

A vision for improving the UK sheep and beef sectors through breeding over the next 10 years

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Executive summary

The aim of this project was to provide an evidence base that can inform decisions related to the development of a future genetic improvement programme for the UK sheep and beef sector. The scope convenes the tools and systems required to understand the role of genetics in the control of important traits and estimates the associated benefits. All approaches related to genetic modification and gene editing are outside the scope of this project.

A future programme must facilitate a step change in how genetic improvement contributes to major areas of strategic challenge/ opportunity for the UK sheep and beef industries. There is urgent need to focus on the use of national genetic improvement programmes to deliver solutions to climate challenges, while driving sustainable economic growth for the sector.

The objectives of the project were to:

1. Understand and quantify the historic and potential future economic and environmental benefits of genetic improvement in the UK sheep and beef sector, including the definition of metrics to monitor progress,
2. Define the most appropriate industry genetic improvement programme for the UK sheep and beef sector, and
3. Establish the potential of a national phenotype and genotype collection programme (to underpin genetic evaluation) to drive genetic improvement and deliver government and industry sustainability and environmental objectives.

Modelling was used to calculate the economic and environmental impacts from historic rates of genetic gain, and to estimate the potential future economic and environmental impacts of genetic improvement, under a range of scenarios (including potential benefits from increased adoption and inclusion of traits that target reduced environmental impact). Historic economic benefits were reported as a net present value (NPV) over 20 years, based on 5% discount rate. To calculate the annualised value of genetic improvement, the equivalent annual value that has the same NPV if payment is received every year for the next 20 years (applying the same discount rate) was calculated. Future economic benefits were reported as the NPV over 30 years, based on 5% discount rate. Environmental benefits were reported in gross and intensity (per kg of carcase weight) terms.

Potential future options were explored, and the most appropriate option identified, by combining a literature and desk-based evaluation along with targeted stakeholder interviews, to identify the option(s) that maximise(s) the benefits and minimise(s) the obstacles in creating an industry genetic improvement programme for the future.

Finally, a range of scenarios were costed for a national phenotype and genotype collection programme and combined with potential benefits in a cost-benefit analysis.

For sheep, the historic rate of genetic gain will deliver annualised benefits of £14.7m (NPV of £183m) over the next 20 years. In parallel, historic environmental benefits in gross terms for sheep amount to -0.521 kg CO₂e/mated female/year and -6,618 tonnes/all mated females/year. This represents a 0.1%

reduction in gross emissions per year. In emissions intensity terms, historic trends reduce the emissions by -0.04 kg CO₂e/kg product/mated female/year. This represents a 0.23% reduction in emissions intensity per year (Historic economic and environmental impacts – page 27). The scale of potential future economic benefits (NPV over 30 years) ranges from £328.1m to £978.8m, while the scale of improvement in future environmental benefits above *status quo* (based on historic trends) ranges from 69.1% to 249.1% and 34.4% to 180.4% in gross and intensity terms, respectively (Future impact modelling – page 33).

For beef, the historic rate of genetic gain will deliver annualised benefits of £6.8 (NPV of £84m) over the next 20 years. In parallel, historic environmental benefits in gross terms for beef amount to -3.38 kg CO₂e/mated female/year and -5,000 tonnes/all mated females /year. This represents a 0.08% reduction in gross emissions per year. In emissions intensity terms, historic trends reduce the emissions by -0.03 kg CO₂e/kg product/mated female/year. This represents a 0.13% reduction in emissions intensity per year (Historic economic and environmental impacts – page 27). The scale of future economic benefits (NPV over 30 years) ranges from £182m to £291.3m, while the scale of improvement in future environmental benefits above *status quo* ranges from -13.3% to 60.9% and -4.3% to 74.5% in gross and intensity terms, respectively (Future impact modelling – page 33).

The future options assessment suggests that there is significant value to be gained by enhancing the genetic improvement programme for sheep and beef in the UK. This is particularly apparent for options that build a national genetic improvement infrastructure with an existing platform or provide for a national genetic improvement infrastructure with a new UK platform. There is a perception that less additional value is created by progressing to a full national genetic improvement programme and integrated infrastructure (Options for the future – page 69). Further consultation is required to clearly identify the most appropriate option. This consultation should focus on discussion with core participants in the provision of genetic evaluation services in the UK.

Cost-benefit ratios suggest that significant benefits are available through implementation of an integrated national phenotype and genotype collection programme. For sheep, benefit to cost ratios range from 8:1 to 18:1. For beef, benefit to cost ratios range from 4:1 to 6:1. Scenarios that can deliver increased selection intensity and adoption generate notably high returns on investment (Results – Cost-benefit analysis – page 81).

The scale of historic and potential future economic and environmental benefits demonstrates that genetic improvement has a cornerstone role to play in driving the sustainability of the UK sheep and beef sector, including as a key tool in the response to the climate challenges the sector faces. The national phenotype and genotype collection programme should focus heavily on building a resource to deliver genetic gain for core genetic traits, as they offer significant opportunity to drive economic and environmental benefits. This will also support adoption and demonstrate commercial value of genetics/differences between sires, improve herd/flock linkages and support multibreed evaluations and across breed comparisons to support higher selection intensity.

Decisions related to investment in the national phenotype and genotype collection programme for feed intake and methane yield should go together with an understanding of how balanced selection for economic/environmental outcomes would accrue economic and environmental benefits. Detailed

approaches to manage phenotyping, considering infrastructure needs and the readiness and potential impact of implementation by different breeds across the industry are also required.

Investment, supported by detailed business planning, should be made to develop a future programme that aspires to maximise the economic and environmental benefit of genetic improvement in the UK sheep and beef sector.

Extended summary

Project overview and approach

The Agriculture and Horticulture Development Board (AHDB), The Department for Environment, Food and Rural Affairs (Defra), and their stakeholders have developed a long-term vision for delivering a step change in the impact of sheep and beef breeding in the UK. The long-term vision is that genetic improvement drives significant benefits in the economic and environmental performance of sheep and beef production in the UK. These benefits will accrue through a coordinated approach to performance recording and genetic evaluation, underpinned by the latest genetic improvement tools, supported using robust data collated from national datasets, commercial farms, and breeders, and using the latest approaches delivered by an active programme of research and development (R&D) and knowledge exchange (KE).

This project represents the first step towards delivering that vision and addresses the core question of how a future model for delivery of genetic improvement can be developed in a way that delivers against both industry and government policy requirements, particularly in response to the climate challenges faced by the industry. The study addresses three main areas and will provide the evidence needed to develop a business plan.

Firstly, this project provides an increased understanding of, and quantifies, the historic and potential future environmental (enteric greenhouse gas emissions) impact of genetic progress in sheep and beef populations and derives suitable metrics to track progress towards this objective. Alongside this, updated estimates of the historic and potential future economic impact of genetic improvement have been determined.

Secondly, the project explores the potential options for an industry genetic improvement programme in the future. This combined a literature and desk-based evaluation along with targeted stakeholder interviews, to identify the option(s) that maximise(s) the benefits and minimise(s) the obstacles in creating an industry genetic improvement programme for the future.

The third element of this project examines the scope and potential for a national phenotype and genotype collection programme based on collecting phenotypes and genotypes to underpin genetic evaluations and drive genetic improvement towards economic and environmental outcomes. Costs of this potential scheme were combined with future benefits in a cost-benefit analysis.

The project delivers the evidence base to inform decisions related to the development of a genetic improvement programme for the UK sheep and beef sector, to improve financial sustainability and reduce the environmental impact of the sector.

Key findings

WP1: Historic and potential future economic and environmental benefits from genetic improvement

The objective of Work Package 1 was to quantify historic and potential future economic and environmental benefits from genetic improvement in the UK sheep and beef industries. The analysis was built in three parts.

Deterministic modelling was used to calculate the economic and environmental impacts from historic rates of genetic gain.

Selection index theory was used to estimate the potential future economic and environmental impacts of genetic improvement (including potential impacts from increased adoption, increased rates of gain, and inclusion of traits that target reduced environmental impact).

Based on the modelling exercise in 1 and 2, metrics were defined that can be used to monitor progress towards economic and environmental goals.

Historic economic and environmental benefits from genetic improvement

Genetic improvement in UK sheep and beef industries has generated substantial economic and environmental benefits. In economic terms, the historic rate of genetic gain will deliver annualised benefits of £14.7m (net present value [NPV] or £183.2m over the next 20 years) and £6.8 (NPV of £84m over the next 20 years) for sheep and beef, respectively.

In parallel, historic environmental benefits in gross terms for sheep amount to -0.521 kg CO₂e/mated female/year and -6,618 tonnes/all mated females/year. This represents a 0.1% reduction in gross emissions per year. In emissions intensity terms, historic trends reduce the emissions by -0.04 kg CO₂e/kg product/mated female/year. This represents a 0.23% reduction in emissions intensity per year.

Historic environmental benefits in gross terms for beef amount to -3.38 kg CO₂e/mated female/year and -5,000 tonnes/all mated females /year. This represents a 0.08% reduction in gross emissions per year. In emissions intensity terms, historic trends reduce the emissions by -0.03 kg CO₂e/kg product/mated female/year. This represents a 0.13% reduction in emissions intensity per year.

Potential future economic and environmental benefits from genetic improvement

For sheep, the scale of future economic benefits (NPV over 30 years) ranges from £328.1m (incorporating an extended set of traits) to £978.8m (full scale genomics with increased selection intensity and greater adoption), or a 14.6% to 241.9% increase above the *status quo*. The scale of improvement in future environmental benefits above *status quo* ranges from 69.1% (incorporating an extended set of traits including feed intake and methane yield) to 249.1% (full scale genomics with increased selection intensity and greater adoption) and 34.4% (incorporating an extended set of traits) to 180.4% (full scale genomics with increased selection intensity and greater adoption) in gross and intensity terms, respectively.

For beef, the scale of future economic benefits (NPV over 30 years) ranges from £182m (incorporating an extended set of traits and feed intake with methane yield at 150% weighting) to £291.3m (full scale genomics with increased selection intensity and greater adoption), or a 10.5% to a 76.8% increase above *status quo* for beef. The scale of improvement in future environmental benefits above the *status quo* ranges from -13.3% (incorporating an extended set of traits including feed intake and methane yield, with methane yield at 150% weighting) to 60.9% (feed intake with methane yield with increased selection intensity and greater adoption) and -4.3% (incorporating an extended set of traits and feed intake with methane yield at 150% weighting) to 74.5% (feed intake with methane yield with increased selection intensity and greater adoption) in gross and intensity terms, respectively.

Future environmental benefit modelling suggests that significant environmental benefits can be obtained by selecting on a broader array of core traits (additional core traits scenarios where a wider suite of core traits have economic weights with base levels of performance records), through increased selection intensity, and greater rates of adoption. Scenarios incorporating feed intake and methane yield do not offer the same scale of environmental benefits, in either gross or intensity terms. This is true for sheep and for beef.

For sheep, the environmental benefits in gross terms realised in scenarios focusing on driving faster rates of economic genetic gain through additional core traits (74.5% greater than the *status quo*) were slightly greater than those offered by either implementing feed intake (71.0%) along with methane yield (69.1%). Only when increased selection intensity and greater adoption were applied on top of feed intake and methane yield, or genomics across all traits (including feed intake and methane yield), or 50% greater emphasis is placed on feed intake and methane yield, did the gross environmental benefits surpass those realised from additional core trait recording alone. In emissions intensity terms, genomics across all traits increases improvement by 82.2%, and the environmental benefits continue to accrue as selection intensity improves (117.4%) and as adoption increases (180.4%).

These outcomes suggest that the net environmental benefit, in gross and intensity terms, of adding feed intake and methane yield (at relatively lower accuracy – see Supplementary material 5: Potential national phenotype and genotype collection programme costing model (Excel file) - and a lower GHG emissions coefficient for feed intake – see Table 38) is less than what can be gained by selection for

core selection index traits that contribute to GHG system efficiency (e.g., earlier slaughter), and/or increased selection intensity and greater adoption.

For beef, like sheep, the environmental benefits in gross terms realised in scenarios focusing on driving faster rates of economic genetic gain through additional core traits (17.1% greater than the *status quo*) were greater than those offered by either implementing feed intake (2.2%) along with methane yield (2.7%) or implementing genomics across all traits (plus feed intake and methane yield) (-7.7%). Only when increased selection intensity and greater adoption were applied on top of feed intake, methane yield and genomics across all traits (plus feed intake and methane yield) did the gross environmental benefits surpass those realised from additional core trait recording. In emissions intensity terms, the same pattern is apparent.

These outcomes suggest that the net benefit, in gross terms, of adding feed intake and methane yield (at lower relative accuracy – see Supplementary material 5: Potential national phenotype and genotype collection programme costing model (Excel file) - and a lower GHG emissions coefficient for feed intake – see Table 46) is less than what can be gained by increased selection for core traits that contribute to GHG system efficiency (e.g., earlier slaughter), and/or increased selection intensity and adoption. The lower net benefit seen in gross terms, when comparing scenarios with feed intake/methane yield/genomics all traits to additional core traits only, is not offset by increased output under emissions intensity calculations.

Along with the dynamics of trait responses, GHG emissions coefficients, and output, there are further contributing reasons for the above responses in environmental benefits. Firstly, the environmental benefits realised under the range of scenarios are entirely a result of selection on indexes that are driven by economic outcomes alone. These economic selection indexes are emphasising economic outcomes and do not drive selection to balance GHG emissions and economic outcomes. There are trade-offs (antagonisms) between positive environmental outcomes and positive economic outcomes.

Secondly, the divergent environmental outcomes in gross terms (in certain scenarios where it might be expected that environmental benefit would be significantly higher), compared to economic outcomes, is partially the result of lower accuracy for feed intake and methane yield relative to other selection index traits (under genomic selection scenarios for all traits). When additional economic emphasis is placed on methane yield, as is done to emphasise the trait, the lower accuracy manifests in lower environmental benefits than the methane yield economic weight implies.

Future target accuracy levels for feed intake and methane yield are driven by the practicalities of reference population design, scale, and cost for these traits. While feed intake and methane yield offer the potential to drive further environmental benefits, potential scenarios that would increase the accuracy of these traits are likely to be cost prohibitive (diminishing returns). Therefore, the modelled accuracies herein are best combined with GHG-driven selection indexes, that balance economic and environmental outcomes, to inform the national phenotype and genotype collection programme for feed intake and methane yield.

Metrics to monitor progress towards economic and environmental goals

The framework best suited to monitoring progress towards economic outcomes includes the following primary, secondary or tertiary metrics:

- Annual rate of economic genetic gain, reported in £ of added profit per all mated cows/ewes per year (primary),
- Adoption in terms of numbers (or %) of herds/flocks submitting genotypes & phenotypes (secondary),
- Industry-weighted genetic trends reported as annual rates progress in key traits across the industry (secondary),
- Accuracy of average breeding values for key traits across the industry, representing the contribution of historic efforts (tertiary),
- Accuracy in terms of annual numbers of genotypes and phenotypes submitted, representing the contribution to future breeding value accuracy (tertiary), and
- Selection Intensity reported as the percentage of calf/lamb registrations originating from recent top-ranked (15%) sires (tertiary).

The framework best suited to monitoring progress towards environmental outcomes is equivalent to the economic framework, with the exception that the primary driver is broken into:

- Annual rate of genetic gain in GHG emissions, in gross emissions terms CO₂e/all mated females/year, and
- Annual rate of genetic gain in GHG emissions, in intensity terms CO₂e/kg product/mated female/year

WP2: Industry consultation and assessment of the most appropriate genetic improvement programme

The objective of Work Package 2 was to identify what the most appropriate industry genetic improvement programme looks like for the UK sheep and beef sector.

Firstly, a process of industry consultation was used to define what good looks like. The aim was to identify critical aspects of a successful genetic improvement programme, needed to deliver both industry and government policy requirements.

Using information from industry consultation and supported by information from the definition of what good looks like, a set of the potential future options for a genetic improvement programme in varying, improved, forms was developed.

Finally, through further stakeholder engagement, a quantitative assessment of potential options was undertaken.

Industry consultation

Targeted interviews (35) were conducted across a range of “user types”. These were represented by commercial breeding companies (5), levy boards (4), sheep and beef farmers (5), livestock specialists (7), food service/retailers (8) and breed societies (6).

Industry consultation highlighted that sheep and beef farmers face challenges in the next ten years related to net zero and wider environmental impact, greater pressures on profitability and efficiency (e.g., loss of subsidies), staff recruitment and retention, and the messaging of the anti-livestock products lobby. All interviewees saw genetics as part of the solution to such challenges. The consultation highlighted future genetic improvement programmes must:

- use a common language for genetic merit (“plain English”) and translate (including visually) genetic information into simple, practical ratings of worth, linked to farm key performance indicators (KPIs).
- use a single data system, independent of genetics service providers, but with data ownership at its core. This should be used to:
 - set up data integrity checks to improve data quality,
 - produce a single national evaluation for each livestock type to produce “national estimates of merit”,
 - generate genetics benchmarks,
 - allow groups to conduct other evaluations as part of their differentiated breeding programmes, and
 - capture and use commercial data e.g., abattoir data,
- widen the definition of overall merit to include all traits with a major effect on farm performance, through adding in “hard to measure” traits,
- make information more accessible in more places, with intuitive tools for examining information,
- not try to be fair to everyone and back “winners” committed to genetic improvement,
- learn from the poultry, pig and dairy sectors who have exploited genetic improvement to a much greater degree, and
- have a strong Knowledge Exchange system at its core, supported by a network of genetic specialists.

There was universal agreement to share data where there was mutual benefit. Overall, the responses obtained show an appetite for change, coupled with a preparedness to work together to deliver that change. All thought that current systems were not delivering to their potential and that the fragmented nature of genetic services provision was part of the problem, confusing ram and bull buyers and failing to make the best of available data.

Options for the future

A set of future genetic improvement programme options (including all aspects of the programme from infrastructure to knowledge exchange systems) were developed. The options were informed by

findings from industry consultation (outlined above and Appendix 5: Industry consultation – structured interviews), a review and assessment of global programmes (Supplementary material 2: International genetic improvement programmes), the definition of what good looks like, and a structured approach to building the range of possible levels across the options i.e., future options can range from enhancements to the current system through to a major overhaul, with each step on the advancement scale offering a different complexity and potential value to the industry. The existing genetic improvement programme (the *status quo*) was considered when building the options. However, the options were developed, presented, and reported in generic terms. That is, the options did not consider, qualify, or quantify if and/or how existing industry stakeholders (e.g., suppliers, societies, or R&D organisations among others) would integrate into, or contribute to, a potential future genetic improvement programme. The integration of existing industry stakeholders and/or the definition of how they may contribute to a potential future genetic improvement programme would form part of a formal business plan to deliver any potential future genetic improvement programme. The options are summarised below.

Option A: Status Quo supported by R&D. The ‘Status Quo supported by R&D’ option builds upon the current programmes and aims to fill some of the gaps that effectively deliver national genetic improvement. The primary developments are concerned with involving commercial farmers in the two-way flow of information. The development and leadership of an all-industry focussed Research, Development and Extension (RD&E) programme will underpin the link with the commercial farmer.

Option B: National genetic improvement infrastructure - existing platform. Further additions to infrastructure include bringing national genetic evaluations to one existing platform. The genetic evaluation development within this option would include genomics. Data for the evaluation would be collated from other individual databases (breed associations, breeding companies, research databases) rather than collected, stored, managed, and governed in a central database (next Option).

Option C: National genetic improvement infrastructure - UK platform. The primary development in this option (in addition to non-redundant elements of Option A and B) is the creation and management of genetic evaluations in-house on a system or platform under the control of a newly created industry-good governing entity. In this option, core data resides in a centrally controlled database and SOP and pipelines are in place.

Option D: Full national genetic improvement programme & integrated infrastructure. Progeny testing, breeding programs (elite herds recruited), advanced R&D, linking with third party databases (health, traceability, GHG inventories) and advanced genetic improvement tools (mate allocation, inbreeding, cull indexes etc.)

