the index was observed, although of note is that thorough testing to set (economic) weights for the resilience & efficiency traits in the index should be done to obtain desired responses to selection and/or reduced unwanted responses to selection.

Changing genetic correlations between MY and FL or FE

Changing the genetic correlation between MY and FL (-0.18 ± 20%) resulted in almost the same relative change in trait emphases and responses to selection. As expected, the response to selection changed for both FL and MY. A correlated change in response to selection was observed for FE, with a change in the genetic correlation between MY and FL .

Changing the genetic correlation between MY and FE (0.80 ± 20%) resulted in slightly different relative trait emphases for traits in the index. As expected, the response to selection changed for both FE and MY, with some correlated responses to selection observed for FL, FC and PC.

Changing the accuracy of genomic breeding values for FL and FE Testing the sensitivity of outcomes to the accuracy of genomic breeding values for FL and FEshowed that:

1. As expected, the relative emphasis of FL and FE in the index changed significantly (average change of 33.6%) as well as their response to selection (average change of 40.0%) when the accuracy of genomic breeding values changed from 50% to either 30% or 70%.

Of the sensitivity analyses, the emphasis on other traits in the index was affected most by the change in accuracy of genomic breeding values for FL and FE (on average 12.6%). The response to selection for PY and FY changed by 5.2% on average.

Outcomes

Relative emphasis on index traits and long-term response to selection

Considering the relative emphasis of traits in the index, the outcomes from the simulated scenarios indicate that:

1. As expected, the relative emphasis of traits in the current TMI reduces when FE and FL are added to the breeding goal, with the most noticeable reductions observed for PY and FY (by 25.2% and 23.2%, respectively) in the scenario including genomic evaluations for FE and FL.
2. When genomics is added as an information source to evaluate FE and FL, their relative emphasis in the index increases from 8.6% and 2.4%, respectively, to 12.7% and 11.8%.

Comparing the long-term (20 year) response to selection of the simulated scenarios, indicates that:

1. Adding FL and FE to the breeding goal results in 0.3 more lactations and an increase of 13.2% in FE (less feed). Genomic evaluations increase the response to selection to a total of 1.3 more lactations and an increase of 21.3% in FE.
2. The response to selection for FY, PY, FC, and PC reduce on average by 19.6% when FL and FE are added to the breeding goal and genomically evaluated.
3. Based on a simulation for the data provided, the current breeding program obtains undesired responses to selection for $LSCS$, TA, UD, and TP.
4. These undesired responses are reduced for TA, UD, and TP in the scenario including genomic evaluations for FE and FL. However, for $LSCS$ the undesired response to selection increases when FE and FL are added to the breeding program.
5. Compared to the current breeding program, the response to selection for MY increases by 29.4% when FL and FE are added to the breeding goal and genomically evaluated.

Detailed outcomes are provided in Appendix IIII – Sensitivity outcomes.

Conclusion – Alpine and Saanen goats

Adding resilience and efficiency traits to the Alpine and Saanen goat breeding programmes can resultin a long-term (20 year) improvement in these traits, depending on several factors: population genetic parameters, the weight given to these traits in the index, and the availability of genomic informationto inform breeding values.

When a 10% relative emphasis is given to RE traits in the Total Merit Index (TMI), Alpine goats are predicted to show a 2 day increase in lifespan and a 0.07 UFL unit increase in feed efficiency after 20 years, relative to the current TMI. Saanen goats are predicted to show a 188 day increase in lifespan and a 0.05 UFL unit increase in feed efficiency after 20 years, relative to the current TMI. Including REtraits reduces the rate of progress in other traits, with most noticeable reductions for protein yield and fat yield.

Genomic evaluations increase RE trait responses significantly. Assuming a genomic accuracy of 50%, the Alpine goat breeding program can achieve a 174 day increase in lifespan and a 0.09 UFL unit increase in feed efficiency after 20 years. The Saanen goat breeding program can achieve a 449 day increase in lifespan and a 0.08 UFL unit increase in feed efficiency.

Genetic parameters like heritability, repeatability, genetic and phenotypic correlations affect responses to selection. The Alpine and Saanen goats breeding programmes are currently experimenting with adding RE traits, so these parameters are currently estimated from preliminary data. In future, once more data is available, a more complete picture of the implications of adding REtraits would be available. It would also help refine the desired gain weight to apply to RE traits in the TMI.

The current TMI uses desired gain weights. Using economic values in the index, instead of desired gains weights, would deliver real world value to breeders and commercial farmers. These economic values result in an index that represents the profit, or cost, to the farmer. This makes index scores easier to interpret and understand. The underlying framework used to calculate economic weights can also be used to calculate CO2e coefficients per trait, and therefore allow the implications of genetic gain on GHG emissions from enteric methane to be estimated.

Conclusion – Lacaune sheep

Adding Functional Longevity (FL) and Feed Efficiency (FE) to the breeding program results in a significant long-term (20 year) response to selection for both traits, with 0.3 more lactations and an increase of 13.2% in feed efficiency (13.2% less feed). Genomic evaluations increase these responses to 1.3 lactations and 21.3% in feed efficiency.

As expected, when adding more traits to the index, the relative trait emphasis and response to selection in other traits in the index reduces, with most noticeable reductions for protein yield (PY) and fat yield (FY).

The sensitivity analyses showed that outcomes were most sensitive to changes in the accuracy of genomic breeding values for FL and FE. The emphasis of FL and FE in the index increased significantly, from 11.8% to 17.7%, and 12.7% to 15.3%, respectively, when the accuracy of genomic breeding values increased from 50% to 70%. The emphasis on FL and FE in the index decreased significantly, by similar proportions, when the accuracy of genomic breeding values decreased from 50% to 30%. Adjusting these accuracies resulted in, on average, a 5.2% change in response to selection for PY and FY. For most sensitivity analyses, only slight differences were observed in responses to selection and emphasis of other traits in the breeding program.

Genetic parameters like heritability, and genetic and phenotypic correlations affect responses to selection. Considering that for FE a genetic and phenotypic correlation was only estimated with MY, estimation of the correlations between FE and other index traits and re-running of simulations would provide a more complete picture of the implications of adding FE and of the sensitivity of responses to the genetic relationship between FE and other traits.

Simulation outcomes from the current breeding program (base scenario) show that $LSCS$, TA, UD and TP have an unwanted long-term (20 year) response to selection; increasing $LSCS$ and TA, whilst decreasing UD and TP. By changing the FL and FE weights in the index, these unwanted responses to selection can reduce. Revisiting the weights applied to the traits in the TMI, including when traits are added to the breeding goal and carefully setting index weights for these additional traits (like FL and FE), would inform a balanced approach to selection. Furthermore, the use of economic values in the index instead of weights based on desired responses, would deliver real world value of breeders and commercial farmers. These economic values result in an index that represents the profit (or loss) to the farmer and are based on price and cost data and other sources of information.

4. Deviations or delays

No deviations. Delayed to month 58: The deliverable was submitted to the coordinator on time (M56), but was submitted to the EU portal with a 6-week delay to ensure revision using the body of work reported in RP4.

5. Acknowledgements

Virginie Clement (INRAE), for genetic parameters and other breeding program data. Jean-Michel Astruc (AINRAE), for genetic parameters and other breeding program data.

6. References

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Zhang, X., & Amer, P. (2021). A new selection index percent emphasis method using subindex weights and genetic evaluation accuracy. *Journal of Dairy Science, 104*(5), 5827-5842.

7. Appendix 1 – Alpine and Saanen goats

Alpine goats genetic parameters: Heritability (h^2), phenotypic variance (σ_p^2), repeatability (r), and trait units are provided in the table below for the recorded traits. The correlation matrix presents genetic correlations above diagonal and phenotypic correlations below diagonal.

Table 9: Genetic parameters used in the Alpine goat simulations.

TRAIT NAME	MY	PY	FY	PC	FC	LSCS	UP	FP	RA	FU	TO	FL	FE	FL-G	FE-G
Trait units	kg	kg	kg	g/kg	g/kg	score	point	point	point	point	point	days	UFL	days	UFL
h^2	0.34	0.36	0.37	0.57	0.58	0.2	0.37	0.31	0.27	0.32	0.32	0.082	0.184	0.99	0.99
σ_p^2	17689	14.44	24.900	5.153	16.322	1.513	1.742	0.737	1.323	0.884	0.656	380689	0.0190	380689	0.0190
r	0.5	0.5	0.5	0.7	0.7	0.45	0	0	0	0	0	0	0.1	1	1

Correlation matrix

	MY	PY	FY	PC	FC	LSCS	UP	FP	RA	FU	TO	FL	FE	FL-G	FE-G
MY	1	0.89	0.77	-0.28	-0.18	0	-0.23	-0.43	-0.17	0.07	-0.24	0.28	0	0	0
PY	0.993	1	0.86	0.19	0.11	-0.04	-0.24	-0.4	-0.18	0.06	-0.27	0.14	0	0	0
FY	0.849	0.884	1	0.14	0.61	-0.13	-0.24	-0.27	-0.17	0.08	-0.24	0.13	0	0	0
PC	-0.384	-0.038	-0.106	1	0.49	-0.06	0.06	0.15	0.04	-0.01	0	0.02	0	0	0
FC	-0.159	0.014	0.377	0.492	1	-0.18	0.04	0.14	-0.01	0.03	-0.06	0.1	0	0	0
LSCS	0	0	0	0	0	1	0.11	-0.24	-0.1	-0.16	0.13	-0.35	0	0	0
UP	0	0	0	0	0	0	1	0.14	0.19	-0.03	0.25	0.02	0	0	0
FP	0	0	0	0	0	0	0	1	0.71	0.55	-0.02	0.26	0	0	0
RA	0	0	0	0	0	0	0	0	1	0.48	0.37	0.17	0	0	0
FU	0	0	0	0	0	0	0	0	0	1	0.07	0.13	0	0	0
TO	0	0	0	0	0	0	0	0	0	0	1	0.08	0	0	0
FL	0.14	0	0	0	0	-0.15	0	0	0	0	0	1	0	0.5	0
FE	0.06	0	0	0	0.08	0	0	0	0	0	0	0	1	0	0.5

FL-G	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
FE-G	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1

Saanen goats genetic parametersHeritability (h^2), phenotypic variance (σ_p^2), repeatability (r), and trait units are provided in the table below for the recorded traits. The correlation matrix presents genetic correlations above diagonal and phenotypic correlations below diagonal.

Table 10: Genetic parameters used in the Saanen goat simulations.

TRAIT NAME	MY	PY	FY	PC	FC	LSCS	UP	FP	RA	FU	TO	FL	FE	FL-G	FE-G
Trait units	kg	kg	kg	g/kg	g/kg	score	point	point	point	point	point	days	UFL	days	UFL
h^2	0.32	0.34	0.4	0.5	0.6	0.24	0.25	0.35	0.29	0.29	0.29	0.072	0.201	0.99	0.99
σ_p^2	20736	15.682	25.806	3.764	14.669	1.21	1.488	0.922	1.850	1.124	0.608	35760	0.0159	357604	0.0159
r	0.5	0.5	0.5	0.7	0.7	0.45	0	0	0	0	0	0	0.1	1	1

Correlation matrix

	MY	PY	FY	PC	FC	LSCS	UP	FP	RA	FU	TO	FL	FE	FL-G	FE-G
MY	1	0.92	0.76	-0.29	-0.1	0.12	-0.3	-0.55	-0.31	0	-0.17	0.16	0	0	0
PY	0.923	1	0.83	0.1	0.1	0.06	-0.09	-0.22	-0.02	-0.03	-0.04	0.02	0	0	0
FY	0.764	0.831	1	0.08	0.61	-0.02	-0.1	-0.21	-0.05	-0.04	-0.05	-0.06	0	0	0
PC	-0.288	0.099	0.079	1	0.51	-0.13	0.12	0.14	0.07	0.1	0.01	0.01	0	0	0
FC	-0.099	0.102	0.614	0.512	1	-0.2	0	0.04	-0.02	0.02	-0.03	0.03	0	0	0
LSCS	0	0	0	0	0	1	-0.11	-0.19	-0.1	-0.01	0.06	-0.29	0	0	0
UP	0	0	0	0	0	0	1	0.09	0.19	-0.17	0.5	-0.03	0	0	0
FP	0	0	0	0	0	0	0	1	0.74	0.53	0.19	0.29	0	0	0
RA	0	0	0	0	0	0	0	0	1	0.49	0.38	0.29	0	0	0
FU	0	0	0	0	0	0	0	0	0	1	-0.05	0.18	0	0	0
TO	0	0	0	0	0	0	0	0	0	0	1	0.04	0	0	0
FL	0	0	0	0	0	0	0	0	0	0	0	1	0	0.5	0
FE	-0.07	0	0	0.05	-0.06	0	0	0	0	0	0	0	1	0	0.5

FL-G	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
FE-G	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1

Information sources

The number of information sources are based on the following assumptions (Clement, V., *pers. Comm*, 2023):

- Phenotypes are measured on the buck's female relatives for all traits, except genomic traits. Therefore, the breeding values for these traits the buck are inferred from its female relatives. Genomic traits are the only traits measured on the buck itself.

- Sexual maturity is reached at 7-8 months for both males and females and therefore, the age at first mating is 7-8 months. Does are 11-12 months at first parity. The buck is 2.5 years when its daughters reach their 1st parity and are first tested for production, type and feed efficiency traits. The buck is 7 years when its daughters reach their 6th parity and are first tested for functional longevity traits.

- Here we also assume that the first mating for a young buck produces 30 daughters. The simulation only includes these 30 daughters, not daughters from any subsequent matings.

- The average litter size is 2, so a buck has 1 full sibling, with a 50% chance that sibling is female. This does not provide much additional phenotype data, so this full-sibling was ignored in this simulation.

- A buck also has approximately 28 (paternal) half-sisters, which provides much more information, so this relative group was included in the analysis.

- The buck's mother is assumed to have a minimum of 1 year of phenotype data.

- The buck may or may not have full aunts, so this relative group was ignored. But the buck has approximately 28 (maternal) half-aunts (mother's half-sisters), so this relative group was included in the simulation. These maternal half-aunts are assumed to have a minimum of 1 year of phenotype data.

These assumptions are summarised in Table 7. The same set of assumptions were used for both Saanen and Alpine goats.

Table 11: Assumptions about information sources used in the Alpine and Saanen goat simulations.