Value ease analysis

A structured framework for scoring the options against key drivers of a successful genetic improvement programme was developed. A Value-Ease scoring evaluation of these options was used to identify the most appropriate option for the UK. Full details of the Value-Ease scoring evaluation are provided in Appendix 6: Genetic improvement programme assessment framework. This process of Value-Ease scoring included four main steps, detailed below.

- i) Illustration of the options and their individual features/elements.
- ii) Evaluation criteria for both value and ease dimensions were assigned (through external expert consultation- detailed found in Supplementary material 4: Stakeholder questionnaire for weighting of criteria and scoring of options (Word & Excel file) a level of importance.
- iii) All options were scored against the value and ease evaluation criteria (through further external expert consultation – details found in Supplementary material 4: Stakeholder questionnaire for weighting of criteria and scoring of options (Word & Excel file).
- iv) Value-Ease calculated by combining criteria importance (weighting) with the scores for each option.

The Value-Ease analysis suggests that there is significant value to be gained by enhancing the genetic improvement programme for sheep and beef in the UK. This is particularly apparent for options that build a national genetic improvement infrastructure with an existing platform (option B) or a national genetic improvement infrastructure with a UK platform (option C). There is a perception that less additional value is created by progressing to a full national genetic improvement programme & integrated infrastructure (option D). Option A (*status quo* supported by R&D) falls into the lower quadrant for its value to the industry. The simpler, smaller development proposed under *status quo* supported by R&D (option A) is considered the easiest to implement and manage. Almost no further decrease in ease of implementation and management is seen when progressing to option B. The scale of decrease in ease of implementation and management is near equivalent for progression from option B to option C and option C to option D.

When quantitatively assessed, option C would be the most appropriate model to take forward into further development and business planning (high relative value to industry and easier to implement and manage for the value gained, compared to option D). However, option B performs well in terms of value to industry, with very little decrease on the ease scale, relative to option A.

WP3: Cost-benefit analysis of potential national phenotype and genotype collection programme

Work package 3 aims to establish the potential, through a cost-benefit analysis, of a national phenotype and genotype collection programme to deliver government and industry sustainability and environmental objectives. The approach focuses on the use of centralised ‘reference populations’ of herds/flocks to support the generation of progeny for genotyping and phenotyping via a structured progeny test model.

Cost-benefit ratios suggest that significant benefits are available through implementation of an integrated national phenotype and genotype collection programme. For sheep, benefit to cost ratios range from 8:1 (implementing feed intake) to 18:1 (implementing methane yield and feed intake + intensity + adoption). For beef, benefit to cost ratios range from 4.2:1 (feed intake with methane yield at 150% weighting) to 6.1:1 (genomics all traits, intensity + adoption (slow)). Scenarios that can deliver

increased selection intensity and adoption generate higher returns on investment. However, the cost of driving additional adoption is not included in this analysis.

Under deployment of genomics for all traits, there is little economic incentive to speed up the delivery of the programme.

The costs incorporated into the potential national phenotype and genotype collection programme are conservative (high) and likely worst case. Costs could be reduced in several potential ways (not modelled), including:

- Through leveraging existing phenotype and genotype datasets for some breeds/traits,
- By adjusting programme scale and structure down once genomics accuracies reach adequate targets,
- By sharing resources/overheads across sheep and beef programmes, and
- By applying a more granular approach to trait by breed by herd/flock combinations.

Further analysis is required to determine how to reduce these fixed costs and deliver efficiencies. The expectation is that the extent to which these fixed costs can be reduced will be limited, due to implicit minimum requirements for programme management and R&D. Fixed costs also restrict the scale of potential cost saving realised by slower/longer implementation. As such, there is little economic incentive to speed up the rate of deployment of the programme.

The relevant scenarios highlight the annual volume of feed intake and methane phenotypes that would be required to meet, conservative, trait accuracy objectives. It is important to consider these phenotyping requirements in planning infrastructure needs, as the forecasts exceed the capacity of current infrastructure. Capital costs associated with additional infrastructure are not captured here. Rather, phenotypes are costed on a per animal basis. Capital costs would be included in a full-scale business plan.

Of note is that changes in environmental outcomes between scenarios do not align entirely (i.e., do not always correlate) with changes in economic outcomes. This is not unexpected given the environmental benefits realised under the range of scenarios are entirely a result of selection on indexes that are driven by economic outcomes alone and there are trade-offs (antagonisms) between positive environmental outcomes and positive economic outcomes. Other drivers of this are mentioned in the section on Potential future economic and environmental benefits from genetic improvement.

National phenotype and genotype collection programmes can be a key tool (indirectly) for achieving outcomes, other than those for which they are designed. These sorts of programmes can support adoption and be used to demonstrate commercial value of genetics/differences between sires, improve herd/flock linkages, and support multibreed evaluations and across breed comparisons.

Recommendations

WP1

1. The scale of historic and potential future economic and environmental benefits demonstrates that genetic improvement has a cornerstone role to play in driving the sustainability of the UK sheep and beef sectors. Investment, supported by detailed business planning, should be made to develop a future genetic improvement programme that aspires to maximise the economic and environmental benefit of genetic improvement in the UK sheep and beef sector.
2. While feed intake and methane offer the potential to drive further environmental benefits, clarity on the scale of these benefits is dependent on first developing industry-wide indexes that drive selection based on GHG coefficients or weighted GHG coefficients/economic weights, rather than economic weights only.
3. The primary and secondary drivers within the economic performance indicator framework should be used to assess the industry-wide annual rate of economic genetic gain and economic impact. Tertiary indicators should be used for further granularity if required.
4. The same primary and secondary drivers within the economic performance indicator framework should be used to assess the industry-wide annual rate of genetic gain in GHG emissions, with the exception that the primary driver is split into gross and emissions intensity measure of environmental impact. Tertiary indicators should be used for further granularity if required.

WP2

5. Options that build a national genetic improvement infrastructure with an existing platform (option B) or a national genetic improvement infrastructure with a UK platform (option C) should be further assessed (via additional industry engagement/consultation as part of business planning) to clearly identify the most appropriate option for the UK. This consultation should focus on discussion with core participants in the provision of genetic evaluation services in the UK.
6. Business planning should draw on learnings from industry consultation and insights from what good looks like to build the appropriate genetic improvement programme (including all aspects of the programme from infrastructure to KE systems).
7. Business planning should also consider, qualify, or quantify if and/or how existing industry stakeholders (e.g., suppliers, societies, or R&D organisations among others) would integrate into, or contribute to, the selected future genetic improvement programme.

WP3

8. The potential for cost reductions in the national phenotype and genotype collection programme should be explored further in business planning, with a focus on leveraging existing phenotype and genotype datasets for some breeds/traits and sharing resources/overheads across sheep and beef programmes, and by applying a more granular approach to trait by breed by herd/flock combinations.
9. The national phenotype and genotype collection programme should focus heavily on building a resource to drive genetic gain for core selection index traits, as they offer significant opportunity to drive economic and environmental benefits. This will also support adoption and demonstrate commercial value of genetics/differences between sires, improve herd/flock linkages, and support multibreed evaluations and across breed comparisons.
10. Decisions related to investment in the national phenotype and genotype collection programme for feed intake and methane yield, at the accuracies modelled herein, should go together with an understanding of how balanced economic/environmental indexes would allocate emphasis to different traits, and of the resultant economic and environmental benefits.
11. In developing a national phenotype and genotype collection programme, phenotyping requirements for feed intake and methane yield should be considered in the context of infrastructure needs and the readiness and potential impact of implementation by different breeds, because forecasted phenotyping needs exceed the capacity of current infrastructure. Capital costs should be included in a full-scale business plan.
12. The benefits available to industry (and the associated benefit costs ratios) through increased selection intensity and greater adoption, regardless of underlying trait and technology implementation, are notably high. To fully realise the economic and environmental benefits that can be obtained by improving recording practices, increasing selection intensity, and greater adoption (core traits and selection tools), a consolidation of genetic merit information into a common language (industry-wide economic/environmental indexes) is required, supported by a strong KE programme. Note that the underpinning elements of a future genetic improvement programme (outlined in WP2) are key to realising the significant benefits available.

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Background

The Agriculture and Horticulture Development Board (AHDB), The Department for Environment, Food and Rural Affairs (Defra), and their stakeholders have developed a long-term vision for delivering a step change in the impact of sheep and beef breeding in the UK. The long-term vision is that genetic improvement drives significant benefits in the economic and environmental performance of sheep and beef production in the UK. The benefits will accrue through a coordinated approach to performance recording and genetic evaluation, underpinned by the latest genetic improvement tools, supported using robust data collated from national datasets, commercial farms and breeders, and using the latest approaches delivered by an active programme of research and development (R&D) and knowledge exchange (KE).

This project represents the first step towards delivering that vision and addresses the core question of how a future model for delivery of industry genetic improvement can be developed in a way that delivers against both industry and government policy requirements. The study addresses three main areas and will provide the evidence needed to develop a business plan.

A key objective of both government and AHDB's own strategy, is to quantify and reduce the impact of agriculture on the environment, as the industry faces a climate emergency. Firstly, this project provides an increased understanding of, and quantifies, the historic and potential future environmental (GHG emissions) impact of genetic progress in sheep and beef populations and derives suitable metrics to track progress towards this objective. Alongside this, updated estimates of the historic and potential future economic impact of genetic progress have been determined.

Secondly, the study explored the potential options for an industry genetic improvement programme fit for the future. This combined a literature and desk-based evaluation, with targeted stakeholder interviews, to identify the option(s) that maximises the benefits and minimises the obstacles.

The third element of this project scoped out the potential for a national phenotype and genotype collection programme to underpin genetic evaluations and drive progress towards government objectives and industry sustainability. The costs of this potential scheme were combined with the future benefits in a cost-benefit analysis.

The project delivers the evidence base to inform decisions related to the development of genetic improvement infrastructure for the UK sheep and beef sector, to improve financial sustainability and reduce environmental impact of the sector.

Project overview

The specific objectives were to:

1. Understand and quantify the historic and potential future economic and environmental benefits of genetic improvement in the UK sheep and beef sector, including the definition of metrics to monitor progress.

2. Define the most appropriate industry genetic improvement infrastructure for the UK sheep and beef sector, through a process of industry consultation, and a quantitative assessment of the potential options available against a set of key assessment criteria.
3. Establish the potential, through a cost benefit analysis, of a national phenotype and genotype collection programme to deliver government and industry sustainability and environmental objectives

This report covers methodology, results, and commentary relating to these 3 work packages and their component deliverables, in 3 separate sections, with additional details in appendices and supplementary material. Recommendations are provided, where appropriate.

WP1: Historic and potential future economic and environmental benefits from genetic improvement

Introduction

The objective of Work Package 1 was to quantify historic and potential future economic and environmental benefits from genetic improvement in the UK sheep and beef industries. The analysis was built in three parts.

Deterministic modelling was used to calculate the economic and environmental impacts from historic rates of genetic gain.

Selection index theory was used to estimate the potential future economic and environmental impacts of genetic improvement (including potential impacts from increased adoption, increased rates of gain, and inclusion of traits that target reduced environmental impact).

Based on the above modelling exercises, metrics were defined that can be used to monitor progress towards economic and environmental goals.

Framework for economic and environmental impact

Definitions for quantifying economic and environmental impact

Table 1 provides a glossary of definitions of inputs and outputs used in the framework for quantifying economic and environmental impact. How these inputs and outputs fit together is also reported in Figure 7 (economic) and Figure 9 (environmental).

Table 1: Glossary of terms for quantifying economic and environmental impact

Term	Definition
Trait genetic trends	Annual rates of genetic gain for selection index traits for each breed
Industry structure	Breed population size and type (dual purpose/maternal or terminal), mating structures, and differences in trait genetic trends between recorded and non-recorded populations
Industry-weighted genetic trend	Weighted aggregation of trait genetic trends, accounting for industry structure
Trait economic weights	Marginal change in profit for a one unit change in each selection index trait
Industry-wide annual rate of economic genetic gain	Industry-wide economic gain (profit) across all selection index traits across all females mated in a single year
Total net present value (NPV)	Total industry-wide value of genetic gain accounting for cumulative expressions of multiple years
Annualised benefit	Industry-wide economic gain (profit) across all selection index traits across all females mated, accounting for cumulative expressions of multiple years (total net present value of genetic gain) converted to a per year value
Trait GHG emission coefficients	Marginal change in emissions (gross and intensity) for a one unit change in each selection index trait
Industry-wide annual rate of genetic gain in GHG emissions	Industry-wide emissions (gross for all females mated and intensity per kg of carcass weight) across all selection index traits in a single year

Approach

In the UK sheep and beef industries, trait genetic trends are measured separately for different breeds, which contribute to the industry-weighted genetic trend for each trait. The industry-weighted genetic trend for each trait is affected by aspects of industry structure including breed population size and breed type (dual purpose/maternal or terminal), mating structures, and differences in trait genetic trends between recorded and non-recorded populations.

For historic impacts, trait genetic trends for each breed for traits under selection covering the last 20 years¹ were compiled and combined with information on breed population sizes and types, recording practices, and mating structures^{2,3} to estimate the contribution of breeds to industry-weighted genetic trends.

Industry-weighted genetic trends were combined with trait economic weights (which measure the change in profit per 1-unit change in each trait) for dual purpose/maternal and terminal selection indexes and breed population size and type (dual purpose/maternal or terminal) to estimate the industry-wide annual rate of economic genetic gain. This industry-wide annual rate of economic genetic gain is defined as the marginal benefit to the industry from one year of improvement.

Genetic improvement is permanent and cumulative, and the benefits from one year of improvement accumulate each year and are expressed indefinitely. Therefore, the economic impact is defined using the annualised benefit, which accounts for this permanent and cumulative expression and is equal to an annual payment with an equivalent net present value (NPV) to the accumulated benefits of expression over a given time.

Environmental impacts, using industry-weighted genetic trends, trait GHG emission coefficients (which measure the change in emissions per 1-unit change in each trait) and breed population size and type (dual purpose/maternal or terminal), were based on the industry-wide annual rate of genetic gain in GHG emissions per year, in gross emissions (all females mated) and emissions intensity (per kg of carcass weight) terms. The environmental benefits in emissions per breeding female per year were calculated between 2001 and 2020.

To assess potential future economic impacts under various scenarios, firstly, the genetic parameters underpinning progress at the current (between 2015 and 2020) industry-weighted genetic trend (trait data records, index standard deviation, selection intensity) were derived, in order to create a future *status quo* scenario. Potential future benefit scenarios beyond the *status quo* were then derived by incorporating changes to the genetic improvement programme and simulating the impact of these changes on the future industry-weighted genetic trend and subsequent industry-wide annual rate of economic genetic gain and industry-wide annual rate of genetic gain in GHG emissions (breed population size and type were assumed to be unchanged in the future). Future scenarios are detailed later in this section of the report.

Potential future economic benefits were then accumulated and annualised in the same way as the historic benefits (i.e., an annual payment with an equivalent total NPV to the accumulated benefits of expression over a given time), while potential future environmental impacts from genetic improvement were based on the annual rate of improvement in emissions per breeding female per

¹ Genetic trends from NBE/ beef and Signet/sheep breed societies compiled and provided by AHDB, Nov 2021.

² Pollot, G. & Boon, S. (2020). Sheep breed proportions from Sheep Breeding in Britain 2020. Report prepared for AHDB, HCC and QMS.

³ Beef breed proportions based on British Cattle Movement Survey (BCMS) registration data. 2011 - 2020.

year, in gross emissions and emissions intensity (per kg of carcase weight) terms, as per historic benefits.

Historic economic and environmental impacts

Sheep

Economic impacts

Economic benefits from genetic improvement in the sheep industry are expressed by ewes, kept for replacements, and by lambs, which are destined for slaughter. Industry-wide annual rates of economic genetic gain (in £m/year) were calculated for ewes mated and for lambs born, for hill, crossing and terminal sired ewes, according to the number of ewes mated by each ram type, the underlying industry-wide genetic trends (per lamb born and per ewe) and trait economic weights.

Industry-wide annual rate of economic genetic gain, based on industry-weighted genetic trends from 2015 to 2020, are presented in Table 2 (progeny from ewes mated to terminal rams do not express maternal traits, because all lambs bred for slaughter).

Table 2: Industry-wide annual rate of economic genetic gain for lambs born and ewes mated for hill, crossing, and terminal sired ewes.

	Lambs born (£m)	Ewes mated (£m)
Hill	0.10	0.04
Crossing	0.45	0.04
Terminal sire	1.49	n/a
Total	2.04	0.07

Ten years of cumulative genetic improvement (at an industry-wide annual rate of economic genetic gain of £2.11m), followed by 10 years where the benefits from genetic improved are “locked-in” is worth £183.2m in total NPV based on 5% discount rate. To calculate the annualised value of genetic gain, the equivalent annual value that has the same NPV if payment is received every year for the next 20 years (applying the same discount rate) is calculated. The annualised benefit is £14.7m.

Figure 1 shows 10 years of genetic improvement, followed by 10 years where genetic gain is “locked-in”, and where the area under the curve is the total NPV (£183m). The slope during the first 10 years is equal to the current industry-wide annual rate of economic genetic gain (£2.11m/year).

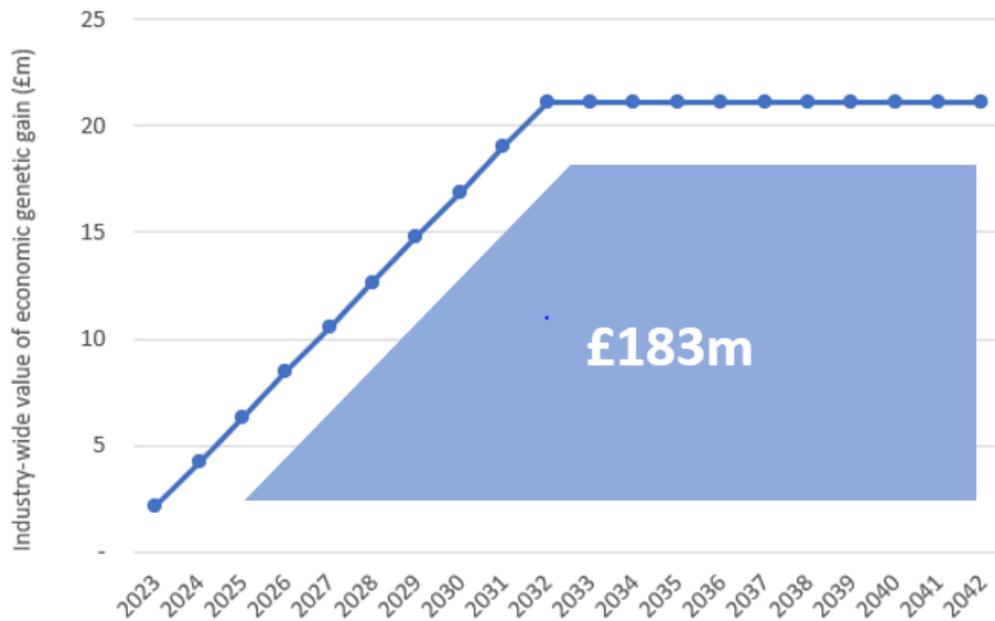


Figure 1: Industry-wide value of economic genetic gain over 20 years, based on 10 years gain at the current industry-wide annual rate of economic genetic gain, followed by 10 years where genetic gain is “locked-in”.

Compared to results from the previous assessment of genetic gain in the UK sheep industry⁴, the annualised benefit of genetic gain has increased from £10.7 to £14.7m. This increase is the result of a combination of population changes, updated economic weights, and changes to trait genetic trends, by breed.

Environmental impacts

Much like economic benefits, environmental benefits from genetic improvement in the sheep industry are expressed by ewes, kept for replacements, and by lambs, which are destined for slaughter. These are calculated based on industry-wide annual rates of genetic gain in GHG emissions for gross emissions (in kg CO₂e/all mated females/year) and for emissions intensity (in kg CO₂e/kg product/mated female/year). To calculate these values, rates of genetic gain per breeding female are calculated by adding emissions from traits expressed per ewe (mature size, litter size, and maternal ability) and emissions expressed per lamb born (scan weight), for hill, crossing and terminal sired ewes. These are then weighted according to the number of ewes mated by each ram type. Industry-wide annual rates of genetic gain in gross GHG emissions and emissions intensity are calculated by scaling up these figures according to the number of ewes mated of each breed type.

Industry-wide annual rates of genetic gain in gross GHG emissions, based on industry-weighted genetic trends from 2015 to 2020, are presented in Table 3 (progeny from ewes mated to terminal

⁴ AbacusBio (2015). Review of the Genetic Improvement of Beef Cattle and Sheep in the UK with Special Reference to the Potential of Genomics. Report prepared for EBLEX (AHDB).

rams do not express maternal traits, because all lambs bred for slaughter). Industry-wide annual rate of genetic gain in gross GHG emissions is -0.521 kg CO₂e/mated female/year, or -6,618 tonnes/all mated females/year, which is equal to a 0.1% decrease in gross emissions per mated female per year (based on gross emissions of 506.6 kg CO₂e/mated female/year).

Table 3: Rate of genetic gain in gross GHG emissions per mated female and industry-wide annual rate of genetic gain in gross GHG emissions for hill, crossing, & terminal sired ewes (all mated females).

	Hill	Crossing	Terminal sire
Mature size (kg)	0.286	0.467	-
Litter size (lambs born)	0.001	0.001	-
Maternal ability (kg)	-0.006	-0.021	-
Scan weight (kg)	-0.550	-0.815	-0.717
Rate of genetic gain in gross GHG emissions (kg/mated female by type/year)	-0.269	-0.369	-0.717
Industry-wide rate of genetic gain in gross GHG emissions (kg/mated female/year)	-0.521		
Rate of genetic gain in gross GHG emissions, by breed type (tonnes/mated females by type/year)	-584	-1,617	-4,418
Industry-wide rate of genetic gain in gross GHG emissions (tonnes/all mated females /year)	-6,618		

Industry-wide annual rates of genetic gain in GHG emissions intensity, based on industry-weighted genetic trends from 2015 to 2020, are presented in Table 4. The industry-wide annual rate of genetic gain in GHG emissions intensity is -0.04 kg CO₂e/kg product/year, which is equal to a 0.23% decrease in emissions per kg of product per year (based on emissions intensity of 17.6 kg CO₂e/kg product).

Table 4: Trends in emissions intensity by trait, rate of genetic gain by breed type, and industry-wide annual rate of genetic gain in GHG emissions intensity for hill, crossing, & terminal sired ewes.

	Hill	Crossing	Terminal sire
Mature size (kg)	-0.053	-0.014	-
Litter size (lambs born)	-0.00015	-0.00004	-
Maternal ability (kg)	0.000	-0.001	-
Scan weight (kg)	-0.008	-0.026	-0.032
Rate of genetic gain in GHG emissions intensity (kg CO ₂ e /kg meat/year, by breed type)	-0.061	-0.042	-0.032
Industry-wide annual rate of genetic gain in GHG emissions intensity (kg CO₂e /kg meat/year)	-0.040		

Beef

Economic impacts

Economic benefits from genetic improvement in the beef industry are expressed on terminal and dual-purpose indexes (where the dual-purpose index measures both terminal and maternal traits). Industry-wide annual rates of economic genetic gain (in £m/year) were calculated according to the contribution from different breeds, the underlying industry-wide genetic trends, and trait economic weights. Contributions from different breeds are determined by the relative numbers of calves and dams registered with the British Cattle Movement Service (BCMS), for the terminal and dual-purpose rates of gain, respectively.

Industry-wide annual rates of economic genetic gain, for terminal and dual-purpose mated females, based on industry-weighted genetic trends from 2015 to 2020, are presented in Table 5.

Table 5: Industry-wide annual rate of economic genetic gain on terminal and dual-purpose indexes.

	Industry-wide annual rate of gain (£m)
Terminal	0.70
Dual purpose	
<i>Terminal</i>	0.83
<i>Maternal</i>	-0.56
Total dual purpose	0.27

Ten years of cumulative genetic improvement in both indexes (at industry-wide annual rates of economic genetic gain of £0.7m and £0.27m for terminal and dual purpose matings, respectively) followed by 10 years where the benefits from genetic improvement are “locked-in” has a total NPV of £84.2m, or £60.5m for terminal matings and £23.7m for dual-purpose matings (NPVs are based on 5% discount rate). The annualised benefit is £6.8m in total (£4.9m and £1.9m for terminal and dual purpose matings, respectively).

Figure 2 shows 10 years of genetic improvement, followed by 10 years where genetic gain is “locked-in”, where the total area under both curves is equal to the total NPV of £84m. The slope during the first 10 years is equal to the combined industry-wide annual rates of economic genetic gain from terminal and dual-purpose matings (£0.97m/year).

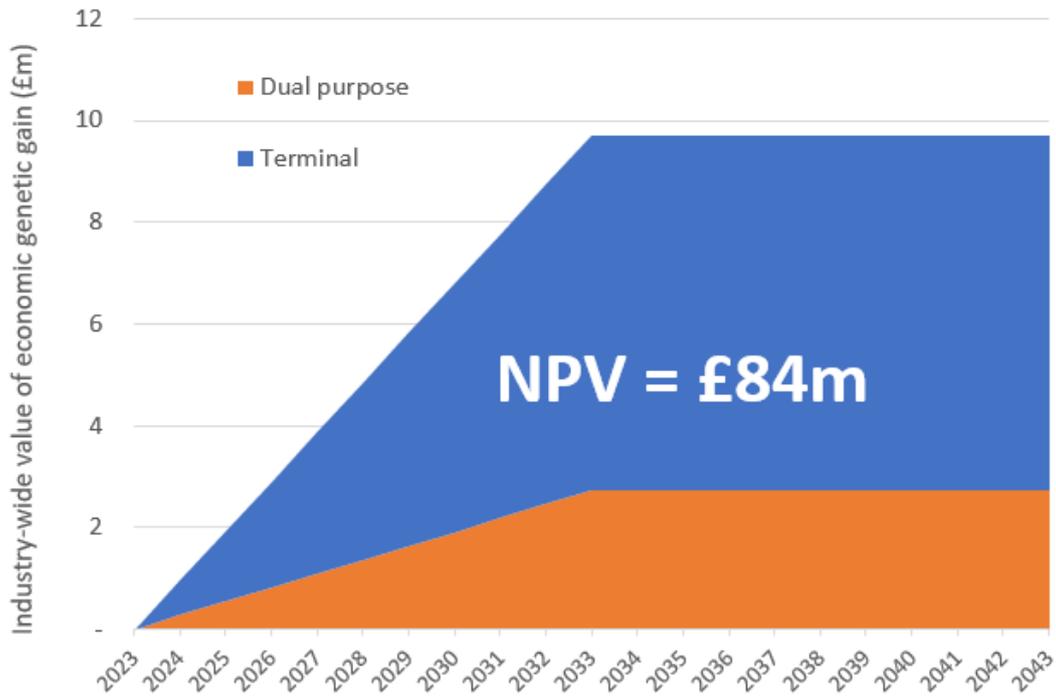


Figure 2: Industry-wide value of economic genetic gain over 20 years for matings on terminal and dual-purpose indexes, based on 10 years gain at the current industry-wide annual rate of economic genetic gain, followed by 10 years where genetic gain is “locked-in”.

Compared to results from the previous assessment of genetic gain in the UK beef industry⁴, the annualised benefit of genetic gain on the terminal index remains largely the same, increasing from £4.8m/year to £4.9m. The annualised benefit of genetic gain on the dual-purpose index increases significantly, from £0.1m to £1.9m (driven due mostly to less negative effects from maternal performance). These changes also reflect an increase in the beef suckler cow population, in addition to updated economic weights, and changes to trait genetic trends, by breed.

Environmental impacts

Environmental benefits from genetic improvement in the beef industry are expressed by suckler cows and by progeny raised for slaughter and are calculated based on industry-wide annual rates of genetic gain in GHG emissions for gross emissions (in kg CO₂e/all mated females/year) and for emissions intensity (in kg CO₂e/kg product/mated female/year). To calculate these values, selection index trends per breeding female are calculated for terminal and dual-purpose indexes. These selection index trends are then scaled up based on the number of females mated on each index to produce the industry-wide annual rates of genetic gain in GHG emissions.

Industry-wide annual rates of genetic gain in gross GHG emissions, based on industry-weighted genetic trends from 2015 to 2020, are presented in Table 6 (females mated on the terminal index do not express maternal traits).

The rate of genetic gain in gross GHG emissions per mated female is -3.38 kg CO₂e/mated female/year, which equates to an industry-wide rate of genetic gain in gross GHG emissions of -5,000 tonnes/per year. This represents a 0.08% decrease in industry-wide gross emissions per year (based on gross emissions of 4,469 kg CO₂e/mated female/year, and a population of 1.48m cows).

Table 6: Rate of genetic gain in gross GHG emissions per mated female and industry-wide annual rate of genetic gain in gross GHG emissions for terminal and dual-purpose mated females.

	Terminal	Dual purpose
Carcase weight (kg)	-2.648	-3.556
Mature cow weight (kg)	-	0.645
Calving interval (days)	-	0.125
Age at first calving (days)	-	0.222
Longevity (years)	-	0.005
Maternal weaning weight (kg)	-	-1.247
Rate of genetic gain in gross GHG emissions (kg/mated female, by index)	-2.648	-3.807
Rate of genetic gain in gross GHG emissions (kg/mated female¹)	-3.378	
Industry-wide rate of genetic gain in gross GHG emissions (tonnes CO ₂ e/year, by index)	-1,450	-3,550
Industry-wide rate of genetic gain in gross GHG emissions¹ (tonnes CO₂e/year)	-5,000	

¹ Combined based on 63% weighting

Industry-wide annual rates of genetic gain in GHG emissions intensity, based on industry-weighted genetic trends from 2015 to 2020, are presented in Table 7. The industry-wide annual rate of genetic gain in GHG emissions intensity is -0.03 kg CO₂e/kg product /year, which is equal to a 0.13% decrease in emissions per kg of product per year (based on emissions intensity of 23.4 kg CO₂e/kg product).

Table 7: Rates of genetic gain in GHG emissions intensity for terminal and dual-purpose mated females.

	Terminal	Dual purpose
Carcase weight (kg)	-0.020	-0.030
Mature cow weight (kg)	-	0.007
Calving interval (days)	-	0.000
Age at first calving (days)	-	-0.001
Longevity (years)	-	0.000
Maternal weaning weight (KG)	-	-0.011
Industry-wide rate of genetic gain in GHG emissions intensity (kg CO ₂ e / kg meat /year, by index)	-0.020	-0.035
Industry-wide rate of genetic gain in GHG emissions intensity¹ (kg CO₂e / kg meat /year)	-0.029	

¹ Combined based on 63% weighting

Future impact modelling

As previously described, historic economic and environmental trends for the UK sheep and beef sector were assessed using a deterministic approach. Further modelling was used to assess the scale of potential future economic and environmental benefits of genetic improvement with a new genetic improvement system, phenotype and genotype collection programmes, and the inclusion of novel environment-focused traits. The model was parameterised using the outcomes from the historic framework to create a *status quo* scenario, from which future benefits could be predicted.

Selection index theory was used alongside a geneflow model to estimate future industry-wide annual rate of economic genetic gain under a series of scenarios that tested the impacts of changes to indexes, rates of adoption, recording/selection practices, and genomic strategies. Selection index theory allows an assessment of the trade-off between and/or synergies in economic and environmental impact.

Gene flow modelling was used to assess the impact at an industry level, and to test the impact of modifying industry practices such as sire selection proportions. The models were developed to predict overall economic and environmental benefits across the industry at an aggregated level based on indexes, i.e., terminal, and dual-purpose for beef, and hill, crossing and terminal for sheep. The industry aggregations are equivalent to those used in the historical modelling and produce the annualised benefit and annual rate of genetic gain in GHG emissions for economic and environmental impact respectively.

Estimating future trends

Selection index theory modelling

Selection index theory^{5,6} predicts the superiority of individuals selected using an index and the annual response to selection in a breeding programme, with the outcomes dependent on the following breeding programme parameters:

- The economic weights used to value a 1 unit change in traits in the breeding objective,
- The trait and/or genomic information available on the selection candidates,
- The selection pressure applied to various candidate types, and
- The genetic parameters for, and genetic relationships between, traits including heritability and repeatability estimates, phenotypic variances, and genetic and phenotypic correlations for selection criteria and breeding objective traits.

⁵ Van Vleck L.D. (1970). Index selection for direct and maternal genetic components of economic traits. *Biometrics* 26(3):477-483

⁶ Dekkers J.C.M. (2007). Prediction of response to marker-assisted and genomic selection using selection index theory. *J Anim Breeding & Genetics* 124:331-341

Selection index theory was used to model the impact of adding new environmental traits (feed intake, methane yield) to existing indexes, including an assessment of changes to the standard deviation of the indexes and the response to selection in existing index traits.

Scenario modelling was used to test the effects of using different traits and numbers of records (genotypes and phenotypes) for key recorded traits on index standard deviation and accuracy. This informs the level of effort required by farmers and the scale of phenotype and genotype collection programmes to generate different levels of genetic gain. These parameters were then used as inputs for the geneflow model to test the impact of these changes on industry level benefits.

The selection index modelling also provides the expected response in each component trait with a 1 unit increase in index. These responses can be converted to trait unit responses and multiplied by the GHG coefficients derived from the historic modelling work to estimate the environmental impact of changes to the index formulation.

Geneflow modelling

Deterministic geneflow models for the UK sheep and beef industries were developed to assess the potential future benefits of modifications to either the breeding indexes or key industry recording/selection practices that influence the lag in flows of genetic merit⁷.

Base models were established for hill, crossing and terminal sheep breed types, and terminal and dual-purpose beef. The models include a set of industry parameters and use the standard deviation of the breeding index derived from the selection index theory modelling as a key input to drive the genetic trend predictions. More information on the methodology is included in Appendix 3: Future modelling framework.

The industry-wide annual rate of economic genetic gain from historic modelling was used as the base line progeny trend, and base selection proportions for sires were set as such that the same level of trend continued, this creating a '*status quo*' future scenario. Separate flows of genetic merit were set up for recorded and non-recorded herds/flocks, and for each index, where the industry-wide annual rate of economic genetic gain was calculated from breed population size and type (constant in the future), trait economic weights, and new industry-weighted genetic trends, to estimate the future benefits. The flows of genetic merit will differ based on the index definition, for example a maternal index per ewe mated would be the trend in index for the breeding females, multiplied by the number of breeding ewes mated per year. As per historic modelling approaches, the industry-wide annual rate of economic genetic gain was used to calculate the annualised benefit, which accounts for this permanent and cumulative expression and is equal to an annual payment with an equivalent total NPV to the accumulated benefits of expression over 20 years plus 10 years "locked in". The industry-wide annual rate of genetic gain in GHG emissions was calculated from the future industry-weighted genetic

⁷ Matthews, D., et al. (2019). Genetic benefits of genomic selection breeding programmes considering foreign sire contributions. GSE 51(40)

trend, per year, in gross emissions (for all mated females) and emissions intensity (per kg of carcass weight) terms. Further details on the environmental impact estimation framework are available in Appendix 3: Future modelling framework.

Breeding programme assumptions

UK sheep

A baseline future breeding programme framework was established for the UK sheep model, using breeding programme assumptions detailed below.

- The records available on various candidate types and relative groups for relevant traits (e.g., sire progeny group sizes) were based on UK performance recorded flock sizes and recording practices.
- Sheep breeds were consolidated into hill, crossing (maternal lowland) and terminal categories
 - o A terminal index was modelled for all sectors (£ per lamb born)
 - o A maternal index was only modelled for hill and crossing (£ per breeding ewe)
 - o The full set of traits considered for each index is shown in Table 8.
- Economic weights were sourced from previous work⁸⁹¹⁰
- The industry-wide annual rate of economic genetic gain was modelled separately for recorded versus non-performance recorded progeny because of the different trait genetic trends.
 - o The non-performance recorded population receive a proportion of the recorded population trend, as per historic modelling.
- The genetic parameters for a methane yield trait (CH₄ g/kg DMI) were sourced from literature¹¹.

Detailed index and industry parameters used are included in Appendix 3: Future modelling framework.

In the *status quo* sheep scenario, the proportion of sires selected (e.g., proportion of ram lambs selected to be sires, on each index within breed type) was derived to match the historic annual rate of economic genetic gain, based on the index standard deviation and accuracies for a base performance recording scenario for indexes using traits with a genetic trend estimated from historic

⁸ AbacusBio (2018). Trait and economic responses to selection for three breeding goals for the UK sheep industry. Report prepared for Defra: Genetic trends from industry breeding goals.

⁹ Conington J., et al. (2004). A bioeconomic approach to derive economic values for pasture-based sheep genetic improvement programs. *Journal of Animal Science* 82, 1290–1304.

¹⁰ AbacusBio (2015). Review of the Genetic Improvement of Beef Cattle and Sheep in the UK with Special Reference to the Potential of Genomics. Report prepared for EBLEX (AHDB).

¹¹ Jonker A., et al. (2018). Genetic parameters of methane emissions determined using portable accumulation chambers in lambs and ewes grazing pasture and genetic correlations with emissions determined in respiration chambers. *Journal of Animal Science* 96, 3031-3042.

modelling. These ranged from selecting from the top 19% (terminal) to the top 78% (hill maternal index).

Table 8: The complete list of traits considered under each index in the sheep future modelling. Only a subset of traits with trends estimated from the historic modelling (indicated with an “H”) were used for the status quo scenario.

Index trait	Terminal	Hill		Crossing	
	Per lamb born	Per lamb born	Per ewe mated	Per lamb born	Per ewe mated
Scan weight	✓(H)	✓(H)	✓	✓(H)	✓
Lean weight	✓(H)				
Fat weight	✓(H)				
Lamb survival direct	✓		✓		✓
IMF	✓				
Mature weight			✓(H)		✓
Litter size			✓(H)		✓
Maternal ability			✓		✓(H)
Lamb survival maternal			✓		✓
Ewe Longevity			✓		✓
Feed intake	✓	✓	✓	✓	✓
Methane yield	✓	✓	✓	✓	✓

UK beef

The base future beef framework was set up using the terminal and dual-purpose (maternal) indexes created for the UK beef industry in previous work carried out by AbacusBio¹². Core breeding programme assumptions are detailed below.

- Impacts were split between terminal and dual-purpose based on the number of cows mated using each index from the historic modelling.
 - o Impacts were also divided across performance/non-performance recording in line with the historic modelling.
- Index (economic weights) were sourced from previous work.¹²
 - o The full set of traits considered for each index is shown in Table 9.
- Genetic parameters from the Limousin breed were sourced and used in selection index modelling
- The genetic parameters for a methane yield trait (CH₄ g/kg DMI) were sourced from literature¹³

¹² AbacusBio (2018). Maternal and Terminal breeding objectives for the UK beef industry. Report prepared for SRUC.

¹³ Donoghue K.A., et al. (2013). Preliminary genetic parameters for methane production in Australian beef cattle. Proc. Assoc. Advmt. Anim. Breed. Genet. 20:290-293

- Sire usage within each industry sector was split into artificial insemination (AI) and natural service (NS) where different sire accuracies and selection proportions were applied to each sire type.

Detailed index and industry parameters used are included in Appendix 3: Future modelling framework.

In the *status quo* beef scenario, the sire selection proportions required to match the historic industry-wide annual rate of economic genetic gain are very modest, with AI sires selected from the top 65% and 92% of calves for terminal and dual purpose, respectively, while natural service sires were selected from the top 85% and 99% of calves, respectively. These selection proportions reflect that fact that the current industry-wide annual rate of economic genetic gain is a small percentage of the index standard deviation, sitting at 2.4% for terminal and 0.6% for dual-purpose. The fragmented nature of the beef industry, where most breeds are running standalone evaluations and breed-specific indexes through BreedPlan, Signet, or Taurus, has resulted in a low level of selection pressure and industry-wide annual rate of economic genetic gain at an industry level. In dairy industry breeding programmes, annual rates of economic genetic gain are typically 10% of the index standard deviation, and previous Australian beef genetic trends have been estimated between 2 and 11% for breed specific indexes¹⁴.