TRAIT NAME	**RELATIVE GROUP**	**YOUNG RAM**		**EMERGING SIRE**		**PROVEN SIRE**	
		Relatives	Records	Relatives	Records	Relatives	Records
Milk Yield	Mother	1	1	1	3	1	8
	Maternal half-aunts	28	1	28	3	28	8
	Paternal half-sisters	28	0	28	2	28	7
	Progeny	0	0	30	1	30	6
Protein Yield	Mother	1	1	1	3	1	8
	Maternal half-aunts	28	1	28	3	28	8
	Paternal half-sisters	28	0	28	2	28	7
	Progeny	0	0	30	1	30	6
Fat Yield	Mother	1	1	1	3	1	8
	Maternal half-aunts	28	1	28	3	28	8
	Paternal half-sisters	28	0	28	2	28	7
	Progeny	0	0	30	1	30	6
Protein Content	Mother	1	1	1	3	1	8
	Maternal half-aunts	28	1	28	3	28	8
	Paternal half-sisters	28	0	28	2	28	7
	Progeny	0	0	30	1	30	6
Fat Content	Mother	1	1	1	3	1	8
	Maternal half-aunts	28	1	28	3	28	8
	Paternal half-sisters	28	0	28	2	28	7
	Progeny	0	0	30	1	30	6
Somatic Cell Score	Mother	1	1	1	3	1	3
	Maternal half-aunts	28	1	28	3	28	3
	Paternal half-sisters	28	0	28	2	28	3
	Progeny	0	0	30	1	30	3
Udder Profile	Mother	1	1	1	1	1	1
	Maternal half-aunts	28	1	28	1	28	1
	Paternal half-sisters	28	0	28	1	28	1
	Progeny	0	0	30	1	30	1
Floor Position	Mother	1	1	1	1	1	1
	Maternal half-aunts	28	1	28	1	28	1
	Paternal half-sisters	28	0	28	1	28	1
	Progeny	0	0	30	1	30	1
Rear Attachment	Mother	1	1	1	1	1	1
	Maternal half-aunts	28	1	28	1	28	1
	Paternal half-sisters	28	0	28	1	28	1
	Progeny	0	0	30	1	30	1

Fore Udder	Mother	1	1	1	1	1	1
	Maternal half-aunts	28	1	28	1	28	1
	Paternal half-sisters	28	0	28	1	28	1
	Progeny	0	0	30	1	30	1
Teat Orientation	Mother	1	1	1	1	1	1
	Maternal half-aunts	28	1	28	1	28	1
	Paternal half-sisters	28	0	28	1	28	1
	Progeny	0	0	30	1	30	1
Functional longevity*	Mother	1	0	1	0	1	1
	Maternal half-aunts	28	0	28	0	28	1
	Paternal half-sisters	28	0	28	0	28	1
	Progeny	0	0	30	0	30	1
Feed efficiency*	Mother	1	4	1	12	1	32
	Maternal half-aunts	28	4	28	12	28	32
	Paternal half-sisters	28	0	28	8	28	28
	Progeny	0	0	30	4	30	24
FL - Genomic[†]	Candidate	1	1	1	1	1	1
FE - Genomic[†]	Candidate	1	1	1	1	1	1

** Functional longevity and feed efficiency only included in Base + RE scenarios*

[†] Genomic functional longevity and genomic feed efficiency only included in Base + RE + Genomics scenarios

Relative groups

Table 8 shows the assumed relationships between the different relative groups used in the simulation. The same set of assumptions were used for both Saanen and Alpine goats.

Table 12: Relative groups and their relationships used in the Alpine and Saanen goat simulations.

GROUP:	**RELATIONSHIPS**					
			BETWEEN GROUPS			
	WITHIN GROUP	WITH CANDIDATE	Mother	Maternal half-aunts	Paternal half-sisters	Progeny
Mother	1	0.5	1	0.25	0	0.25
Maternal half-aunts	0.25	0.5	0.25	0.25	0	0.0625
Paternal half-sisters	0.25	0.125	0	0	0.25	0.125
Progeny	0.25	0.25	0.25	0.0625	0.125	0.25
Candidate	1	0.5	0.5	0.125	0.25	0.5

Selection proportions

Table 9 shows the assumed selection proportions used in the simulation. The same set of assumptions were used for both Saanen and Alpine goats.

Table 13: Selection proportions by buck lifecycle used in the Alpine and Saanen goat simulations.

SELECTION PROPORTIONS:	YOUNG	EMERGING	PROVEN
Age	1	2	7
Selection proportion (at each stage)	0.70	0.30	0.70
Selection proportion (of initial population)	0.70	0.21	0.15

8. Appendix II – Lacaune sheep

Genetic parameters and trait units : Heritability (h^2), phenotypic variance (σ_p^2), repeatability (r), and trait units are provided in Table 14 for the recorded traits. The correlation matrix presents genetic correlations above diagonal and phenotypic correlations below diagonal.

Table 14: Genetic parameters and trait units.

TRAIT NAME	MY	FY	PY	FC	PC	LSCS	TA	UC	UD	TP	FL	FE
Trait units	l	kg	kg	g/l	g/l	score	point	point	point	point	days	%
h^2	0.266	0.258	0.286	0.404	0.581	0.124	0.375	0.326	0.233	0.25	0.15	0.12
σ_p^2	4,044.96	18.0625	9	59.7529	14.5924	1.803649	0.9409	1.203409	0.273529	0.600625	266,256	396.01
r	0.5	0.5	0.5	0.6	0.7	0.3	0	0	0	0	0	0.4

Correlation matrix

	MY	FY	PY	FC	PC	LSCS	TA	UC	UD	TP	FL	FE
MY		0.07	0.83	-0.37	-0.46	0.19	0.04	0.14	-0.48	-0.08	-0.18	0.80
FY	0.82		0.79	0.30	-0.05	0.26	0.12	0	-0.50	-0.09	0	0
PY	0.93	0.82		-0.14	0.06	0.21	0.08	0.06	-0.51	-0.08	0	0
FC	-0.23	0.41	-0.04		0.61	0.05	0.06	-0.11	0.05	0.01	0.06	0
PC	-0.35	-0.02	0.09	0.45		-0.03	0	-0.01	0.09	0.03	0.03	0
LSCS	-0.17	-0.07	-0.07	0.08	0.13		0.05	-0.14	-0.30	-0.06	0.17	0
TA	0.02	0.06	0.04	0.04	0	0.05		-0.30	-0.27	-0.31	-0.06	0
US	0.13	0.07	0.10	-0.05	-0.04	-0.09	-0.21		0.18	0.09	0.03	0
UD	-0.33	-0.28	-0.31	0.02	0.04	-0.08	-0.13	0.06		0.24	0.14	0
TP	-0.05	-0.04	-0.04	0	0.01	-0.02	-0.16	0.05	0.11		0	0
FL	0	0	0	0	0	0	0	0	0	0		0
FE	0.57	0	0	0	0	0	0	0	0	0	0	

Relative groups and assumptions on available information sources

Relative groups

Relationships between groups needed to be modelled and are provided in Table 15 below.

Table 15: Relationships between relatives (groups)

Groups	Group_name	Within_group_rel	Rel_with_cand	G1	G2	G3	G4	G5
G1	Mother	1	0.5	1	0.25	0.25	0.5	0.5
G2	Progeny with records	0.25	0.5	0.25	0.25	0.0625	0.125	0.5
G3	Aunts	0.25	0.125	0.25	0.0625	0.25	0.125	0.125
G4	Maternal half sibs	0.25	0.25	0.5	0.125	0.125	0.25	0.25
G5	Candidate	1	1	0.5	0.5	0.125	0.25	1

Information sources

The available information sources (Table 16) (were generated from information provided (pers. Comm. Jean-Michel Astruc) about the breeding program, were:

- A candidate (ram) has 1 mother;
- The mother already has had one litter, so phenotypes from the mother available for young rams;
- Average litter size of 2 (one male, one female), with full-sib of the male selection candidate therefore being female. As this full-sib will hardly contribute to the candidate's EBV (reliability), this information source was disregarded;
- A candidate (ram) has 29 aunts (mother's sister), as 30 daughters are born from 1 ram each year;
- 4 years of breeding for rams;
- MY is measured during first 3 years of production;
- FY, PY, FC, PC, and LSCS are measured during first 2 years of production;
- TA, UC, UD, and TP are only measured once, and FE, and FL are assumed to be measured only once.

The number of records on other information sources (except self) increase the older the ram gets, the more records become available on female relatives. Available information sources for the 3 candidate groups were:

- Young rams do not have progeny records;
- Emerging sires have had their first year of breeding, resulting on average in 30 daughters with records for each sire;
- Proven sires have been breeding for 4 years, resulting on average in 120 daughters (4 years x 30 daughters per year).

Table 16: Information sources on candidate types, across traits.

		CANDIDATES number of individuals x number of repeated records by individual e.g., for an emerging sire 30 progeny are available with 1 record on milk yield each		
TRAIT NAME	Relative group	Young ram	Emerging sire	Proven sire
Milk yield	Mother	1x1	1x2	1x3
Milk yield	Progeny	0	30x1	120x3
Milk yield	Aunts (mother’s sisters)	29x2	29x2	29x3
Milk yield	Maternal half-sibs	1x1	1x2	3x3
Fat yield	Mother	1x1	1x2	1x2
Fat yield	Progeny	0	30x1	120x2
Fat yield	Aunts (mother’s sisters)	29x2	29x2	29x2
Fat yield	Maternal half-sibs	1x1	1x2	3x2
Protein yield	Mother	1x1	1x2	1x2
Protein yield	Progeny	0	30x1	120x2
Protein yield	Aunts (mother’s sisters)	29x2	29x2	29x2
Protein yield	Maternal half-sibs	1x1	1x2	3x2
Fat content	Mother	1x1	1x2	1x2
Fat content	Progeny	0	30x1	120x2
Fat content	Aunts (mother’s sisters)	29x2	29x2	29x2
Fat content	Maternal half-sibs	1x1	1x2	3x2
Protein content	Mother	1x1	1x2	1x2
Protein content	Progeny	0	30x1	120x2
Protein content	Aunts (mother’s sisters)	29x2	29x2	29x2
Protein content	Maternal half-sibs	1x1	1x2	3x2
Somatic cell score	Mother	1x1	1x2	1x2
Somatic cell score	Progeny	0	30x1	120x2
Somatic cell score	Aunts (mother’s sisters)	29x2	29x2	29x2
Somatic cell score	Maternal half-sibs	1x1	1x2	3x2
Teat angle	Mother	1x1	1x1	1x1
Teat angle	Progeny	0	30x1	120x1
Teat angle	Aunts (mother’s sisters)	29x1	29x1	29x1
Teat angle	Maternal half-sibs	1x1	1x1	3x1
Udder cleft	Mother	1x1	1x1	1x1
Udder cleft	Progeny	0	30x1	120x1
Udder cleft	Aunts (mother’s sisters)	29x1	29x1	29x1
Udder cleft	Maternal half-sibs	1x1	1x1	3x1
Udder depth	Mother	1x1	1x1	1x1
Udder depth	Progeny	0	30x1	120x1
Udder depth	Aunts (mother’s sisters)	29x1	29x1	29x1
Udder depth	Maternal half-sibs	1x1	1x1	3x1

Teat position	Mother	1x1	1x1	1x1
Teat position	Progeny	0	30x1	120x1
Teat position	Aunts (mother's sisters)	29x1	29x1	29x1
Teat position	Maternal half-sibs	1x1	1x1	3x1
Functional longevity	Mother	0	0	1x1
Functional longevity	Progeny	0	0	30x1
Functional longevity	Aunts (mother's sisters)	0	0	29x1
Functional longevity	Maternal half-sibs	0	0	1x1
Functional longevity	Candidate*	1x1	1x1	1x1
Feed efficiency	Mother	1x1	1x1	1x1
Feed efficiency	Progeny	0	30x1	120x1
Feed efficiency	Aunts (mother's sisters)	29x1	29x1	29x1
Feed efficiency	Maternal half-sibs	1x1	1x1	3x1
Feed efficiency	Candidate*	1x1	1x1	1x1

*Based on genotypes.

9. Appendix III – Percent emphasis on index traits – Lacuane

The relative weights of traits in the TMI and of FL and FE when added to the index, was calculated using desired gains weights, where the percentage weight was calculated by dividing the trait weight by the sum of the weights across all traits, to obtain the relative weight.

The weights applied to FL and FE were set through a trial-and-error approach, finding weights that would produce a meaningful response to selection, when considering the trait architectures.

The relativity between trait weightings, and particularly between scenarios, helps to understand what the addition of the resilience and efficiency traits does to the emphasis on other traits in the index, prior to running any of the simulations.

However, it is important to note that the TMI is not an economic index. Weights are set on the principle of desired gains using units that are different across traits (e.g., kg, days, and %) with significant differences in standard deviations too. For an economic index, all trait weights would have the same unit, being monetary (e.g., € or $), that would allow for a much more informative comparison of relative trait weights and emphasis.

Nonetheless, the relative percentage weights of traits in the TMI reduces when FL and FE are added to the index. Across the different scenarios, the relative emphasis of traits in the TMI is reduced by 1-2%, depending on the weight assigned to FL and FE (Table 17).

Table 17: Relative weightings of traits based on the desired gains weight in the index.

TRAIT	UNIT	WEIGHTS	RELATIVE EMPHASIS	
			BASE SCENARIO	INDEX INCLUDES R&E TRAITS
Current index traits				
FY	kg	0.5	20.2%	19.0-19.3%
PY	kg	0.925	37.3%	35.1-35.8%
FC	g/l	1/25	1.6%	1.5%
PC	g/l	1/64	0.6%	0.6%
LSCS	score	-0.5	20.2%	19.0-19.3%
TA	point	0.5 x -0.25 = -0.125	5.0%	4.7-4.8%
UD	point	0.5 x 0.5 = 0.25	10.1%	9.5-9.7%
TP	point	0.5 x 0.25 = 0.125	5.0%	4.7-4.8%
Resilience and efficiency (R&E) traits				
FL	days	0.004-0.006	-	0.2%
FE	%	0.10-0.15	-	3.9-5.7%

10. Appendix IIII – Sensitivity outcomes – Lacaune

Changing R&E trait weights

Reducing or increasing the weights on both FL (being X) and FE (being Y) by 20% in the index affected the relative emphasis of the other traits in the index to a small degree. Most noticeable changes are again observed in PY and FY, with a 4.7% (from 35.0% to 33.4%) and 4.5% reduction in emphasis, respectively, when weights on FL and FE were increased by 20%. Reducing the weights of FL and FE by 20% resulted in an increase in emphasis of 4.3%and 4.0% for PY and FY, respectively.

The emphasis of FL and FE in the index increased 42.5% (from 2.4% to 3.4%) and 35.0% (from 8.6% to 11.7%), respectively, when their weights (X and Y) were increased by 20%. Similarly, the emphasis of FL and FE in the index decreased by 37.3% and 31.7%, respectively, when their weights were decreased by 20%.

Table 18: Relative goal trait emphasis, based on response, with changes to R&E trait weights.

	RELATIVE TRAIT EMPHASIS IN THE INDEX		
TRAITS* (UNIT)	BASE + R&E	BASE + R&E +20% WEIGHT	BASE + R&E -20% WEIGHT
$FY\ (kg)$	35.0%	33.4%	36.4%
$PY\ (kg)$	49.1%	46.8%	51.2%
$FC\ (g/l)$	1.0%	1.0%	1.0%
$PC\ (g/l)$	0.2%	0.2%	0.2%
$LSCS\ (score)$	2.4%	2.4%	2.5%
$TA\ (point)$	0.1%	0.1%	0.2%
$UD\ (point)$	1.1%	1.0%	1.1%
$TP\ (point)$	0.1%	0.1%	0.1%
$FL\ (lactation)$	2.4%	3.4%	1.5%
$FE\ (\%)$	8.6%	11.7%	5.9%

*FY = fat yield, PY = protein yield, FC = fat content, PC = protein content, LSCS = somatic cell score, T = teat angle, UD = udder depth, TP = teat position, FE = feed efficiency, and FL = functional longevity.