Table 9: The complete list of traits considered under each index in the beef future modelling. Only the subset of traits with trend estimated from the historic modelling (indicated with an “H”) were used for the status quo scenario.

Index trait	Terminal	Dual Purpose
Weight 400 d	✓ (H)	✓ (H)
Gestation length	✓ (H)	✓ (H)
Calving ease direct	✓ (H)	✓ (H)
Calving interval		✓
Age first calving		✓
Longevity		✓
Milk 200 d		✓ (H)
Maternal calving ease		✓ (H)
Mature Cow Size		✓ (H)
Conformation score	✓ (H)	✓ (H)
Fat score	✓	✓
Feed Intake	✓	✓
Methane yield	✓	✓

Scenario modelling

The future modelling framework allowed scenario testing of both changes at the trait and index level (including genomics) as well as changes to key recording/selection practices. The impact of changes

¹⁴ Johnston, D.J. (2007). Genetic trends in Australian beef cattle – Making real progress. Proc. Assoc. Advmt. Anim. Breed. Genet. 17:8-15

flow through the model in various ways, with further details on this in Appendix 3: Future modelling framework.

A set of potential future scenarios were selected, with the changes implemented in a stepwise manner (except for 4b - increased weighting on feed efficiency and methane yield by 50%):

1. *Status quo* - base traits, those with an “H” in Table 8 and Table 9, in the selection index formulations, as modelled in AbacusBio 2015 report¹⁵.
2. Additional core traits – all traits in Table 8 and Table 9 included (except feed intake and methane yield) in selection index formulations¹⁶
3. Feed efficiency trait (via genomics) added to all sheep and beef selection indexes
4. Methane yield added to all sheep and beef selection indexes
 - a. Adding a methane yield trait (via genomics) with 20% emphasis
 - b. Increase weighting on feed efficiency and methane yield by 50%
 - c. 25% improvement in selection proportions for sires
 - d. Improvement in adoption at 50% for sheep (up from 20-25%) and to 90% in beef (up from 80%¹⁷).
5. Include carcass records as information sources in beef selection indexes
6. Full scale genomics
 - a. Implement genomics across the industry (all traits in all indexes)
 - b. 25% improvement in selection proportions for all sires
 - c. Improvement in adoption at 50% for sheep (up from 20-25%) and to 90% in beef (up from 80%).

Future modelling results

Sheep

The total NPV realised under the 11 future modelling scenarios in sheep are shown in Table 10, split into those from lambs selected on the ‘per lamb born’ indexes, and breeding ewes selected on the maternal indexes, where benefits have been aggregated based on the proportion of lambs born/ewes mated on each index. The economic benefits from lambs are significantly higher than the economic benefits from improvement in breeding ewes. In the additional core traits scenario, where all traits

¹⁵ AbacusBio (2015). Review of the Genetic Improvement of Beef Cattle and Sheep in the UK with Special Reference to the Potential of Genomics. Report prepared for EBLEX (AHDB).

¹⁶ To include all traits in beef - AbacusBio (2018). Maternal and Terminal breeding objectives for the UK beef industry. Report prepared for SRUC, and sheep - AbacusBio (2018). Trait and economic responses to selection for three breeding goals for the UK sheep industry. Report prepared for Defra: Genetic trends from industry breeding goals.

¹⁷ High baseline recording levels, at 80%, are the result of how “recording” is defined. For example, in some cases birth records alone may imply a herd is “recording”. This produces a high level of baseline recording. Modelling lower baseline recording levels would have minimal impact on the benefits of genetic improvement, because non-recorded trait trends are similar to recorded trait trends.

from the 2018 Defra work are included with economic weights and base performance recording assumptions, the total NPV only increases for the per ewe mated indexes, with an increase of 280%, as the base recording scenario covers all traits available for the per lamb born indexes. This is driven by the increased standard deviation for the selection index, resulting in increased variation and increased selection differentials for sires at the same selection proportions. The addition of the new traits for sheep, feed intake and methane yield, also increased the index standard deviations and led to increases of 20% and 296% over *status quo* for lambs and ewes respectively when feed intake was added, and this increased to 67% and 410% for lambs and ewes with methane yield added.

One of the key industry parameters that drives genetic gain is the selection proportion applied when selecting sires. Scenario 4c tested the impact of improving this by 25% across all indexes with feed intake and methane yield incorporated into indexes, and scenario 4d looked at the impact of increasing adoption alongside the improvement in selection proportions. Improving selection intensity alone results in an 114% increase over *status quo* for lambs and 615% for ewes, and these rise to 166% and 839% respectively for lambs and ewes when adoption is also increased. Three scenarios were modelled incorporating genomic predictions for all traits: rolling out genomic predictions across all traits, then with the increased selection proportions from scenario 4c, and lastly with the increase in adoption added. In the per lamb born indexes, the shift to genomic predictions across all traits increased the total NPV by 110% over base with higher benefits than all previous scenarios, with the increased selection intensity and greater adoption further lifting this to 145% and 203% respectively. In the per ewe mated indexes which incorporate a wider range of traits, including lower heritability traits such as lamb survival and longevity, the shift to genomics for all traits without the improvements to selection proportions and adoption was more modest and produced lower total NPV when compared to scenarios 4c and 4d, with a 469% increase over *status quo*.

Table 10: The total NPV of genetic gain from lambs and ewes after 20 years gain, followed by 10 years where the gain is “locked in”.

Future modelling scenario	Net present value (£M)		
	Lambs	Ewes	Total
1: Status quo	271.4	14.9	286.3
2: Additional core traits	271.5	56.6	328.1
3: Feed intake	324.4	58.9	383.3
4a: Methane yield	452.1	75.8	527.9
4b: Feed intake/methane yield x 150%	614.7	94.3	708.9
4c: Intensity	580.9	106.4	687.3
4d: Intensity + adoption	720.9	139.6	860.6
6a: Genomics all traits	570.0	84.6	654.5
6b: Increased intensity	664.7	118.3	783.1
6c: Intensity + adoption	822.8	156.1	978.8

Figure 3 and Figure 4 present the underlying selection index trends in profit per lamb born indexes (aggregated by proportion of lambs produced under each index) and profit per ewe mated indexes (aggregated by the proportion of ewes mated under each index) over the 20-year modelling timeframe, for each of the future modelling scenarios.

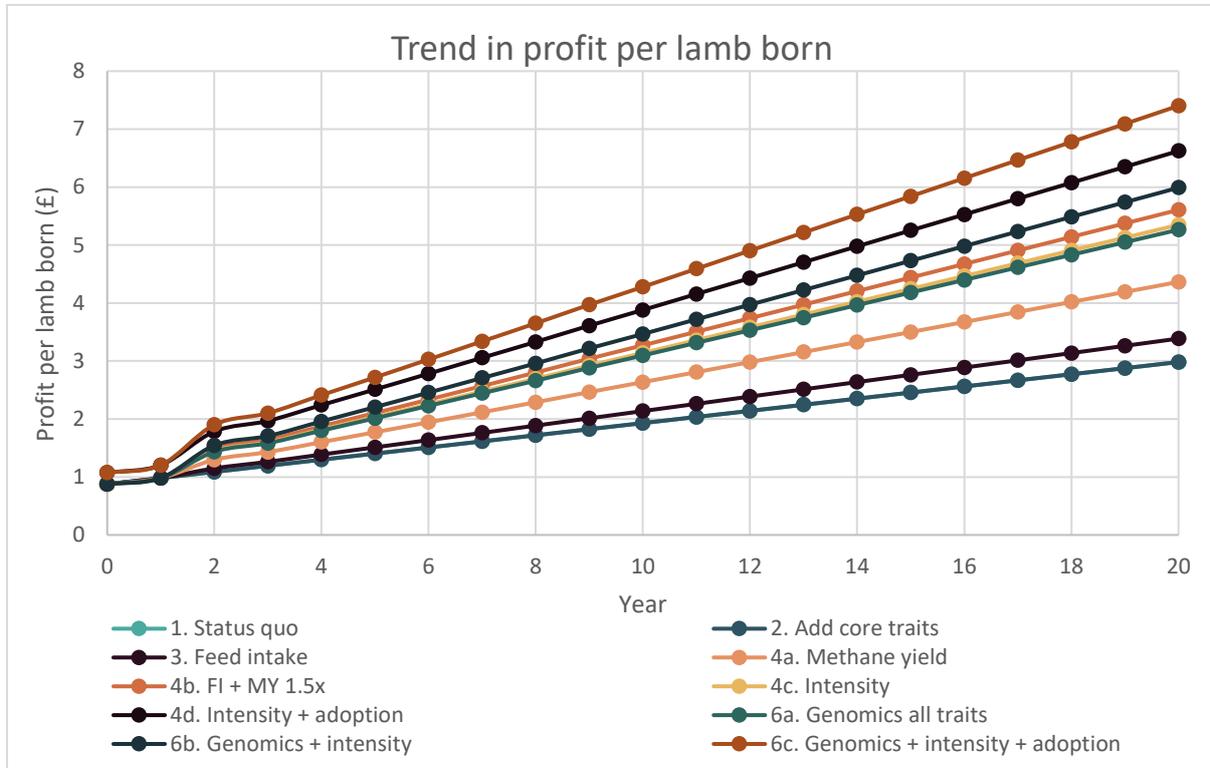


Figure 3: Selection index trends in profit per lamb born indexes (aggregated by proportion of lambs produced under each index) over the 20-year modelling timeframe, for each of the future modelling scenarios.

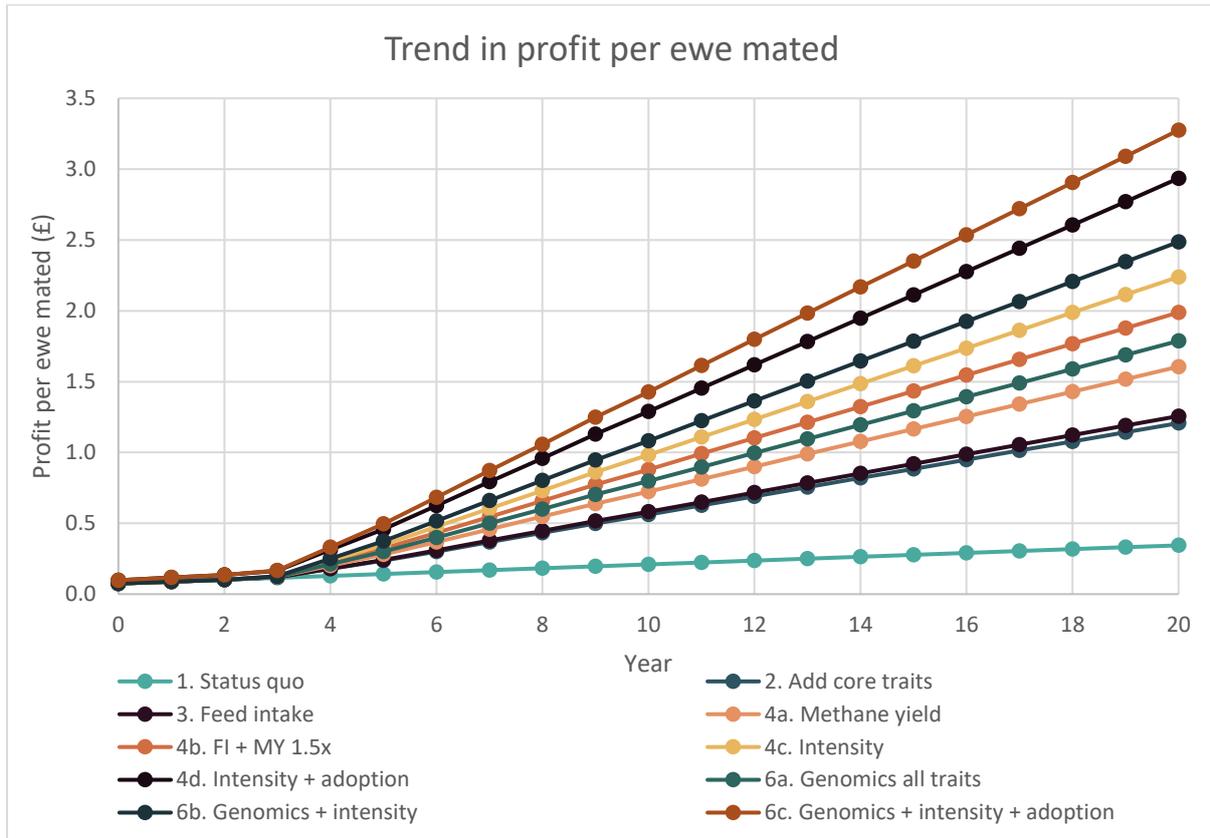


Figure 4: Selection index trends in profit per ewe mated indexes (aggregated by proportion of ewes mated under each index) over the 20-year modelling timeframe, for each of the future modelling scenarios.

Table 11 presents trends in gross CO₂e emissions per mated female and scaled up industry-wide annual rate of genetic gain in GHG emissions, for each of the future modelling scenarios. The scale of improvement in future environmental benefits above *status quo* ranges from 69.1% (scenario 4a - incorporating an extended set of traits, feed intake and methane yield) to 249.1% (scenario 6c - full scale genomics with increased selection intensity and greater adoption). In emissions intensity terms, the benefits range from 34.4% (scenario 4a - incorporating an extended set of traits, feed intake and methane yield) to 180.4% (scenario 6c - full scale genomics with increased selection intensity and greater adoption) (Table 12).

Table 11: Trends in gross CO₂e emissions per mated female, industry-wide annual rate of genetic gain in GHG emissions (all females mated), and % change relative to status quo, for each of the future modelling scenarios.

Future modelling scenario	Trends per ewe (kg CO ₂ e/yr)	Industry-wide trend (tonnes)	% change
1: Status quo	-0.52	-6,620	-
2: Additional core traits	-0.91	-11,551	74.4%
3: Feed intake	-0.89	-11,321	71.0%
4a: Methane yield	-0.88	-11,193	69.1%
4b: Feed intake/methane yield x 150%	-0.93	-11,869	79.3%
4c: Increased intensity	-1.17	-14,806	123.6%
4d: Intensity + adoption	-1.48	-18,867	185.0%
6a: Genomics all traits	-1.21	-15,422	132.9%
6b: Increased intensity	-1.43	-18,233	175.4%
6c: Intensity + adoption	-1.82	-23,111	249.1%

The scale of future economic benefits (NPV over 30 years) ranges from £328.1m (incorporating an extended set of traits) to £978.8m (full scale genomics with increased selection intensity and greater adoption). The scale of benefits ranges from a 14.6% to a 241.9% increase above the *status quo* (Table 12).

Table 12: Total NPVs and industry-wide annual rate of genetic gain in GHG emissions (gross and intensity terms) for each future modelling scenario, along with the percentage change compared to status quo.

Future modelling scenario	30yr NPV (£m)	% change	Industry-wide trend (tonnes)	% change	Trend in EI (kg CO ₂ /kg output)	% change
1: Status quo		-	-6,620	-	-0.040	-
2: Additional core traits	328.1	14.6%	-11,551	74.5%	-0.057	43.7%
3: Feed intake	383.3	33.9%	-11,321	71.0%	-0.055	38.0%
4a: Methane yield	527.9	84.4%	-11,193	69.1%	-0.054	34.4%
4b: Feed intake/methane yield x 150%	708.9	147.6%	-11,869	79.3%	-0.056	38.8%
4c: Increased int.	687.3	140.0%	-14,806	123.6%	-0.072	80.6%
4d: Int. + adoption	860.6	200.6%	-18,867	185.0%	-0.094	134.8%
6a: Genomics all traits	654.5	128.6%	-15,422	132.9%	-0.073	82.2%
6b: Imp. intensity	783.1	173.5%	-18,233	175.4%	-0.087	117.4%
6c: Int. + adoption	978.8	241.9%	-23,111	249.1%	-0.112	180.4%

Future environmental benefit modelling suggests that significant environmental benefits can be obtained by driving improved selection practices on core selection index traits such as growth, reproductive rate and lamb survival, longevity, and (reduced) mature weight (additional core traits), through higher selection intensity, and higher rates of adoption. Scenarios incorporating feed intake and methane yield, or feed intake and methane yield along with genomics for all traits do not offer the same scale of environmental benefits, particularly when quantified in gross terms.

The environmental benefits in gross terms realised in scenarios focusing on driving faster rates of economic genetic gain through additional core traits (74.5% greater than the *status quo*) were greater than those offered by either implementing feed intake (71.0%) along with methane yield (69.1%). Only when increased selection intensity and greater adoption were applied on top of feed intake, methane yield and genomics across all traits (plus feed intake and methane yield) did the gross environmental benefits surpass those realised from additional core trait recording. This pattern of benefits was also reflected in the emissions intensity results. (Table 12).

These outcomes suggest that the net environmental benefit, in gross terms, of adding feed intake and methane yield (at relatively lower accuracy – see Supplementary material 5: Potential national phenotype and genotype collection programme costing model (Excel file) - and a lower GHG emissions coefficient for feed intake – see Table 38) is less than what can be gained by selection for core selection index traits that contribute to GHG system efficiency (e.g., earlier slaughter), and/or increasing selection intensity and achieving greater adoption. The lower net benefit seen in gross terms, when comparing scenarios with feed intake/methane yield/genomics for all traits to additional core traits, is offset under emissions intensity calculations, where the lesser improvement in gross emissions is diluted by improvements in output (while dilution is the result of emissions intensity coefficients¹⁸, in the analysis herein changes in output of product have not been quantified).

¹⁸ Wall, E., et al. (2010). The potential for reducing greenhouse gas emissions for sheep and cattle in the UK using genetic selection. Commercial report by AbacusBio prepared for AHDB & Defra.

Beef

Table 13 shows the total NPV of genetic gain from females mated on dual-purpose and terminal indexes over a 30-year period (at the current, fixed, population), along with the total NPV. This period includes 20 years of genetic gain, followed by 10 years where the gain is “locked-in”. This longer period of gain reflects time taken for genomics to be implemented and allows adequate time for benefits to be fully realised.

Table 13: The total NPV of genetic gain from beef after 20 years gain, followed by 10 years where the gain is “locked in”.

Future modelling scenario	Net present value (£M)		
	Dual purpose	Terminal	Total
1: Status quo	118.1	46.7	164.7
2: Additional core traits	130.4	51.7	182.1
3: Feed intake	130.4	53.0	183.3
4a: Methane yield	131.3	53.3	184.6
4b: Feed intake/methane yield x 150%	126.6	55.2	181.8
4c: Intensity + adoption	186.5	89.1	275.6
5: Carcase records	134.0	54.6	188.6
6a: Genomics all traits	135.7	56.5	192.2
6b: Improved intensity	188.1	92.5	280.6
6c: Intensity + adoption	194.1	97.1	291.3

Figure 5 and Figure 6 each present selection index trends in profit per mated female, on the terminal and dual-purpose indexes, respectively, over the 20-year modelling timeframe, for each of the future modelling scenarios.

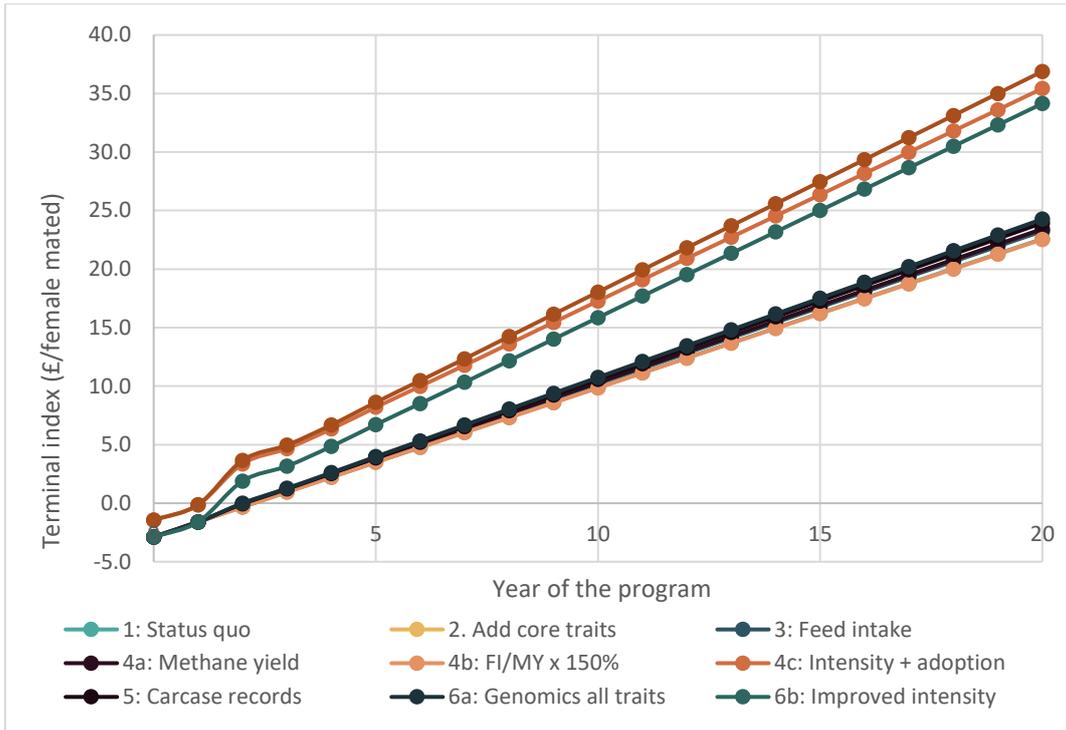


Figure 5: Selection index trends in profit per female mated animal on the terminal index over the 20-year modelling timeframe, for each of the future modelling scenarios.

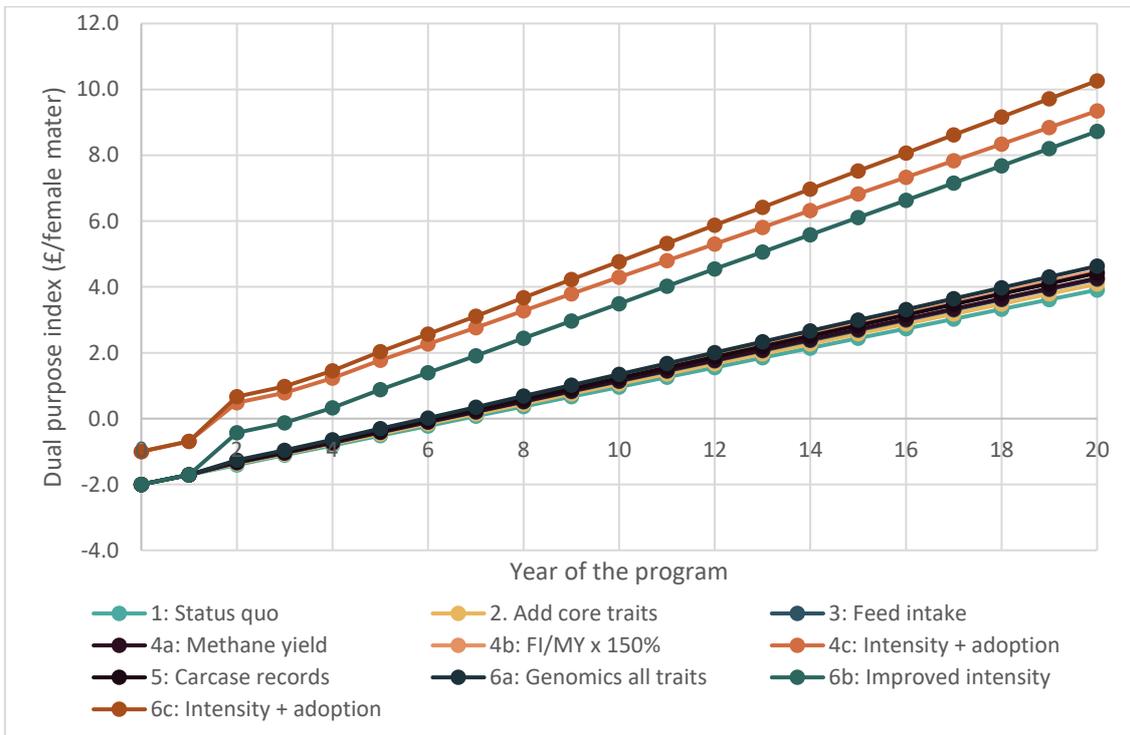


Figure 6: Selection index trends in profit per female mated animal on the dual-purpose index over the 20-year modelling timeframe, for each of the future modelling scenarios.

Table 14 presents trends in gross CO₂e emissions per mated female and scaled up to industry-wide annual rate of genetic gain in GHG emissions, for each of the future modelling scenarios. The scale of improvement in future environmental benefits above the *status quo* ranges from -13.3% (incorporating an extended set of traits and feed intake with methane yield at 150% weighting) to 60.9% (feed intake with methane yield with increased selection intensity and greater adoption). In intensity terms, the benefits range from -4.3% (incorporating an extended set of traits and feed intake with methane yield at 150% weighting) to 74.5% (feed intake with methane yield with increased selection intensity and greater adoption) (Table 15)

Table 14: Trends in gross CO₂e emissions per mated female, industry-wide annual rate of genetic gain in GHG emissions (all females mated), and % change relative to status quo, for each of the future modelling scenarios.

Future modelling scenario	Trends per cow (kg CO ₂ e/yr)	Industry-wide trend (tonnes)	% change
1: Status quo	-3.38	-5,000	
2: Additional core traits	-3.96	-5,856	17.1%
3: Feed intake	-3.45	-5,109	2.2%
4a: Methane yield	-3.47	-5,133	2.7%
4b: Feed intake/methane yield x 150%	-2.93	-4,335	-13.3%
4c: Intensity + adoption	-5.44	-8,045	60.9%
5: Carcase records	-3.35	-4,962	-0.8%
6a: Genomics all traits	-3.12	-4,617	-7.7%
6b: Intensity only	-4.72	-6,981	39.6%
6c: Intensity + adoption	-4.90	-7,254	45.1%

The scale of future economic benefits (NPV over 30 years) ranges from £182m (incorporating an extended set of traits and feed intake with methane yield at 150% weighting) to £291.3m (full scale genomics with increased selection intensity and greater adoption). This represents a 10.5% to a 76.8% increase above *status quo* (Table 15).

Table 15: Total NPVs and industry-wide annual rate of genetic gain in GHG emissions (gross and intensity terms) for each future modelling scenario, along with the percentage change compared to status quo.

Future modelling scenario	30yr NPV (£m)	% change	Industry-wide trend (tonnes)	% change	Trend in EI (kg CO ₂ /kg output)	% change
1: Status quo	164.7	-	-5,000	-	-0.029	-
2: Additional core traits	182.1	10.5%	-5,856	17.1%	-0.037	28.6%
3: Feed intake	183.3	11.3%	-5,109	2.2%	-0.033	13.8%
4a: Methane yield	184.6	12.1%	-5,133	2.7%	-0.033	13.6%
4b: Feed intake/methane yield x 150%	181.8	10.4%	-4,335	-13.3%	-0.028	-4.3%
4c: Intensity + adoption	275.6	67.3%	-8,045	60.9%	-0.051	74.5%
5: Carcase records	188.6	14.5%	-4,962	-0.8%	-0.032	9.8%
6a: Genomics all traits	192.2	16.7%	-4,617	-7.7%	-0.031	7.1%
6b: Intensity only	280.6	70.3%	-6,981	39.6%	-0.046	59.5%
6c: Intensity + adoption	291.3	76.8%	-7,254	45.1%	-0.048	65.4%

Future environmental benefit modelling suggests that significant environmental benefits can be obtained by driving improved selection practices on core selection index traits such as growth, longevity, and (reduced) mature weight (additional core traits), through higher selection intensity, and higher rates of adoption. Scenarios incorporating feed intake and methane yield or feed intake and methane yield along with genomics for all traits do not offer the same scale off environmental benefits, particularly when quantified in gross terms.

Like sheep, the environmental benefits in gross terms realised in scenarios focusing on driving faster rates of economic genetic gain through additional core traits (17.1% greater than the *status quo*) were greater than those offered by either implementing feed intake (2.2%) along with methane yield (2.7%) or implementing genomics across all traits (plus feed intake and methane yield) (-7.7%). Only when increased selection intensity and greater adoption were applied on top of feed intake, methane yield and genomics across all traits (plus feed intake and methane yield) did the gross environmental benefits surpass those realised from additional core trait recording. In emissions intensity terms, the same pattern is apparent (Table 15). A more detailed breakdown of the contributing factors to this are provided in Appendix 3: Future modelling framework.

These outcomes suggest that the net benefit, in gross terms, of adding feed intake and methane yield (at lower relative accuracy – see Supplementary material 5: Potential national phenotype and genotype collection programme costing model (Excel file) - and a lower GHG emissions coefficient for feed intake – see Table 46) is less than what can be gained by improved selection for core traits that contribute to GHG system efficiency (e.g., earlier slaughter), and/or increasing selection intensity and achieving greater adoption. The lower net benefit seen in gross terms, when comparing scenarios with

feed intake/methane yield/genomics for all traits to additional core traits, is not offset by increased output under emissions intensity calculations.¹⁹

Discussion

Along with the dynamics of trait responses, GHG emissions coefficients, and output, there are further contributing reasons for the above responses in environmental benefits. Firstly, the environmental benefits realised under the range of scenarios are entirely a result of selection on indexes that are driven by economic outcomes alone. These economic selection indexes are emphasising economic outcomes and do not drive selection to balance GHG emissions and economic outcomes. There are trade-offs (antagonisms) between positive environmental outcomes and positive economic outcomes.

Secondly, the divergent environmental outcomes in gross terms (in certain scenarios where it might be expected that environmental benefit would significantly higher), compared to economic outcomes, is partially the result of lower accuracy for feed intake and methane yield relative to other selection index traits (under genomic selection scenarios for all traits). When additional economic emphasis is placed on methane yield, as is done to emphasise the trait, the lower accuracy manifests in lower environmental benefits than the methane yield economic weight implies.

Future target accuracy levels for feed intake and methane yield are driven by the practicalities of reference population design, scale, and cost for these traits. While feed intake and methane yield offer the potential to drive further environmental benefits, potential scenarios that would increase the accuracy of these traits are likely to be cost prohibitive (diminishing returns). Therefore, the modelled accuracies herein are best combined with GHG-driven selection indexes, that balance economic and environmental outcomes, to inform the national phenotype and genotype collection programme for feed intake and methane yield.

¹⁹ Wall, E., et al. (2010). The potential for reducing greenhouse gas emissions for sheep and cattle in the UK using genetic selection. Commercial report by AbacusBio prepared for AHDB & Defra.

Metrics for monitoring progress

The purpose of this section is to identify and describe a range of metrics that could be used to monitor progress toward industry economic and environmental goals. Selected metrics will ultimately be used to measure the impact of AHDB/Defra and industry initiatives to enhance industry-wide rates of genetic progress and support greater contribution of genetics to industry economic and environmental goals.

To ensure suitability as an appropriate performance metric, adopted metrics must be:

- **Measurable** – data is available to support accurate and timely measurement or estimation of the target metric.
- **Relevant** – the metrics need to directly contribute to the desired outcome/s – increased industry value and sustainability via genetic improvement.
- **Under the control or influence of AHDB/Defra** – the metrics must be able to be influenced by AHDB/Defra strategies, activities, and investments.

Economic metrics

Primary metrics

Industry economic impacts are a function of the underlying industry-weighted genetic trend – driven by trait genetic trends per breed and industry structure (breed population size and type, mating structures, and differences in trait genetic trends between recorded and non-recorded populations) – and trait economic weights (creating dual-purpose/maternal and terminal selection indexes). The combination of these things produces the industry-wide annual rate of economic genetic gain (in trait units or £/all cows or ewes mated per year). The industry-wide annual rate of economic genetic gain – expressed as £/all mated females/year – represents the key primary indicator of the efficacy of the industry genetic improvement programme.

Aligned with the framework for accumulating impact within work package 1, the components of the industry-wide annual rate of economic genetic gain are presented in Figure 7.

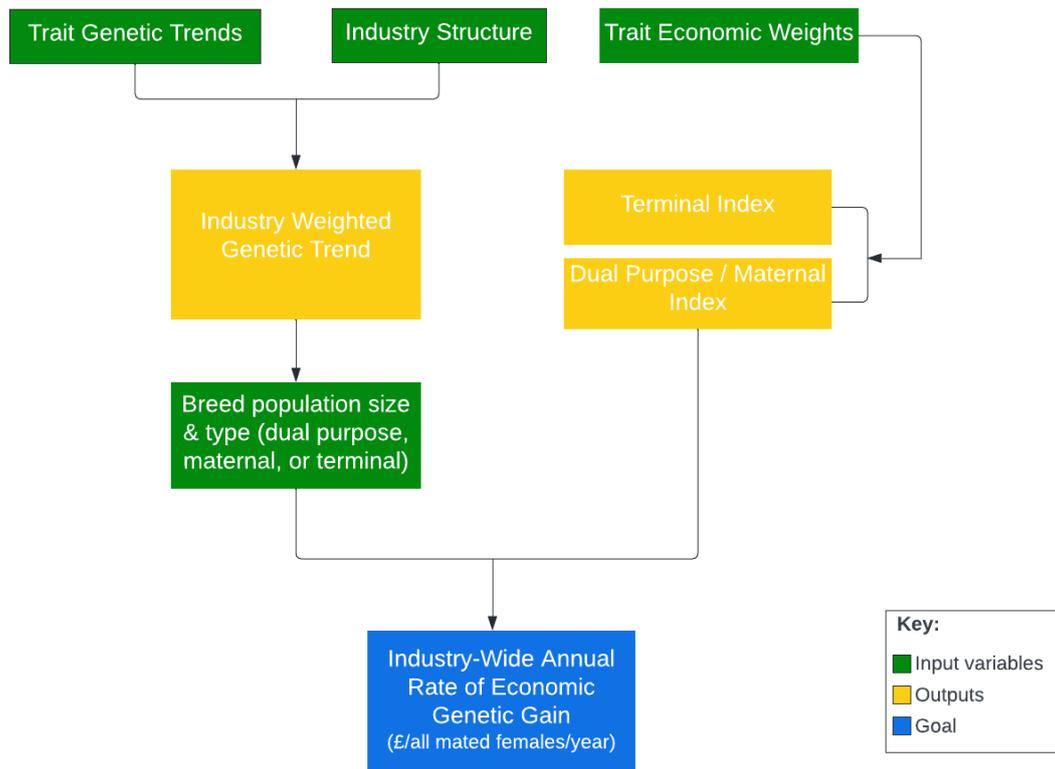


Figure 7 Computation of industry genetic trends and economic impact

To complement the use of the industry-wide annual rate of economic genetic gain as the primary performance indicator, secondary and tertiary indicators can support greater granularity and understanding of the underlying drivers of the primary indicator. The addition of secondary and tertiary indicators can also pinpoint opportunities to generate greater impact via the identification of areas where progress is sub-optimal.

Potential secondary and tertiary metrics

Based on Figure 7, the underlying industry-weighted genetic trends for the key trait represents obvious secondary metrics. These trends should be benchmarked over time. Trait genetic trends, by breed and benchmarked over time, could also be used as secondary metrics.

For simplicity, the genetic trend analysis could be restricted to major traits within key trait groups (e.g., fertility, growth, carcass, maternal and longevity, environmental etc.), or limited to the major 4-5 traits within the respective trait groupings (sub-indexes).

Whilst the use of these secondary indicators provides an excellent insight into the performance of the industry's genetic improvement nucleus (seedstock/pedigree breeders), there is opportunity to

integrate additional tertiary indicators to support greater understanding of underlying drivers of the observed trends.

Figure 8 highlights key tertiary factors associated with observed industry-wide annual rate of economic genetic gain (as the primary indicator). Drivers of the observed trait genetic trends reflect the different components of the breeder’s equation (selection intensity, accuracy of selection, genetic variation and generation interval), while influential aspects of industry structure include number and diversity of breeds, population sizes, and level of recording). Input to the trait economic weights include prices, costs, productivity and performance parameters, and market and social requirements).

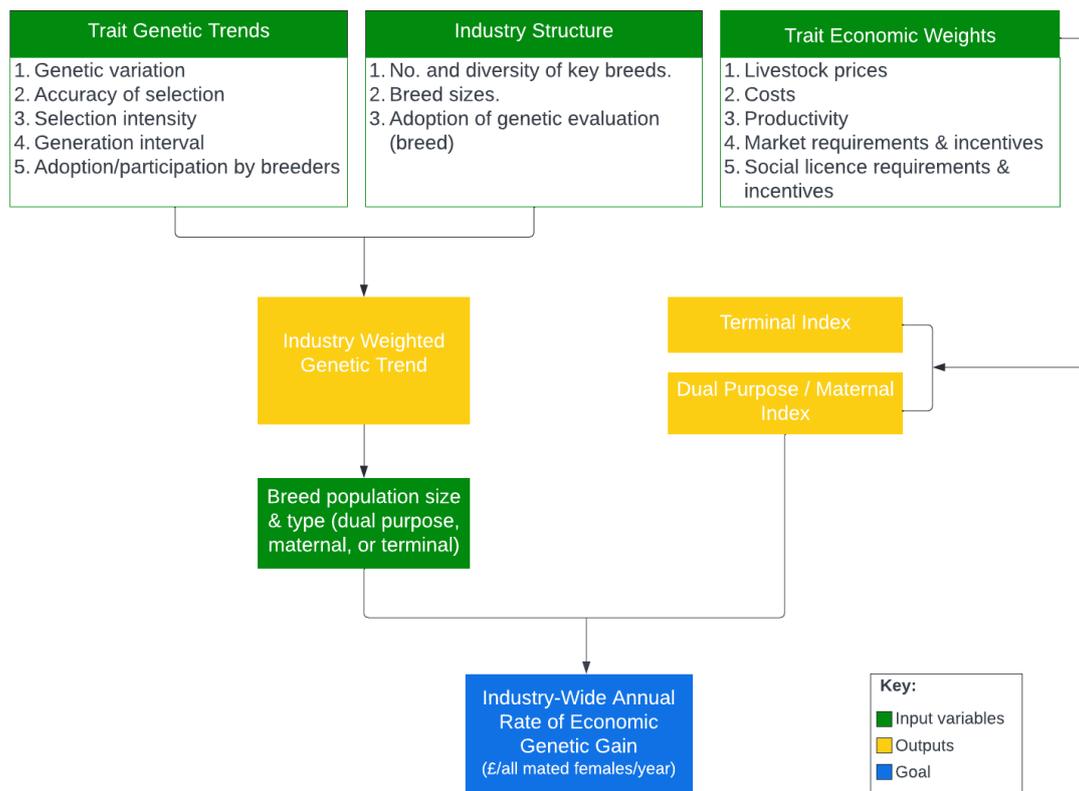


Figure 8 Key drivers of industry genetic trends

Table 16 describes recommended tertiary indicator metrics that could be utilized to better assess progress/impact within the primary and secondary indicators. The indicators presented in Table 16 are derived from an assessment of each potential tertiary indicator against the key characteristics identified (measurability, relevance, and control/influence). This assessment is presented in Appendix 4: Tertiary .

The proposed indicators are measured primarily within the pedigree sector as a proxy for genetic progress within the broader commercial industry. This reflects the complexity of accurately measuring genetic progress within the commercial industry (requires genomics and multi-breed evaluations) and

recognizes the traditional model of genetic dissemination from pedigree herds/flocks to the commercial sector (with a generational lag).