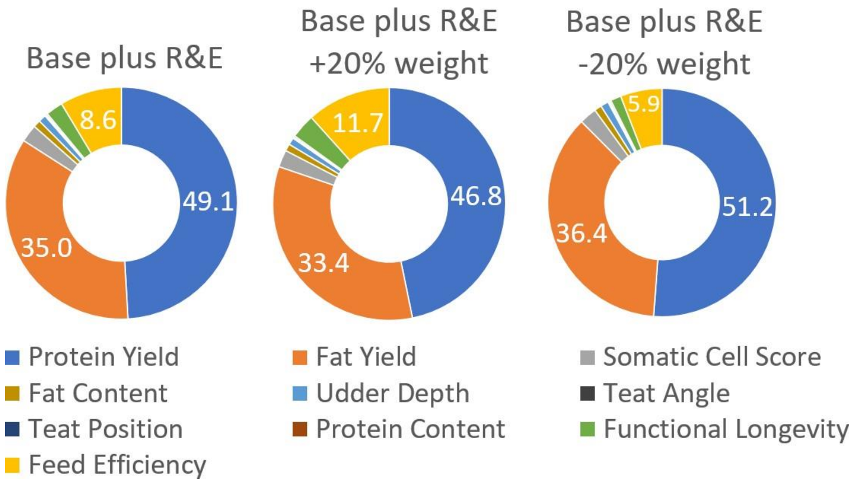
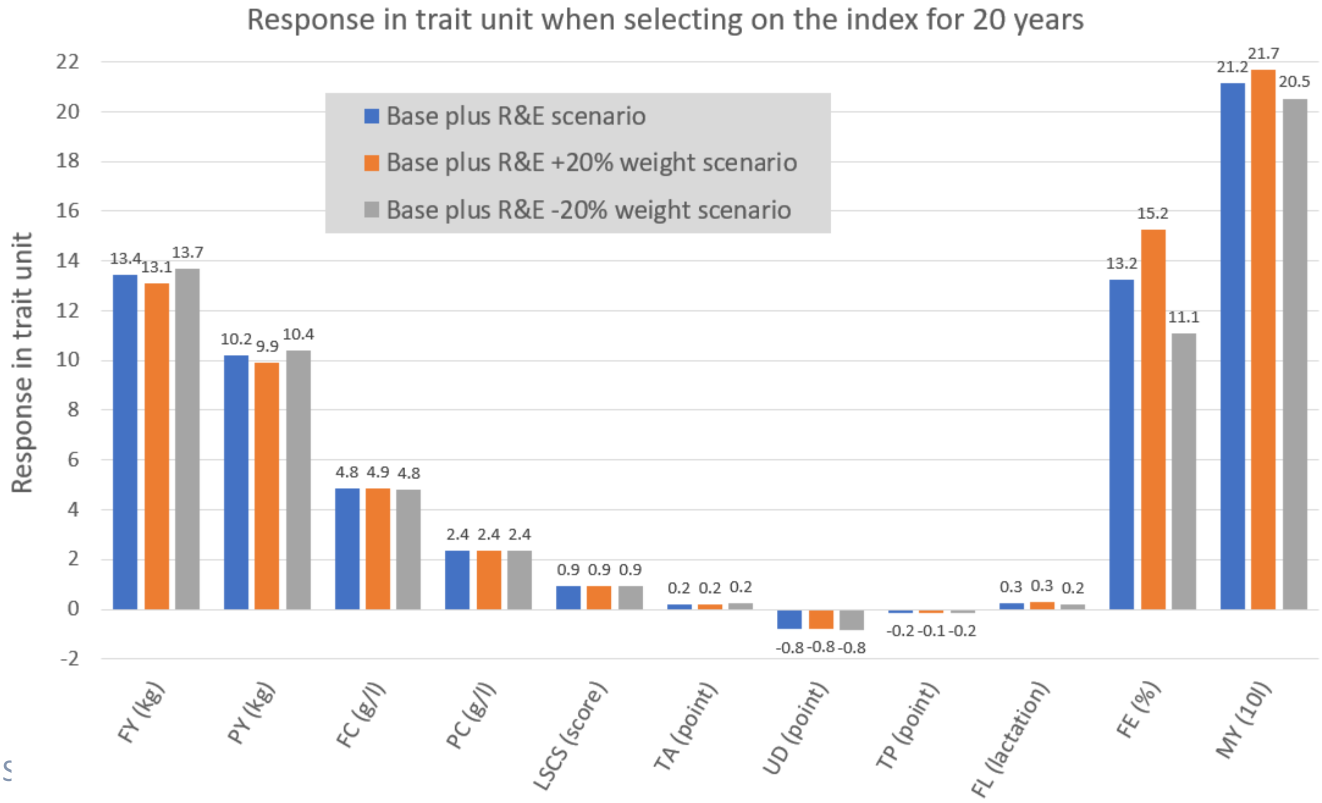


Figure 23: Relative goal trait emphasis, based on response, with changes to R&E trait weights.

The long-term responses to selection (
Figure 24) for FL and FE are most affected when their weights in the index are changed by 20%. The response to selection of FL and FE increases by 21.4% (from 13.2% to 15.2%) and 15.0% (from 0.25 to 0.30 lactations), respectively, when their weights are increased by 20%. Similarly, with a 20% reduction in weights, a 23.1% reduction in response to selection is observed for FL and a 16.2% reduction for FE. Response to selection in all other traits remains near the same, with observed changes ranging from 0% to 2.6%.



MY = milk yield; despite not being a profit trait (milk yield is not included in the index), response to selection is reported as the only available genetic correlation for FE was between MY and FE.

Figure 24: Long-term response to selection (trait change after 20 years) for index traits and milk yield, across scenarios with higher or lower emphasis (+/-20%) on R&E traits.

Changing focus on FL or FE

When changing the focus in the index to more of either FL or FE, (increasing either X or Y by 20%) their relative trait emphasis increases by 34.8% (from 2.4% to 3.2%) and 33.0% (from 8.6% to 11.5%), respectively (Table 19 and Figure 25). Small differences in relative trait emphasis on other traits in the index are observed when the weight of either FL or FE is increased by 20%.

Table 19: Relative goal trait emphasis, based on response, with change in fucus of R&E traits.

	RELATIVE TRAIT EMPHASIS IN THE INDEX		
TRAITS* (UNIT)	BASE + R&E	BASE + R&E FL FOCUS	BASE + R&E FE FOCUS
$FY\ (kg)$	35.0%	34.6%	33.8%
$PY\ (kg)$	49.1%	48.5%	47.4%
$FC\ (g/l)$	1.0%	1.0%	1.0%
$PC\ (g/l)$	0.2%	0.2%	0.2%
$LSCS\ (score)$	2.4%	2.5%	2.3%
$TA\ (point)$	0.1%	0.1%	0.1%
$UD\ (point)$	1.1%	1.0%	1.0%
$TP\ (point)$	0.1%	0.1%	0.1%
$FL\ (lactation)$	2.4%	3.2%	2.5%
$FE\ (\%)$	8.6%	8.8%	11.5%

*FY = fat yield, PY = protein yield, FC = fat content, PC = protein content, LSCS = somatic cell score, T = teat angle, UD = udder depth, TP = teat position, FE = feed efficiency, and FL = functional longevity.

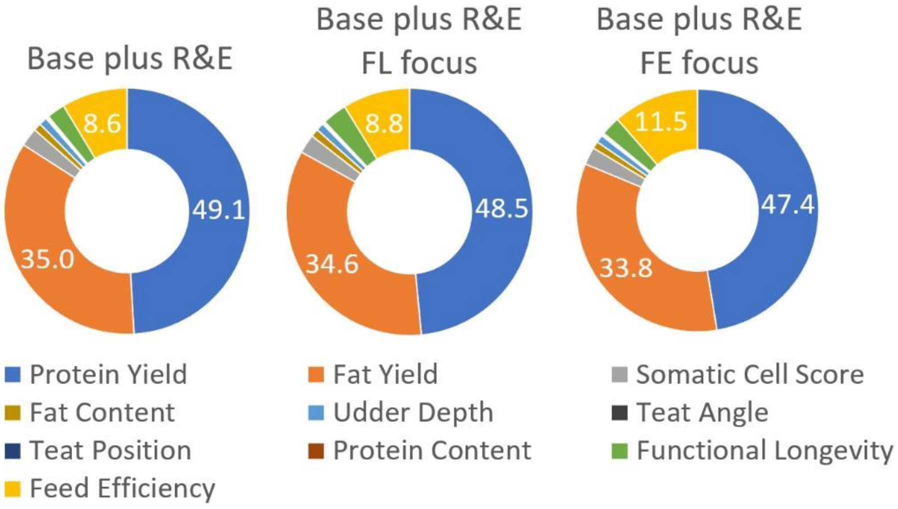


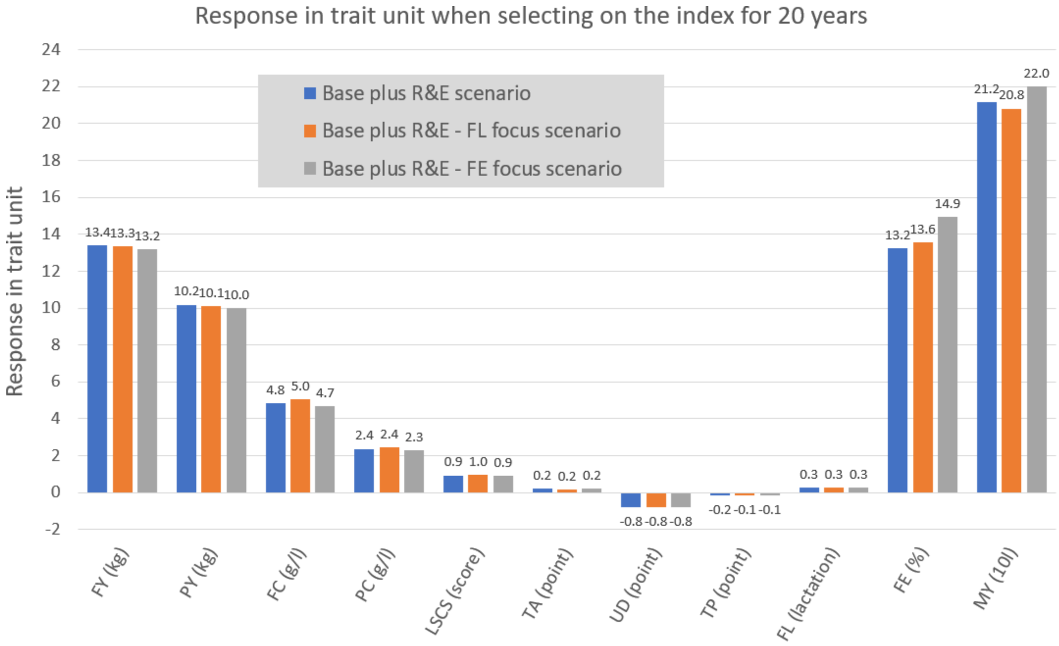
Figure 25: Relative goal trait emphasis, based on response, with change in fucus of R&E traits.

In the long-term, changing the focus on FL in the index (increase its weight by 20%) resulted in an increase in response to selection for FL, but also for FC, PC, and FE (comparing base plus R&E scenario with base plus R&E - FL focus scenario) (Figure 26). When the weight of FE in the index was increased, only an increase in response to selection was observed for FE and FL. This difference is likely caused by the lack of information on genetic correlations between FE and other traits (see

Appendix 1), whereas for FL many genetic correlations with other traits were estimated.

Increasing the weight of FL in the index resulted in a 12.9% increase in response to selection (from 0.25 to 0.28 more lactations). For FE, the response to selection increased by 12.7% (from 13.2% to 14.9%) when its weight in the index was increased by 20%.

Long-term response to selection of other traits in the index did not change much, with either an FL or FE focus. However, of note is the outcomes of changing the focus in the index to either FL or FE, which resulted in a reduction, though small, of unwanted response to selection for TA, UD, and TP, whilst having a similar response to selection impact for the other traits (not visible in the figure below due to rounding).



MY = milk yield; despite not being a profit trait (milk yield is not included in the index), response to selection is reported as the only available genetic correlation for FE was between MY and FE.

Figure 26: Long-term response to selection (trait change after 20 years) for index traits and milk yield, across scenarios with higher or lower emphasis (+/-20%) on FL or FE.

Sensitivity to genetic correlations between MY and R&E traits

Functional longevity

Changing the genetic correlation between MY and FL (-0.18 ± 20%) resulted in almost the same relative change in response to selection and trait in FL (Table 20 and Figure 27). As expected, the response to selection changed for both FL and MY. With an increase in genetic correlation, long-term response to selection for FL and MY decreased from 0.25 to 0.20 lactations, and from 212 to 208 litres, respectively (Figure 28). A change in response to selection is observed for FE as well.

Table 20: Relative goal trait emphasis, based on response, with change in MY-FL genetic correlation.

	RELATIVE TRAIT EMPHASIS IN THE INDEX		
TRAITS* (UNIT)	BASE + R&E	BASE + R&E +20% $r_g\,MY\text{-}FL$	BASE + R&E -20% $r_g\,MY\text{-}FL$
$FY\ (kg)$	35.0%	35.0%	34.9%
$PY\ (kg)$	49.1%	49.2%	49.0%
$FC\ (g/l)$	1.0%	1.0%	1.0%
$PC\ (g/l)$	0.2%	0.2%	0.2%
$LSCS\ (score)$	2.4%	2.5%	2.4%
$TA\ (point)$	0.1%	0.1%	0.1%
$UD\ (point)$	1.1%	1.1%	1.1%
$TP\ (point)$	0.1%	0.1%	0.1%
$FL\ (lactation)$	2.4%	1.9%	2.8%
$FE\ (\%)$	8.6%	8.8%	8.4%

*FY = fat yield, PY = protein yield, FC = fat content, PC = protein content, LSCS = somatic cell score, T = teat angle, UD = udder depth, TP = teat position, FE = feed efficiency, and FL = functional longevity.