Table 16 Recommended tertiary metrics (economic impact)

Driver	Indicator/Metric	Rationale
Adoption/Participation	Numbers (or %) of herds/flocks submitting phenotypes and genotypes.	Good indicator of the adoption of best practice performance recording standards and broader participation across the pedigree sector.
Accuracy of selection	Average breeding value accuracy trends	<p>Good indicator of the efficacy of performance recording and genotyping programs. Also potentially highlights quality of genetic linkage within the underlying genetic evaluation system.</p> <p>It is a retrospective indicator that doesn't account for new phenotypes being collected for new traits. Nor does it highlight potential future challenges of declining phenotype/genotype volumes. Also requires perspective when comparing accuracy of different traits e.g., differences in heritability and influence of correlated traits/phenotypes.</p>
Accuracy of selection	Annual numbers of genotypes and key phenotypes submitted.	<p>Useful indicator to track contribution of phenotypes from sources additional to pedigree herds/flocks – e.g., reference populations, commercial data and research herds/flocks.</p> <p>Ultimately greater volumes of phenotypes/genotypes will increase breeding value accuracy.</p> <p>Secondary indicator of gaps and trends within performance recording programs – better snapshot than breeding value accuracy of potential future outcomes.</p>
Selection intensity	Percentage of calf/lamb registrations originating from recent top-ranked sires.	<p>Potentially a useful indicator for highlighting the influence of top genetics within the industry. This can serve as a general proxy or indicator for tracking trends in selection intensity.</p> <p>Likely to miss progeny from sires that enter the commercial herd/flock. As these commercial sires have effectively been lost to the genetic improvement nucleus this might be revealing and useful to track.</p> <p>Also revealing to track and highlight contribution of imported genetics versus elite domestic sires.</p>
Generation interval	Average age of sires for new calves/lambs.	Younger average sire age will contribute to shorter generation interval. Could also highlight greater use of AI and artificial breeding to accelerate access to new genetics, and faster turnover of sires.
Genetic variation	Standard deviation of key indexes.	<p>General indicator of genetic variation/diversity. Also, a potential indicator of the impact of new traits and increased breeding value accuracy to index variation and future progress.</p> <p>Provides good perspective to measured genetic progress (incremental change in average index value) by supporting expression as % of index SD.</p>

Economic impact framework

In the context of the influence of tertiary indicators presented in Table 16, adoption contributes far more significantly to the industry-wide annual rate of economic genetic gain and economic impact than the other tertiary indicators. This is visibly demonstrated within the assessment presented in Appendix 4: Tertiary .

To better reflect the relative importance of the proposed primary, secondary and tertiary indicators Table 17 presents the summarised economic performance indicator framework. This recommended framework incorporates the proposed adoption/participation metric as a secondary indicator to better reflect its influence on the industry-wide annual rate of economic genetic gain and economic impact.

Table 17 Recommended economic indicator framework

Indicator Type	Indicator	Performance Metric	Implementation
Primary	Industry-wide annual rate of economic genetic gain	£ of added profit for all mated cows/ewes per year	<ul style="list-style-type: none"> Will require development of generic national indexes with standard traits used across all/most breeds. Can break into sub-indexes that reflect common breeding goals and aggregate based on expected proportion of the industry adopting each sub-index.
Secondary	Industry-weighted genetic trend	Annual progress of key traits.	<ul style="list-style-type: none"> Can simplify by focusing on major traits common across all/most breeds. Can report trends based on specific trait units (e.g., kg/year for growth), and/or express as a % of a standard deviation to support comparison of relative progress across traits.
	Adoption	Numbers (or %) of herds/flocks submitting phenotypes and genotypes.	<ul style="list-style-type: none"> Should implement a system similar to BREEDPLAN's 'completeness of performance' ratings²⁰ to provide a more granular measure of overall participation. Metric should be reported and analysed by breed (and potentially additional demographic segments) to help identify gaps and opportunities.
Tertiary	Accuracy	Average breeding value accuracy.	<ul style="list-style-type: none"> For consistency and relevance this should be measured annually on each new cohort as it approaches mating age.

²⁰ <https://breedplan.une.edu.au/products/completeness-of-performance/#:~:text=The%20E2%80%9CCompleteness%20of%20Performance%20reports,informati%20could%20potentially%20be%20recorded.>

Indicator Type	Indicator	Performance Metric	Implementation
			<ul style="list-style-type: none"> For simplicity this can be measured on key traits across each trait group.
	Accuracy	Annual numbers of phenotypes and genotypes submitted.	<ul style="list-style-type: none"> Could be focused on phenotypes aligned to major traits (and novel/new traits) for simplicity. Could be reported as both annual and cumulative totals. Easy to record and report, could be expressed on a breed-basis to further highlight gaps/opportunities.
	Selection Intensity	Percentage of calf/lamb registrations originating from recent top-ranked sires.	<ul style="list-style-type: none"> Rankings can be derived from major indexes prior to first mating of each new bull/ram cohort, subsequently aligning with the sire IDs of calf/lamb registrations over next 2-3 mating seasons.
	Generation Interval	Average age of sires for new calves/lambs.	<ul style="list-style-type: none"> Easy to record and report. Could be expressed on a breed-basis or mating type to further highlight gaps/opportunities.
	Genetic Variation	Standard deviation of key indexes.	<ul style="list-style-type: none"> For simplicity this could utilize the generic indexes associated with the primary indicator, as opposed to the more niche indexes used at industry level.

Environmental metrics

Primary metrics

Figure 9 describes the current framework for measuring environmental impact. The framework is broadly similar to the economic impact framework (Figure 7). Final outputs include:

- Industry-wide annual rate of genetic gain in GHG emissions, in gross emissions terms expressed as CO₂e/all mated females/year.
- Industry-wide annual rate of genetic gain in GHG emissions in emissions intensity terms expressed as CO₂e/kg product/mated female/year.

These outputs reflect the need to monitor both gross emissions and emissions intensity and capture the objectives of both public stakeholders (reduced national GHG inventories) and the commercial industry and consumer (reduced emissions intensity of red meat products). Both metrics should be reported concurrently as primary environmental indicators/metrics.

It is important to note that the current environmental impact framework (Figure 9) is focussed on measuring the impact of the industry-wide annual rate of economic genetic gain on GHG emissions. It is likely that a future environmental impact framework will be driven by selection on indexes that

incorporate trait GHG emission coefficients and may need to monitor broader social, animal welfare and environmental outcomes. Consequently, the environment framework described in Figure 9 will evolve as the scope and focus of genetic improvement shifts further towards GHG emissions reductions and beyond.

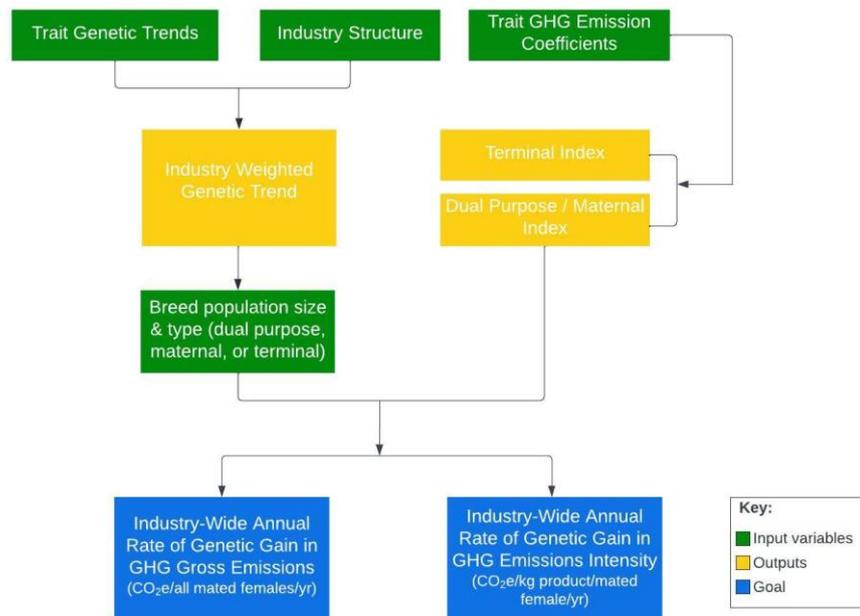


Figure 9 Computation of industry genetic trends and environmental impact

The environmental impact framework utilizes similar basic inputs (trait genetic trends and industry structure parameters) as the economic impact framework (Figure 7). The key difference revolves around the use trait GHG emission coefficients instead of economic weights. These GHG coefficients describe the change in gross emissions (CO₂e/mated female) and emissions intensity (CO₂e/kg product/mated female) per unit change in each trait.^{21 22}

Potential secondary & tertiary Indicators

Comparison of Figure 7 and Figure 9 demonstrates the significant overlap in inputs, outputs, and tertiary drivers that influence the annual rate of genetic gain in GHG emissions and environmental impact. As per Figure 9, the underlying industry-weighted genetic trends and adoption/participation

²¹ Wall, E., et al. (2010). The potential for reducing greenhouse gas emissions for sheep and cattle in the UK using genetic selection. Commercial report by AbacusBio prepared for AHDB & Defra.

²² AbacusBio (2018). Maternal and Terminal breeding objectives for the UK beef industry. Report prepared for SRUC.

will still form the key secondary indicators, these will subsequently be underpinned by the same tertiary drivers as the economic framework.

Whilst this largely supports the adoption of the same secondary and tertiary performance indicator framework as described in Table 17, several adjustments are required.

Reporting of industry-weighted genetic trends should recognize that key traits underpinning economic outcomes may be different to those that drive environmental impact. Furthermore, key traits (e.g., calving interval) may have antagonistic economic and environmental outcomes, whereby the trend for a particular trait may be economically favourable but environmentally unfavourable. Lastly, industry-weighted genetic trends for a given trait may produce divergent/antagonistic responses for the two primary environmental indicators (annual rate of genetic gain in GHG emissions in gross and intensity terms, respectively). Gross emissions are primarily driven by the relationship between a trait and feed requirements, whilst emissions intensity incorporates the relationship between a trait and broader output dimensions as well as feed requirements.

Consequently, the use of industry-weighted genetic trends as secondary indicators will require customization, to meet the needs of performance monitoring for both economic and environmental outcomes. This will impact both the scope of traits that are monitored and reported, and the structure of the reporting outputs, such that they can adequately reflect the different economic and environmental outcomes attributable to a specific trait.

It is important to recognise that the environmental impact framework will evolve over time, and this will require the addition of new indicators, particularly at the secondary and tertiary levels. The trait emissions coefficients currently reflect the underlying relationship between each trait and feed requirements. This incorporates fixed assumptions relating to both the level of feed intake required to support a unit increase in each trait, and the GHG yield attributable to a unit of intake. Future development of feed intake/efficiency traits and methane yield traits will need to be reflected in the emissions coefficients, as the addition of these traits will influence fixed assumptions/parameters. Future development of non-methane mitigation traits (e.g., traits targeting urinary/faecal nitrogen) will also require adaptation of the GHG coefficients.

Environmental impact framework

Table 18 describes the proposed environmental indicators that could be applied to monitor progress toward industry environmental goals. As previously described, this framework utilizes the same secondary and tertiary indicators as the economic indicator framework (with customization to reflect the potentially divergent economic and environmental outcomes). This framework also reflects the current scope of environmental impact monitoring and will require adaptation as industry needs and genetic improvement capability evolves.

Table 18 Recommended environmental indicator framework

Indicator Type	Indicator	Performance Metric	Implementation
Primary	Industry-wide annual rate of genetic gain in GHG emissions, in gross emissions terms	CO ₂ e/all mated females/year	<ul style="list-style-type: none"> Utilises the same indexes and sub-indexes as the economic framework. Output may not reflect outcomes within national GHG inventory if herd size is expanding.
	Annual rate of genetic gain in GHG emissions, in intensity terms	CO ₂ e/kg product/mated female/year	<ul style="list-style-type: none"> Utilises the same indexes and sub-indexes as the economic framework. Output may not reflect outcomes within national GHG inventory if overall production is growing at a faster rate than the improvement in intensity.
Secondary	Industry-weighted genetic trend	Annual progress of key traits	<ul style="list-style-type: none"> As per economic impact framework. Ensure reported traits reflects key drivers of environmental outcomes. Ensure reporting reflects potential divergent economic and environmental outcomes for specific traits.
	Adoption	Numbers (or %) of herds/flocks submitting genotypes & phenotypes.	<ul style="list-style-type: none"> As per economic impact framework.
Tertiary	Accuracy	Average breeding value accuracy.	<ul style="list-style-type: none"> As per economic impact framework. Ensure reported traits reflects key drivers of environmental outcomes.
	Accuracy	Annual numbers of genotypes and phenotypes submitted.	<ul style="list-style-type: none"> As per economic impact framework. Ensure reported phenotypes reflects traits that are key drivers of environmental outcomes.
	Selection Intensity	Percentage of calf/lamb registrations originating from recent top-ranked sires.	<ul style="list-style-type: none"> As per economic impact framework.
	Generation Interval	Average age of sires for new calves/lambs.	<ul style="list-style-type: none"> As per economic impact framework.
	Genetic Variation	Standard deviation of key indexes.	<ul style="list-style-type: none"> As per economic impact framework.

WP2: Industry consultation and assessment of the most appropriate genetic improvement programme

Introduction

The objective of Work Package 2 was to identify the most appropriate industry genetic improvement programme for the UK sheep and beef sector.

Firstly, a process of defining what good looks like was undertaken. The aim was to identify critical aspects of a successful genetic improvement programme, needed to deliver both industry and government policy requirements.

A process of industry consultation, supported by information from the definition of what good looks like, was used to define a set of the potential future options for a genetic improvement programme in varying, improved, forms.

Finally, through further stakeholder engagement, a quantitative assessment of potential options was undertaken.

A genetic improvement programme for the future

Industry consultation

Industry consultation was carried out to support the definition of what good looks like, and to identify appropriate potential industry genetic improvement programme options for the UK sheep and beef sector in 10 years' time. A summary of the approach and responses from 35 interviews with people from the UK beef & sheep industry is provided below.

Approach

For this information gathering, targeted interviews (35) were conducted across a range of "user types". These were represented by commercial breeding companies (5), levy boards (4), beef and sheep farmers (5), livestock specialists (7), food service/retailers (8) and breed societies (6). A series of questions were developed after discussion of the needs specific to the type of questions to be asked. The final set of questions comprised a combination of open questions, without constraints on how they be answered, and quantitative questions. All interviews were carried out using video calls. Questions put to the interviewees and the full consultation outcomes can be found in Appendix 5: Industry consultation – structured interviews. Data from the structured interviews can be found in Supplementary material 3: Responses from structured interviews (Excel file).

Key findings

Sheep and beef farmers face challenges in the next ten years related to net zero and wider environmental impact, greater pressures on profitability and efficiency (e.g., loss of subsidies), staff

recruitment and retention, and the messaging of anti-livestock product groups. They all saw genetics as part of the solution to such challenges.

- Future systems must:
 - use a common language for genetic merit (“plain English”),
 - translate genetic information into simple, practical ratings of worth, linked to farm key performance indicators (KPIs). Visual depictions of data would help more people use genetic information,
 - have a strong Knowledge Exchange system at its core, supported by a network of genetic specialists,
 - eliminate complexity and duplication to reduce confusion,
 - use a single data system, independent of genetics service providers, but with data ownership at its core. This should be used to
 - set up data integrity checks to improve data quality,
 - produce a single national evaluation for each livestock type to produce “national estimates of merit”,
 - generate genetics benchmarks,
 - allow groups to conduct other evaluations as part of their differentiated breeding programmes,
 - capture and use commercial data e.g., abattoir data,
 - widen definition of overall merit to include all traits with a major effect on farm performance, through adding in “hard to measure” traits,
 - make information more accessible in more places, with intuitive tools for examining information,
 - not try to be fair to everyone and back “winners” committed to genetic improvement,
 - learn from the poultry, pig & dairy sectors who have exploited genetic improvement to a much greater degree.

There was universal agreement to share data where there was mutual benefit. A range of views were held regarding the value of current services, from poor to very good. Awareness of overseas systems was good but not universal.

Overall, the responses obtained show an appetite for change, coupled with a preparedness to work together to deliver that change. All thought that current systems were not delivering to their potential and that the fragmented nature of genetic services provision was part of the problem, confusing ram and bull buyers and failing to make the best of available data. The key findings above were used, along with a review of international genetic improvement programmes (see Supplementary material 2: International genetic improvement programmes (Excel file)), to define what good looks like.

What does good look like?

Critical aspects were identified from industry consultation and by exploring genetic improvement programmes internationally and noting common themes in the strengths and weaknesses of each system. A summary of the international systems has been provided in Supplementary material 2: International genetic improvement programmes (Excel file). Beyond these critical aspects, there can be varying levels of ideal depending on the industry and its structure. The definition of these critical

aspects focused on the UK, using knowledge of the agricultural sector and the role of a service provider in delivering a new genetic improvement programme.

Critical aspects of a successful genetic improvement programme for the UK are detailed below.

Governance

Given the likely requirement for an industry and/or government owned genetic improvement programme, an effective governance framework is critical to realisation of the full benefits of genetic improvement. Consequently, there is a need to implement a governance framework that can guide transparent and responsive delivery of genetic improvement services to the livestock industries.

A potential best practice model would feature a governance board involving representatives from the owners/funders, key stakeholders, and technical experts. The board would be supported by advisory and consultation groups. The key role of the board would be to oversee the:

- Delivery of genetic evaluation capability, using a common platform, to the industry.
- Running of core national evaluations for industry wide benchmarking.
- Development of the data and genetic evaluation infrastructure.
- Identification of investment priorities for the supporting research, development, and adoption programmes.

Through genetic improvement the performance of the entire commercial supply chain can be improved, including but not limited to, commercial farmers, processors, retailers, society, etc. This governance framework needs to be broader than the primary users of genetic improvement services (e.g., pedigree/seedstock breeders and breed societies) and must support representation and engagement with key stakeholders along the livestock value chain. This will help ensure the system is aligned to the needs of the broader commercial industry. In addition, effective governance also requires appropriate technical expertise and recognition of extension/adoption experts to ensure the delivery of genetic improvement services is technically robust and has an embedded focus on commercial adoption.

Funding and customers

Funding

Ultimately, the objective should be for a largely user-pays system that can minimise reliance on industry levy or government funding to support routine service delivery. Internationally there are examples of genetic evaluation services that are self-funded (e.g., major US beef industry evaluations), or are self-funded for service delivery, KE, and basic maintenance/development, with reliance on levy or government funding to support R&D or major infrastructure development (e.g., ICBF). The level of self-funding that could be achieved within the UK is uncertain, given the relative size of the livestock industry compared to other markets. User fees need to be internationally competitive and benchmarked against equivalent user-pays services. Funding for supporting R&D and KE, plus major infrastructure development projects could be pursued through Industry/levy bodies and/or

government – this underlines the importance of an effective overarching governance framework to identify investment priorities based on industry need/opportunity and communicate these to funders.

Customers

Customers paying for the genetic improvement service should be the end user; UK pedigree/seedstock and commercial farmers. Many international examples incorporate breed societies as the primary customer for genetic evaluation services, subsequently on-charging fees to members as part of their overall membership and registration fees. This model is sub-optimal, lacking transparent participation costs for end users and in some cases, mandating breed society membership for farmers to receive genetic improvement services. Engaging directly with end users is preferable, decoupling participation from breed society membership and animal registration requirements. This can support broader participation particularly among commercial farmers whose herds/flocks may not currently meet breed society registration requirements. Breed societies can still be engaged in a support, coordination, or breed promotion role, similar to the bureaus in the New Zealand sheep industry or beef breed societies in Ireland.

Genetic evaluation system and key infrastructure

Genetic evaluation system

Optimal genetic improvement in the future is likely to require a genomic-based evaluation that incorporates a modern single step system to maximise the value of underlying genotypic and phenotypic data. This is particularly the case for strategic traits of interest that can deliver solutions to the climate emergency, which are hard and costly to measure. There is a need for ongoing development/enhancement of the system to incorporate the latest genetic evaluation methodologies/models. Hence, the capacity to fund and resource the ongoing development of the platform is critical. Underlying trait modules need to be robust and suitable for use within a sophisticated, multi-trait analysis and underpinned by genetic parameters (heritability and, variance/covariance estimates) derived from UK datasets.

The genetic evaluation should ideally support the evaluation of crossbred animals and be a multi-breed analysis. Whilst technically challenging, this supports user adoption by identifying elite genetics regardless of breed and can support extension to commercial herds where untapped opportunity exists to utilise genomics in commercial herds (and support greater capture/use of commercial data).