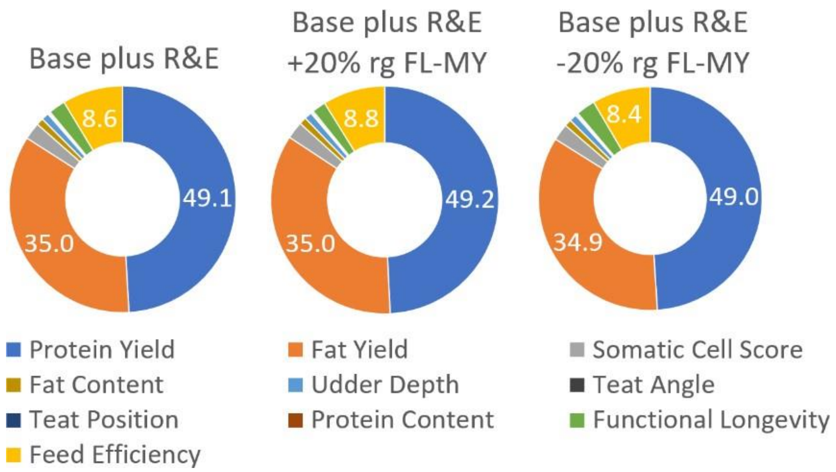
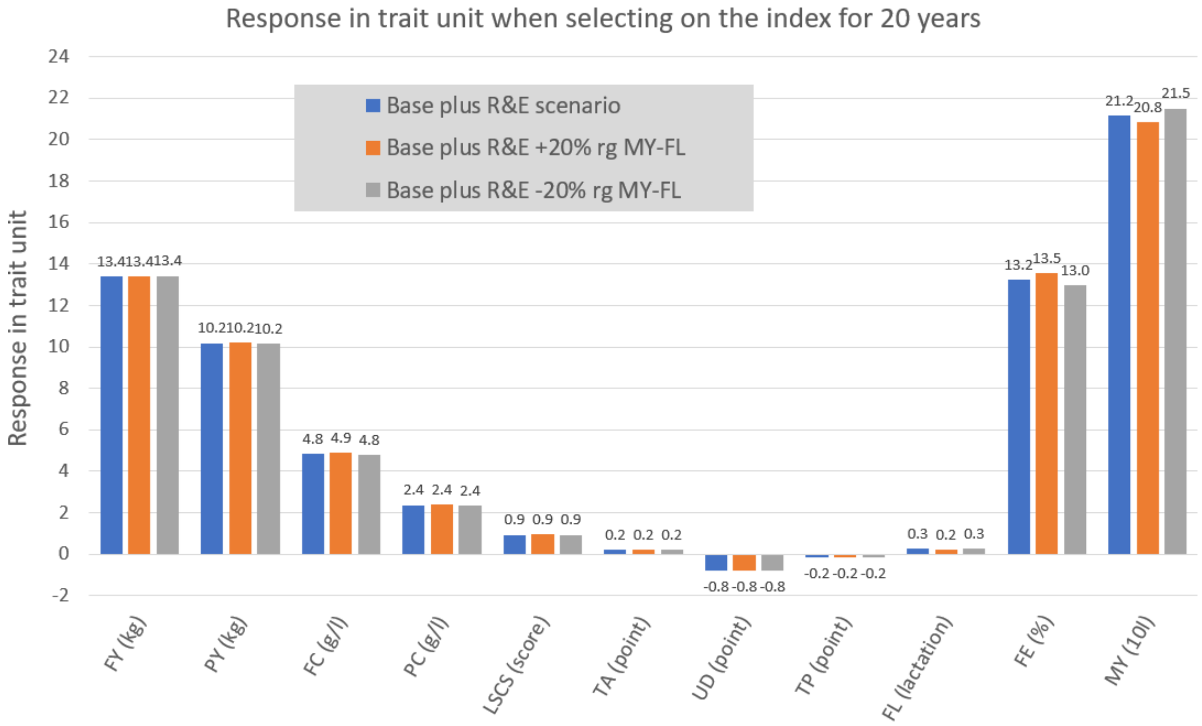


Figure 27: Relative goal trait emphasis, based on response, with change in MY-FL rg.



MY = milk yield; despite not being a profit trait (milk yield is not included in the index), response to selection is reported as the only available genetic correlation for FE was between MY and FE.

Figure 28: Long-term response to selection (trait change after 20 years) for index traits and milk yield, across scenario with higher or lower rg (+/-20%) between MY and FL.

Feed efficiency

Changing the genetic correlation between MY and FE (0.80 ± 20%) resulted in differing responses in FE for +20% compared to -20% change in the genetic correlation (Table 21 and Figure 29). In the long-term, the response to selection changed for both FE and MY, with some correlated responses to selection observed for FL, FC and PC (Figure 30).

Table 21: Relative goal trait emphasis, based on response, with change in MY-FE genetic correlation.

	RELATIVE TRAIT EMPHASIS IN THE INDEX		
TRAITS* (UNIT)	BASE + R&E	BASE + R&E +20% $r_g\,MY$-FE	BASE + R&E -20% $r_g\,MY$-FE
$FY\ (kg)$	35.0%	35.0%	35.1%
$PY\ (kg)$	49.1%	48.9%	49.6%
$FC\ (g/l)$	1.0%	1.0%	1.1%
$PC\ (g/l)$	0.2%	0.2%	0.2%
$LSCS\ (score)$	2.4%	2.4%	2.5%
$TA\ (point)$	0.1%	0.1%	0.1%
$UD\ (point)$	1.1%	1.0%	1.1%
$TP\ (point)$	0.1%	0.1%	0.1%
$FL\ (lactation)$	2.4%	3.1%	1.4%
$FE\ (\%)$	8.6%	8.2%	8.8%

*FY = fat yield, PY = protein yield, FC = fat content, PC = protein content, LSCS = somatic cell score,
T = teat angle, UD = udder depth, TP = teat position, FE = feed efficiency, and FL = functional longevity.

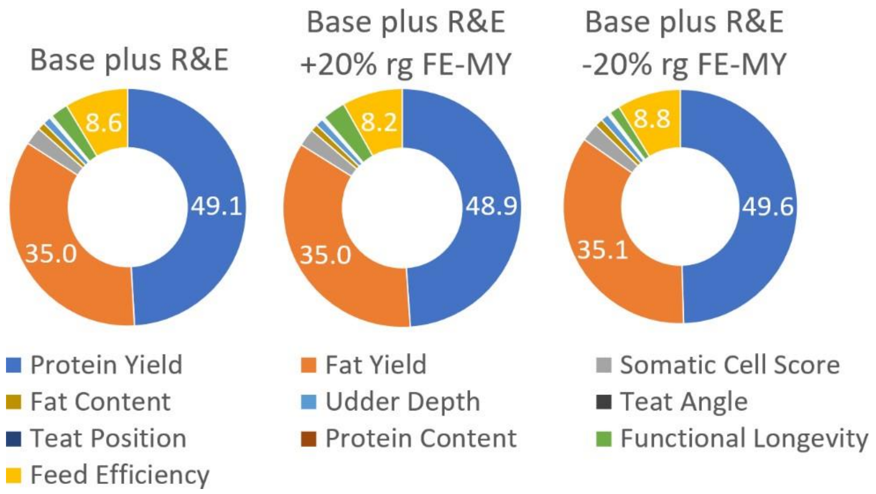
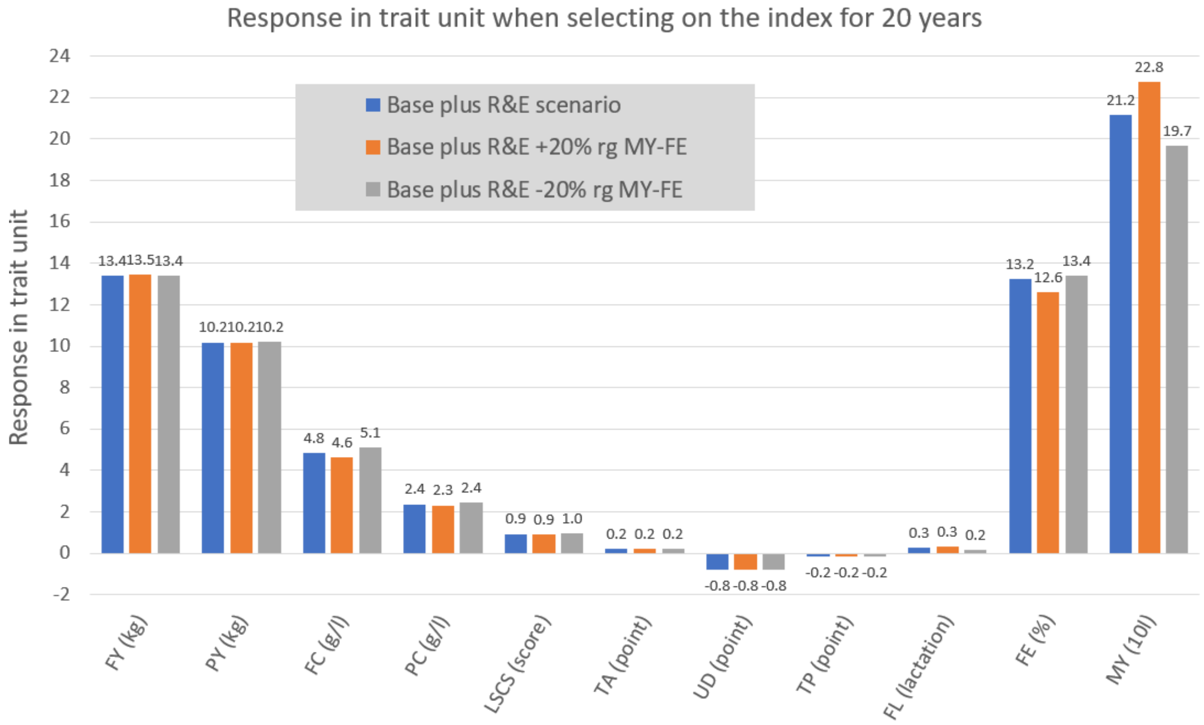


Figure 29: Relative goal trait emphasis, based on response, with change in MY-FL rg.



MY = milk yield; despite not being a profit trait (milk yield is not included in the index), response to selection is reported as the only available genetic correlation for FE was between MY and FE.

Figure 30: Long-term response to selection (trait change after 20 years) for index traits and milk yield, across scenario with higher or lower rg (+/-20%) between MY and FE.

Sensitivity to accuracy of genomic breeding values for R&E traits

Testing the sensitivity of outcomes to the accuracy of genomic breeding values for FL and FE shows that the relative emphasis on other traits in the index reduces when the accuracy of genomic breeding values for FL and FE increases from 50% to 70%, e.g., PY and FY from 41.5% to 36.7%, and 29.5% to 26.1%, respectively. Similar changes are observed, in the opposite direction, when the accuracy of genomic breeding values for FL and FE decreases from 50% to 30%. The emphasis of FL and FE in the index increased significantly, from 11.8% to 17.7%, and 12.7% to 15.3%, respectively, when the accuracy of genomic breeding values increased from 50% to 70%. Similarly, the emphasis of FL and FE in the index decreased significantly when the accuracy of genomic breeding values decreased from 50% to 30%.

Table 22: Relative goal trait emphasis, based on response, with change in accuracy of genomic breeding values for FL and FE.

	RELATIVE TRAIT EMPHASIS IN THE INDEX		
TRAITS* (UNIT)	BASE + R&E + G	BASE + R&E + G 70% ACCURACY	BASE + R&E + G 30% ACCURACY
$FY\ (kg)$	29.5%	26.1%	32.7%
$PY\ (kg)$	41.5%	36.7%	45.9%
$FC\ (g/l)$	0.9%	0.9%	1.0%
$PC\ (g/l)$	0.2%	0.2%	0.2%
$LSCS\ (score)$	2.4%	2.4%	2.4%
$TA\ (point)$	0.1%	0.0%	0.1%
$UD\ (point)$	0.8%	0.7%	1.0%
$TP\ (point)$	0.1%	0.1%	0.1%
$FL\ (lactation)$	11.8%	17.7%	6.4%
$FE\ (\%)$	12.7%	15.3%	10.4%

*FY = fat yield, PY = protein yield, FC = fat content, PC = protein content, LSCS = somatic cell score, T = teat angle, UD = udder depth, TP = teat position, FE = feed efficiency, and FL = functional longevity.

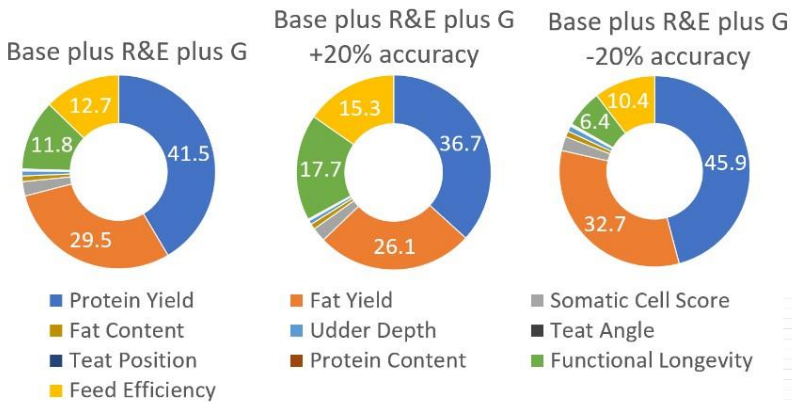
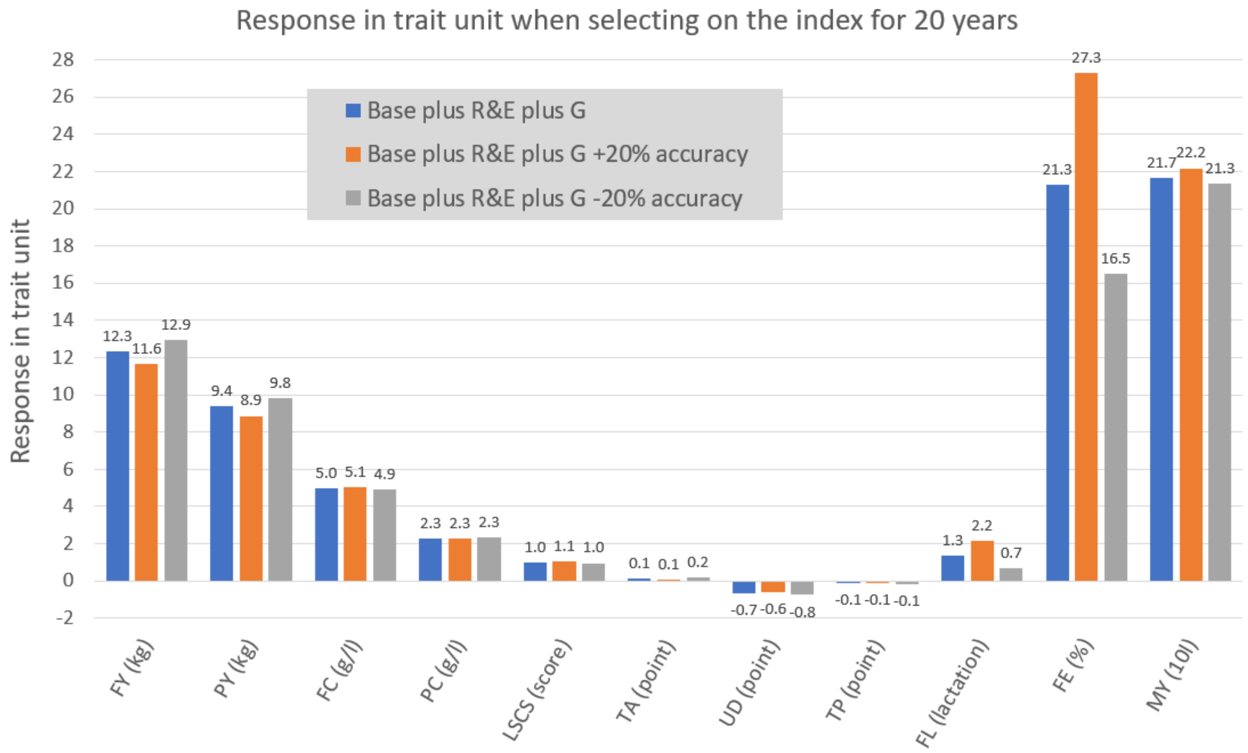


Figure 31: Relative goal trait emphasis, based on response, with change in accuracy of genomic breeding values for FL and

Aligned with the change in emphasis, the long-term response to selection for FL and FE increases by 60.3% (from 1.3 to 2.2 lactations) and 28.3% (from 21.3% to 27.3%), respectively, when the accuracy increases from 50% to 70% (Figure 32). Similarly, when the accuracy reduces to 30%, a 48.7% reduction in response to selection is observed for FL and a 22.5% reduction for FE. An on average 5.2% change in response to selection for FY and PY is observed when the accuracy of genomic breeding values for FL and FE change.



MY = milk yield; despite not being a profit trait (milk yield is not included in the index), response to selection is reported as the only available genetic correlation for FE was between MY and FE.

Figure 32: Long-term response to selection (trait change after 20 years) for index traits and milk yield, across scenario with higher or lower accuracy (+/-20%) of genomic breeding values for FL and FE.