The genetic evaluation should also consider opportunities for international alignment (e.g., Interbeef), reflecting the ongoing importance of import and export of genetics. This will need to consider permissions/protocols for exchanging data, animal identification systems, and development of traits/definitions that can support international compatibility.

Core traits

There is a strong incentive for a standardised set of core traits. These traits need to be relevant to, and aligned with, UK users and the broader UK industry needs, such that they will drive adoption. Standardised traits reduce complexity and promote understandability for end users by ensuring greater consistency of language, metrics, and definitions. Standardisation requires standardised trait definitions (e.g., consistent definitions of fertility traits), standardised trait units and standardised protocols for collection and processing of phenotypic data. Given this, there is also potential for greater efficiencies within industry data pipelines through economies of scale and enhanced data volumes, leading to more robust parameter estimations and more accurate genetic merit predictions. Efficiencies also exist for delivery of R&D and KE activities whereby phenotyping/genotyping programmes can be more easily scaled up and integrated with routine evaluation. Addition of new traits to the core trait panel (including redevelopment and enhancement of existing traits) should be addressed through the R&D pipeline and prioritised in accordance with established investment prioritisation frameworks/processes.

Novel/custom traits

Whilst a standardised set of core traits is desirable, care needs to be taken to ensure that specific groups of breeders and specific industry segments can develop and implement novel/custom traits to meet their unique requirements and/or differentiate themselves. This is an important source of innovation in the genetics value chain. User dissatisfaction and fragmentation is a key risk emanating from a rigid approach to standardisation. The key challenge is to ensure there is flexibility to support novel requirements but ensure that this does not unnecessarily erode the robustness of the genetic improvement programme/genetic evaluation or undermine the benefits of a largely standardised approach. Responsibility for funding the development and implementation of novel/custom traits also requires consideration. This issue highlights the critical role an effective governance framework provides for evaluating the technical, commercial, and strategic basis for customisation and innovation.

Infrastructure

To support standardisation and avoid inefficiencies associated with data being stored across isolated, incompatible data islands, there is a requirement for either a centralised database or a centralised data repository that can efficiently access data from separate databases via application programming interfaces (APIs - clearly defined methods of communication between various software components). A single centralised database is simplest and most efficient, but could be difficult to establish due to commercial, structural, and data ownership considerations. The ability to pool large volumes of phenotypic and genotypic data centrally is critical to the genetic evaluation and to breeding value accuracy. This also supports simplification for key users and consolidates data for research purposes.

It is important that the capability and resources exist to maintain and develop the database infrastructure into the future. A model where maintenance and development can be strategically outsourced allows industry to avoid bottlenecks, enabling users to access new features and

customisations more readily. To manage data quality and make the best use of the data available, it is crucial that a state-of-the-art database infrastructure (including APIs) is available. This is particularly important if collaborative arrangements allow integration with other national and industry databases.

Data pipelines

Phenotypic and genotypic data underpinning the genetic evaluation will be collected/submitted from several key sources:

- Genotypes either directly from herds/flocks or from genotyping laboratories.
- Pedigree/seedstock data collected within pedigree/seedstock flocks/herds (e.g., weights, birth dates and other standard phenotypes) or by service providers (e.g., ultrasound scan data).
- Reference herd/flock data that is collected from coordinated progeny test or reference herd/flock programmes that are undertaken to support collection and scaling up of hard-to-measure phenotypes (e.g., feed efficiency, methane emissions, and carcass), generating genetic linkage and commercial benchmarking.
- Research herd/flock data that is collected to evaluate novel research phenotypes (e.g., methane phenotypes) to understand potential to scale up into breeding traits.
- Commercial and supply chain data could be evaluated for inclusion within genetic evaluation datasets in the future, subject to appropriate R&D.

This will require appropriate collection, submission and processing protocols that are appropriate for the key data sources, in particular data collected directly from farms. Ease of collection/submission of farm data is a priority, particularly given the direct interaction with farmers as end users under this preferred model. Investment in online portals and user interfaces is vital for ease of collection and submission. Resourcing requirements to simplify data processing and submission requirements for data originating from pedigree/seedstock and commercial farms should also be considered. The objective should be to simplify the collection and submission of farm-level data to encourage more farmers to performance record, even if this creates a level of resourcing burden associated with the processing of this data.

Using a single point of data entry minimises duplication, time, and errors that can occur when there are numerous data entry points. This approach streamlines the data entry process, minimising the need for integration software to collect data from multiple sources which aside from being costly, adds to the complexity of the system and has potential to create unnecessary challenges.

Pipelines must also consider the ease of accessing and retrieving data, particularly to support Research, Development and Extension (RD&E) activities (see below).

Data ownership & access

Ultimately data should be owned by the animal owner(s). However, there is a need to consider broader data access permissions to support use of data for R&D and KE activities. This is particularly important when new data is generated by the merging of existing data from different owners.

Enhanced genetic improvement outcomes require continual investment in R&D that is contingent on access to high quality data. The genetic evaluation data pipeline must have mechanisms for data to be readily shared with research organisations, with sensible/workable protocols regarding the associated permissions, IP ownership and usage restrictions. The goal should be to ensure data is available for industry-good R&D but with appropriate protections to prevent unlicensed commercial exploitation of private data. Legislation may be required to support and promote data sharing, while standards of recording and data sharing protocols will also be important.

Service Delivery

Genetic Evaluation Services

The core service revolves around the delivery of genetic evaluation information to customers (pedigree/seedstock and commercial farmers) and the broader industry. This requires the delivery of routine 'runs' to update breeding value and index information for the population that incorporates the latest genotypic, pedigree and phenotypic data.

Standard run frequency varies internationally from quarterly, monthly to weekly, where greater frequency is desirable but carries obvious resourcing constraints. Some international platforms that operate in conjunction with breed societies can stagger their scheduled runs, but this may not be possible under a multi-breed analysis.

In addition to the core genetic evaluation service, there will also be a need to develop and provide selection indexes to support the use of genetic improvement information. Indexes should be established for major national production systems and supply chains; however, the development of custom indexes could also be provided to support specific contexts (but potentially withheld from the general evaluation service).

There are also requirements to consider broader tools and services such as mating optimisation systems to manage inbreeding trade-offs, sire finder/selection tools, and tools for managing deleterious recessive conditions etc.

Reporting and benchmarking

Genetic evaluation data from each run can be released through online portals with both standard and customisable reports. The portal needs to be accessible to both member/participating owners (pedigree/seedstock herds/flocks or participating commercial farmers) and non-member/non-participating farmers seeking information to support stock purchases, acknowledging that these users will have different levels of access and information offered.

Reports and public data should extend beyond traditional delivery of breeding values and indexes to include objective benchmarking of herd/flock breeding values, national statistics, genetic trends/progress, and data quality/completeness, where appropriate comparisons can be made (i.e., depending on genetic connectedness and/or accuracy, for example). Public interfaces/portals should enable users to search/filter pedigree/seedstock herds/flocks by these performance benchmarks.

Industry impact relies on adoption by commercial farmers (as participants or users). Consequently, there is a need to consider how to leverage the national genetic evaluation to better support and engage commercial farmers. This requires provision of tools and interfaces that simplify access to the core information that commercial farmers need; that being, the identification of optimal sire genetics for their enterprises. Additional opportunities to add value to commercial participants (rather than user) enterprises could comprise:

- Herd profile (inventory, management stats, annual averages of key metrics).
- Genetic evaluation of the cow herd/ewe flock.
- Benchmarking/analysis of commercial herd/flock genetics.
- Analysis of herd/flock breed composition.
- Providing the opportunity for sire information and commercial genotypes to support QA programmes, compliance requirements etc. Recording/data completeness/quality score for each breeder flock/herd.
- Commercial tools and benchmarking reports to support marketing of calves/lambs to finisher farmers and processors.

A strong overarching governance framework should actively target opportunities for greater relevance and value-add to commercial users.

User support

User support is considered as a separate requirement from broader industry adoption programmes that seek to promote and encourage the use of genetic evaluation information and tools by pedigree/seedstock breeders and commercial farmers.

User support is focussed on the provision of support to existing users of the genetic evaluation service and is generally the responsibility of the service provider. This broadly captures the provision of support to users in:

- Collection and submission of phenotypic and genotypic data.
- Use of online portals and interfaces.
- Use of online tools.
- Integration with on-farm recording software/equipment.

In addition to the above, subject to the scope of services provided by the service provider, there could be a requirement to provide more customised support to individual herds/flocks around the use of mate allocation systems and custom selection indexes.

There is potentially also an opportunity for the service provider to deliver a broader range of complementary services, e.g., the provision of online sale catalogue services for seedstock breeders, that can support additional revenue streams. Competition between the providers of data of the service provide and the service providers would need to be managed, in this context.

Research & development and knowledge exchange

Phenotype and genotype collection programmes

There is a compelling argument for a centrally coordinated approach to the development of phenotype and genotype collection programmes (reference herds/flocks) to support:

- Collection of phenotypes and genotypes for traits that deliver solutions to the climate emergency (e.g., feed efficiency and methane traits) and adaptation (e.g., longevity, fertility, and heat tolerance), as well as broader social licence challenges (e.g., traits to support enhanced animal welfare outcomes).
- Enhanced sire progeny testing and benchmarking to improve breeding value accuracy on emerging industry sires.
- Enhancing genetic linkage across herds, breeds (for development of multi-breed evaluations) and international populations.

Central coordination of these phenotype and genotype collection programmes is required to ensure subsequent delivery of new trait modules and infrastructure within the national genetic improvement programme and national evaluation. Cost efficiencies from combining reference populations (where practical) and technical oversight, are also generated through a centralised approach. Finally, central coordination also ensures these programmes are implemented on a timely basis in accordance with industry needs, as opposed to being implemented and controlled by third parties (breed societies and breeding companies etc).

Design, prioritisation, and oversight of these programmes can fall within the remit of the governance body and its relevant advisory groups, in collaboration with AHDB/Government (as a key funder of major R&D, phenotype and genotype collection programme, and KE initiatives) and its research partners.

Applied research

There is a strong requirement for a centrally coordinated approach to applied research activities for the same rationale as above. This would incorporate central coordination of research and development associated with:

- Novel traits and gene discovery research.
- Novel phenotyping strategies and systems.
- R&D associated with the genetic evaluation infrastructure.
- Genotyping and sequencing platforms.

Design, prioritisation, and oversight of these programmes can fall within the remit of the governance body and its relevant advisory groups, in collaboration with AHDB/government (as a key funder of major R&D, phenotype and genotype collection programme, and KE initiatives) and its research partners.

Industry KE programmes

To realise the benefits of a national genetic improvement programme and evaluation and its supporting R&D programmes, there is a critical need for a well-resourced and independent knowledge exchange/adoption programme.

This programme should be focussed on engaging both pedigree/seedstock herds/flocks and commercial producers to:

- Promote the benefits of genetic evaluation as a fundamental strategy to underpin improved economic and environmental performance on farm.
- Support user understanding of the application of genetic evaluation information and associated tools.
- Support greater pedigree, seedstock and commercial understanding of genetic improvement, and its role and application within broader livestock management.

In addition to pedigree, seedstock and commercial farmers there is also a need to promote the value of genetic improvement to broader members of the supply chain to support greater engagement and increase market pull. Different messaging and information format will be required for the different target audiences.

Knowledge exchange/adoption programmes need to be aligned with the broader national genetic improvement strategy and delivered by an independent, industry-good organisation to avoid stakeholder concerns about real/perceived conflicts.

These programmes should include both a recurrent investment in the delivery of routine knowledge exchange/adoption services (e.g., regular industry meetings to update, understand, consult), with flexibility to pursue larger, targeted programmes as required. Investment into larger, strategic programmes should be identified and prioritised by the overarching governance framework.

As part of KE, there should also be a focus and framework for validation of the outcomes of a national genetic improvement programme especially for novel traits linked to environment impact reduction. For example, methane traits driven by genomic evaluation will likely rely on somewhat lower quality phenotypes. Reasonably large scale and powerful validation efforts will be critical to recognition of these genetic gains, as part of any support or legislative schemes.

Futureproofing

Data integration as a national asset

Development of a national genetic improvement programme and evaluation needs to consider the use of the data infrastructure for applications broader than genetic improvement of seedstock and commercial livestock. In addition, there is a requirement to consider opportunities to link the genetic

evaluation to other large industry databases (e.g., supply chain databases, health records, GHG inventory) to support greater volumes of phenotypes/data for use within the genetic evaluation.

Development of the genetic evaluation infrastructure and associated data pipelines needs to consider both current and future opportunities to integrate with other key industry databases.

Due to the ongoing evolution of genetic evaluation systems/models, it is vital to recognise the importance of futureproofing to ensure the platform can adapt to future opportunities and is agile enough to allow rapid upgrades to processes.

Sustainability and social licence

With a focus on farm sustainability and the climate emergency, as well as broader social licence challenges (e.g., animal welfare), there is opportunity for data captured within a national genetic evaluation to be leveraged across these areas. Examples include:

- Using phenotypic data (on sires, or samples of commercial animals) to inform more accurate assessment of GHG emissions inventories at both national and individual herd/flock levels.
- Development of environmental traits and indexes within the national genetic evaluation can form the basis of industry GHG inventory and GHG emissions reduction programmes.
- Genotypic data can be used to support/verify animal movements/origins for traceability and GHG auditing, as well as validating animal status for welfare purposes (e.g., horn/poll status, resistance traits etc).

To support opportunities to leverage the national genetic evaluation for these emerging purposes, it is important that the development of the national genetic evaluation infrastructure considers:

- IP, data ownership and data access barriers that may need to be addressed to support broader use of the national genetic evaluation.
- Connectivity with other key data sources, in particular national animal movement and identification database systems.
- Potential data pipelines that may be required to support these uses.
- Customer and service delivery models that may be required to support these uses.

Provenance and quality assurance

There is also opportunity for the national improvement programme and genetic evaluation to support provenance and quality assurance programmes. Examples include:

- Verifying breed composition or sire for breed-related product branding.
- Verifying herd/flock of origin.
- Verifying traits and gene status.

As above, development of the national genetic improvement programme and evaluation needs to consider how to support these alternate uses.

Options for the future

A set of future genetic improvement programme options (including all aspects of the programme from infrastructure to knowledge exchange systems) were developed. The options were informed by findings from industry consultation (outlined above and Appendix 5: Industry consultation – structured interviews), a review and assessment of global programmes (Supplementary material 2: International genetic improvement programmes), the definition of what good looks like, and a structured approach to building the range of possible levels across the options i.e., future options can range from enhancements to the current system through to a major overhaul, with each step on the complexity scale offering a different complexity and potential value to the industry. The existing genetic improvement programme (the *status quo*) was considered when building the options. However, the options were developed, presented and reported in generic terms. That is, the options did not consider, qualify, or quantify if and/or how existing industry stakeholders (e.g., suppliers, societies, or R&D organisations among others) would integrate into, or contribute to, a potential future genetic improvement programme. The integration of existing industry stakeholders and/or the definition of how they may contribute to a potential future genetic improvement programme would form part of a formal business plan to deliver any potential future genetic improvement programme.

Delivering genetic improvement of the national herd/flock will require the coordination of existing resources and the investment in new. What the overall genetic improvement programme should look like depends on the current genetic improvement programme, the complexity to build and maintain different future genetic improvement programme (including investment), the potential value of different levels of development, and the trade-off between these factors.

Outlined below are four levels (options) of genetic improvement programmes for the future, alongside the *status quo*, and a detailed outline of the approach used to evaluate these options, using a value-ease analysis. Each option, beyond the *status quo*, represents a cumulative level of improvement to the genetic improvement programme.

Status quo

Currently, sheep and beef both achieve a level of genetic improvement because of various initiatives and tasks led by AHDB, SRUC and Defra in conjunction with, or in complement to, breed associations, government agencies, interest groups and individual farmers. This approach can be characterised as "dispersed" genetic improvement activities with the industry being served by several platforms with farmers having access via breed societies, directly, or through private providers (breeding companies).

Beef tends to collate national data for specific projects only and genetic improvement efforts are otherwise largely siloed (by farm, breed society, group etc.). Genetic improvement is more centralised in sheep with more frequent centralised genetic evaluation runs and ability for progeny testing but is still limited to a small proportion of the national flock. Data recording procedures are well laid out for both species and herd profile and genetic evaluation reporting is available to paying members.

Option A: Status quo supported by R&D

The 'status quo supported by R&D' option builds upon the current programme and aims to fill some of the gaps that effectively deliver national genetic improvement. The primary developments are concerned with involving commercial farmers in the two-way flow of information i.e., commercial farmer data submitted to national evaluations easily and evaluation, herd profiles and knowledge transfer returned. Abattoirs are another entity included, to add data to carcass evaluations. The development and leadership of an all-industry RD&E programme will underpin the link with the commercial farmer. This RD&E would be centrally managed and led.

Option B: National genetic improvement infrastructure - existing platform

Further additions to infrastructure include bringing national genetic evaluations to one platform. In this instance, the service platforms (providers) currently used would be examined and through data collation and organisation, by a newly created industry-good governing entity, engaged to deliver genetic improvement. The genetic evaluation development within this option would include genomics and all parameters that lead to a successful genomic evaluation. Data for the evaluation is collated from other individual databases (breed associations, breeding companies, research databases) rather than collected, stored, managed and governed in a central database (unlike Option C below). This will, pending data availability, include commercial and crossbred data. The newly created industry-good governing entity would be responsible for publishing breeding values making them available to herds and flocks with commercial animals and the knowledge transfer activities required to utilise generated genetic evaluation results.

Option C: National genetic improvement infrastructure - UK platform

The primary development in this option is the creation and management of genetic evaluations in-house (and under the control of newly created industry-good governing entity). The advantages of owning the genetic evaluation in-house are many but chief of these is the ability to add new traits when desired, run more routine evaluations, increased transparency in the process and the opportunity for across breed comparisons (if required). A secondary development over the previous option is the way in which data is collected and stored. In this option, data resides in a centrally controlled database and standing operating procedure and pipelines are in place. Again, knowledge transfer must be optimised to reflect new changes and deal with increased volume of detail being generated for producers to utilise.

Option D: Full national genetic improvement programme & integrated infrastructure

Option D adds progeny testing, breeding programmes (elite herds recruited), advanced R&D, linking with third party databases (health and welfare, traceability, GHG inventories) and advanced genetic improvement tools (mate allocation, inbreeding, cull indexes etc.)

Value-ease analysis

Approach

All the previously detailed options have varying degrees of conceivable value to offer, and different degrees of deployment and maintenance ease (or conversely, difficulty). A structured framework for scoring the options against key drivers of a successful genetic improvement programme was developed. A value-ease scoring evaluation of these options was used to identify the most appropriate option for the UK. Full details of the value-ease scoring evaluation are provided in Appendix 6: Genetic improvement programme assessment framework. This process of value-ease scoring included four main steps, detailed below.

- v) Illustration of the options and their individual features/elements.
- vi) Evaluation criteria for both value and ease dimensions were assigned (through external expert consultation – details found in Supplementary material 4: Stakeholder questionnaire for weighting of criteria and scoring of options (Word & Excel file)) a level of importance.
- vii) All options were scored against the value and ease evaluation criteria (through further external expert consultation – details found in Supplementary material 4: Stakeholder questionnaire for weighting of criteria and scoring of options (Word & Excel file)).
- viii) Value-Ease calculated by combining criteria importance (weighting) with the scores for each option.

Results

The scaled and weighted scores are plotted in Figure 10. The trade-off between value drivers and ease of implementation drivers is small, given all options are positioned in the upper right quadrant. This implies that these options offer value to the industry and can be implemented with relative ease. There is significantly more spread in the value offered by different options than there is in ease with which they can be deployed and maintain. A detailed summary of the weights (for criteria) and scores (for options) is presented in Appendix 6: Genetic improvement programme assessment framework. also presented along with the scaled and weighted scores, as defined by the project team.

The value-ease analysis suggests that there is significant value to be gained by enhancing the genetic improvement programme for sheep and beef in the UK. This is particularly apparent for options that build a national genetic improvement infrastructure with an existing platform (option B) or a national

genetic improvement infrastructure with a UK platform (option C). There is a perception that less additional value is created by progressing to a full national genetic improvement programme and integrated infrastructure (option D). Option A (*status quo* supported by R&D) falls into the lower quadrant for its value to the industry. The simpler, smaller development proposed under *status quo* supported by R&D (option A) is considered the easiest to implement and manage. Almost no further decrease in ease of implementation and management is seen when progressing to option B. The scale of decrease in ease of implementation and management is near equivalent for progression from option B to option C and option C to option D.

Based on the value-ease analysis alone, option C would be the most appropriate model to take forward into further development and business planning (high relative value to industry and easier to implement and manage for the value gained, compared to option D). However, option B performs well in terms of value to industry, with very little decrease on the ease scale, relative to option A.

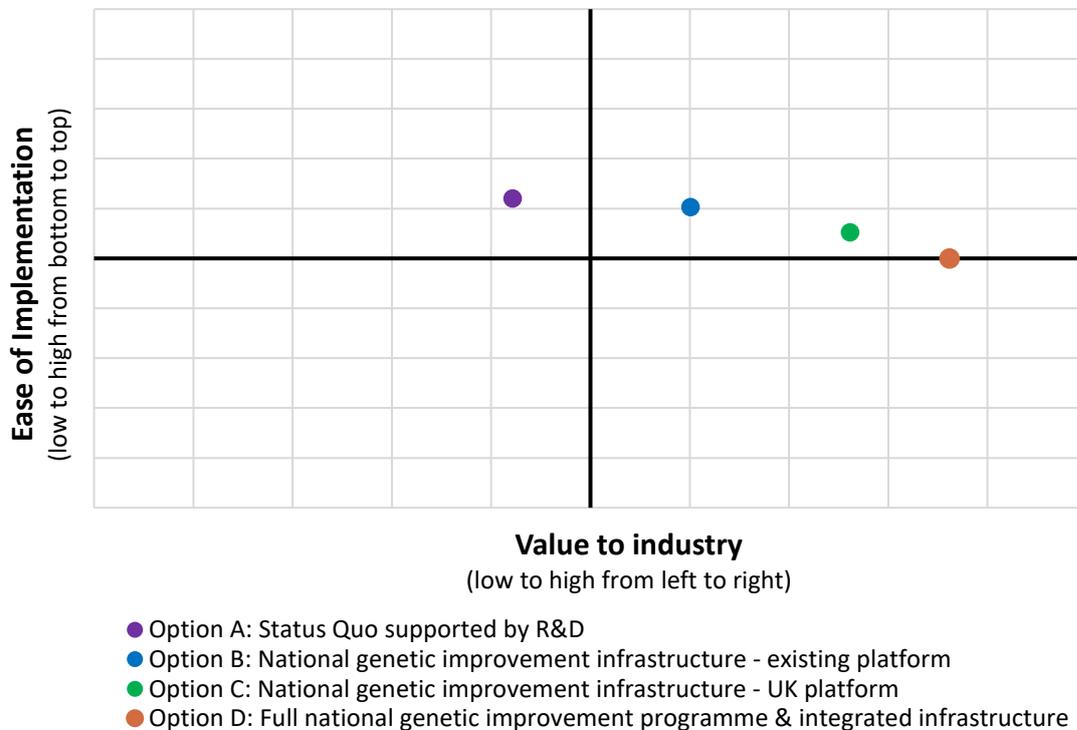


Figure 10: Value ease matrix for 4 potential genetic improvement programmes, as assessed by stakeholders.

WP3: Cost-benefit analysis of potential national phenotype and genotype collection programme

Introduction

Work package 3 aims to establish the potential, through a cost benefit analysis, of a national phenotype and genotype collection programme to deliver government and industry sustainability and environmental objectives. The approach focuses on the use of centralised 'reference populations' of herds/flocks to support the generation of progeny for genotyping and phenotyping via a structured progeny test model.

The model is well established within dairy breeding programmes to support identification of high accuracy, daughter-proven sires and, more recently, to facilitate collection of genotypic and phenotypic data for genomic evaluation. Use of reference populations within sheep and beef genetic improvement programmes has evolved more gradually, but is now increasingly implemented to support:

- Development of training and validation datasets to expedite implementation of genomic evaluation systems,
- Collection of phenotypic data for traits that are hard to measure in pedigree herds/flocks (e.g., carcass traits and novel phenotypes such as feed intake and methane emissions), and
- Strengthening of genetic linkage and connectedness both within and across breeds by supporting head-to-head comparison of progeny cohorts under common environmental conditions.

Design of the reference population programme will require the balancing of several operational aspects, including:

- Optimising the volume and quality of the collected phenotypes to support rapid development of new traits at desired accuracy,
- Ensuring appropriate representation of the industry gene pool and the scale required to achieve that representation,
- Budget/funding, technical resources/capacity, and logistical constraints linked to programme size and scope, and
- The burden on participating farmers in collecting the number and range of phenotypes in their breeding herds/flocks.

A number of these aspects are antagonistic and create key areas of tension that need to be managed in the programme design. The desire to collect as many phenotypes/genotypes as quickly as possible favours a larger programme, but with obvious implications for both the overall cost of the programme and the burden placed on farmer participants.

In essence, the optimal design of the future phenotyping and genotyping programme requires a strategic approach to balance the competing objectives described above. This is achieved via an analysis that considers:

- The value of each phenotype/genotype to the industry and the urgency with which implementation is required,
- The cost and practicality of collecting each phenotype, and
- The number of phenotypes required to achieve target breeding value accuracy (based on heritability of the target trait).

To support the design of the phenotype/genotype programme, a model was developed to analyse the impact of key reference population design inputs on outcomes (programme cost, phenotype numbers and breeding value accuracy).

Model description

Figure 11 provides a description of the model framework. The model encompasses two primary outputs, detailed below.

- The projected cost of the programme, based on:
 - o The number of herds/flocks and average herd/flock size,
 - o The scope of traits to be recorded and the costs of individual trait measurements,
 - o Overheads,
 - o Variable costs (not related to phenotyping – e.g., mating costs etc), and
 - o Genotyping costs.
- The annual forecasts of the accuracy of genomic prediction, influenced by:
 - o Heritability of the target traits,
 - o Proportion of herds/flocks measuring the traits,
 - o The breed make-up within the programme,
 - o Animal classes targeted for collection of specific phenotypes and subsequent timing of expression of traits, and
 - o Effective population size, and genome size for target breeds^{23,24}.

²³Daetwyler, H.D., et al. (2008) Accuracy of Predicting the Genetic Risk of Disease Using a Genome-Wide Approach. PLoS ONE 3(10): e3395. Parameters were required to enable estimation of genomic BV accuracy.

²⁴ Hall, S.J.G. (2016). Effective population sizes in cattle, sheep, horses, pigs and goats estimated from census and herdbook data. Animal 10(11):1778-1785. Estimates of Ne.

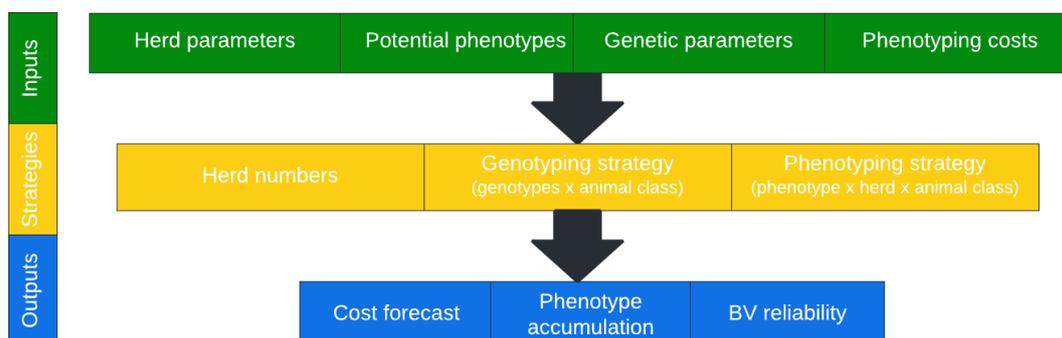


Figure 11: Model framework for national phenotype (and/or genotype) collection programme

Model development and parameterisation

Key assumptions in development and parameterisation of the programme are provided below.

- Average herd/flock size for the reference population herds/flocks reflects an above average size, equivalent to the 25th percentile. This drives efficiencies through working across fewer, larger participant herds/flocks.
- Participant herds/flocks were assumed to be commercial enterprises due to their larger scale and the ability to access full contemporary groups of progeny for slaughter data.
- Nominated breeds capture the key breeds currently undertaking genetic evaluation. Multi-breed herds/flocks were included to capture smaller breeds. In practice, these multi-breed units could also facilitate across breed linkage.
- Target traits were chosen to reflect a focus on key profit and functional trait groups. Critical novel traits (methane and feed intake) were also included. Traits were grouped into generic categories (e.g., fertility traits and carcass traits) where multiple phenotypes (reflecting traits of similar heritability) were collected on the same animals.
- Mating was assumed to occur via artificial insemination to ensure access to relevant and influential sire genetics from pedigree herds/flocks and to support linkage across the individual programme herds/flocks.
- Costs of genotyping, artificial breeding and phenotyping were assumed to be incurred by the programme as opposed to the participants.

Table 19 presents the basic scope of the reference population programme for both sheep and beef.

Table 19 Scope of proposed reference population programme.

	Beef Programme	Sheep Programme
Breeds	Aberdeen Angus Charolais Hereford Limousin Shorthorn Simmental South Devon Multi-breed	Welsh mountain Cheviot Scottish blackface Romney Wool shedding (various) Lleyn Blue-faced Leicester Multi-breed Maternal Suffolk Texel Multi-breed Terminal
Target Traits	Fertility Calving difficulty Marble score /carcase Yearling weight Mature weight Feed intake Methane Health/resistance	Prolificacy (lambs born) Lambing difficulty Lamb survival (lambs reared) Longevity Methane Lamb growth rate Ultrasound muscle and fat Parasite traits Ewe mature weight Carcase CT scan traits Feed intake
Average Herd/Flock Size	75 mated cows	200 mated ewes

Model application and scenario development

National phenotype and genotype collection programme (reference population) scenarios and associated costs were developed to align with a subset of the WP1 future modelling scenarios that require integration with a genomics programme. These scenarios are:

3. Addition of feed intake,
4. Addition of feed intake and methane yield, and
6. Genomics for all traits.

The reference population model was configured to deliver the required scale and structure to attain specified genomic breeding value accuracy targets within 5 years. However, to assess sensitivity of the outcomes to programme scale and structure, Scenario 6a incorporated both fast (5-year horizon) and slow (10-year horizon) scenarios, reflecting different time scales to reach accuracy targets.

Genomic breeding value accuracy targets were defined with reference to current accuracy benchmarks for existing traits (assessed for young animals prior to first progeny records) and nominal accuracies of 0.3 for new traits. Table 20 (beef) and Table 21 (sheep) provide an overview of the genomic accuracy targets.

Table 20: Accuracy target for beef reference population programme.

Trait	Accuracy target	Collection Cost per Phenotype
Fertility	0.5	£0
Calving Difficulty	0.5	£0
Marble score/carcase	0.6	£0.85
Yearling weight	0.7	£0.85
Mature weight	0.7	£0.85
Feed intake	0.3	£500 ¹
Methane	0.3	£200 ¹
Health/Resistance	0.3	£0

¹ Costings assume methane phenotypes are collected in conjunction with feed intake.

Table 21: Accuracy target for sheep reference population programme.

Trait	Accuracy target	Collection Cost per Phenotype
Prolificacy (lambs reared)	0.3	£0
Lambing difficulty	0.3	£0
Lamb survival	0.3	£0
Longevity	0.3	£0
Methane	0.3	£25
Lamb growth rate	0.6	£0
Ultrasound muscle and fat	0.6	£3
Parasite traits	0.3	£6.50
Ewe mature weight	0.6	£0
Carcase traits	0.6	£0
CT scan traits	0.5	£100
Feed Intake	0.3	£300

Table 22 provides an overview of indicative programme establishment and recurrent overhead costs. Projected costs were estimated at high-level. Greater detail of programme scale/structure and objectives, during business planning, is required in order to calculate more robust estimates. Engagement with potential participants would also support greater understanding of support and incentives to foster participation.

Table 22: Indicative programme establishment and overhead costs

	Beef Programme	Sheep Programme
Participant incentive (£/breeding female/year)	£10	£4
Participant equipment subsidy (£ - Year 1)	£0	£1,500
Participant support/admin (£/participant/year)	£2,500	£2,500
Programme management (£/year)	£570,000	£570,000
Research overheads (£/year)	£460,000	£460,000
Programme establishment costs (£ - Year 1)	£500,000	£500,000

Each scenario incorporated a 20-year forecast of programme expenditure. Programme scale and structure was fixed throughout the forecast period.

In practice, scope exists to shift the reference population programme into a maintenance phase once an acceptable/target level of genomic breeding value accuracy has been achieved. The number phenotypes required annually to maintain reference population linkage to contemporary selection candidates and genomic breeding value accuracy are typically significantly lower than volumes required to build a suitable reference population. For example, in sheep Van der Werf et al. (2014)²⁵ suggest refreshing the reference population every two generations with (e.g., every 6 years for a 3-year generation interval, where generation interval is based on the average age of the parents) $N/6$ animals added per year, where N is the target size of the reference population for a given trait.

In the context of this analysis, adjusting programme scale and structure was not considered, on the basis that:

- Accuracy targets in Table 20 and Table 21 are conservative and reflect current target levels of accuracy. There is scope to enhance accuracy beyond these thresholds and this will require ongoing accumulation of phenotypes/genotypes.
- Accuracy targets associated with key new traits (e.g., feed intake and methane) are very modest and reflect a minimum accuracy required to implement a worthwhile genomic breeding value. These novel hard to measure traits are key drivers of the cost of the programme, and it is likely that programme structure would be retained to some degree to support ongoing accuracy improvements in these traits.
- Future development of additional novel traits is likely to require maintenance of programme scale and structure.
- National phenotype and genotype collection programmes fill several roles and purposes beyond development of genomic breeding values (e.g., benchmarking, knowledge exchange, creating an industry focal point). Consequently, there are other imperatives to maintain programme scale and structure.

²⁵ Van der Werf, J.H.J., et al. (2014). Genomic Selection in Sheep Breeding Programs. Proc 10th WCGALP, paper 351.

Based on the above, the cost forecasts reflect a fixed programme scale and structure. The costs can therefore be considered conservative (i.e., higher costs than might be expected), as there could be potential to revise future scale and structure once initial objectives are achieved.

Results – Programme structure & costings

Beef programme

Table 23 summarises the basic structure of each beef reference population across the costed scenarios. Full spreadsheet model provided in Supplementary material 5: Potential national phenotype and genotype collection programme costing model (Excel file).

Table 23: Basic structure of each beef reference population across costed scenarios.

Scenario	Herds	Annual Cows Mated	Annual Methane Phenotypes	Annual Feed Intake Phenotypes	Annual Carcase Phenotypes	Annual Fertility Phenotypes
3	42	3,822	0	1,386	0	0
4	42	3,822	1,386	1,386	0	0
6 (Fast)	157	14,287	1,424	1,424	5,181	14,287
6 (Slow)	80	7,280	728	728	2,640	7,280

Table 24 summarises the cost forecast of each beef reference population across the costed scenarios. Full spreadsheet model provided in Supplementary material 5: Potential national phenotype and genotype collection programme costing model (Excel file).

Table 24: Cost forecast of each beef reference population across costs scenarios.

Scenario	20 Year Cost (£M)	Avg Annual Cost (£M)	NPV (£M)	Cost Breakdown by Category					
				% Breeding Costs	% Genotyping Costs	% Phenotyping Costs	% Participant Support Costs	% Programme Management Costs	% R&D Costs
3	£41.31	£2.07	£29.53	5%	4%	34%	7%	29%	22%
4	£46.85	£2.34	£33.47	4%	3%	41%	6%	25%	20%
6 (fast)	£65.19	£3.26	£46.65	12%	9%	31%	16%	18%	14%
6 (slow)	£43.59	£2.18	£31.21	9%	7%	24%	12%	27%	21%

By way of comparison, cost saving attained by pursuing scenario 3 versus 6 (fast) amounts to 37%. The drivers of this are:

- Fixed costs (programme management and R&D) are approximately 32% of the total cost of Scenario 6 (fast), while this increases to 51% under scenario 3.

- Feed intake is the highest cost phenotype – reducing from a full programme with all traits (6 fast) to a single trait programme (3) only reduces phenotyping costs by 32%.

Sheep programme

Table 25 summarises the basic structure of each sheep reference population across the costed scenarios. Full spreadsheet model provided in Supplementary material 5: Potential national phenotype and genotype collection programme costing model (Excel file).

Table 25: Basic structure of each sheep reference population across the costed scenarios.

Scenario	Flocks	Annual Ewes Mated	Annual Methane Phenotypes	Annual Feed Intake Phenotypes	Annual Carcase Phenotypes	Annual Fertility Phenotypes
3	23	4,600	3,450	3,450	0	0
4	23	4,600	3,450	3,450	0	0
6 (Fast)	80	16,000	2,903	2,903	8,700	11,200
6 (Slow)	45	9,000	1,410	1,410	6,400	4,890

Table 26 summarises the cost forecast of each sheep reference population across the costed scenarios. Full spreadsheet model provided in Supplementary material 5: Potential national phenotype and genotype collection programme costing model (Excel file).

Table 26: Cost forecast of each sheep reference population across costs scenarios.

Scenario	20 Year Cost (£M)	Avg Annual Cost (£M)	NPV (£M)	Cost Breakdown by Category					
				% Breeding Costs	% Genotyping Costs	% Phenotyping Costs	% Participant Support Costs	% Programme Management Costs	% R&D Costs
3	£50.84	£2.54	£36.31	7%	7%	41%	3%	23%	18%
4	£52.57	£2.63	£37.54	7%	7%	43%	3%	23%	18%
6 (Fast)	£83.65	£4.18	£59.76	15%	15%	37%	7%	14%	11%
6 (Slow)	£54.82	£2.74	£39.19	13%	13%	29%	6%	22%	17%

Sheep programme costs are approximately 30% higher than beef due to:

- Greater number of breeds with associated requirement for more phenotypes to reach accuracy targets across all breeds.
- More diverse range of traits, particularly complex traits such as Worm FEC and CT scanning.
- Higher relative genotyping costs due to smaller animal size and numbers per flock at same overall cost per test.

These additional costs are partly offset by the ability to use lower cost PAC chamber for methane traits in sheep. Like beef, fixed costs are 25% of Scenario 6 (Fast) and the cost saving attained from pursuing scenario 3 versus 6 (fast) amount to 40%.

Results – Cost-benefit analysis

Sheep

Table 27 presents benefits, costs, NPVs, and benefit-to-cost ratios for 30-year projections of future modelling scenarios (including slow and fast implementation for genomics scenarios) for sheep. Benefit to cost ratios range from 8.2:1 (scenario 3: feed intake) to 17.8:1 (scenarios 4d: methane yield and feed intake + intensity + adoption). Scenarios that can deliver increased selection intensity and or adoption generate high returns on investment. However, the cost of driving additional adoption is not included in this analysis.

Under deployment of genomics for all traits, there is little economic incentive to speed up the delivery of the programme.

Table 27: Benefits (economic & gross GHG trend), costs, NPVs, and benefit-to-cost ratios for 30-year projections of future modelling scenarios (including slow and fast implementation for genomics scenarios) for sheep.

Future modelling scenario	Benefits		Cost (£m)	NPV (£m)	Benefit: cost ratio
	Economic (£m)	Industry-wide trend (tonnes CO2e/yr)			
1: Status quo	286.3	-6.6	-	-	-
2: Additional core traits	328.1	-11.5	-		n/a
3: Feed intake	383.3	-11.3	46.9	336.4	8.2
4a: Methane yield	527.9	-11.1	48.5	479.4	10.9
4b: Feed intake/methane yield x 150%	708.9	-11.8	= 4a	660.4	14.6
4c: Improved intensity	687.3	-14.8	= 4a	638.8	14.2
4d: Improved intensity + adoption	860.6	-18.8	= 4a	812.1	17.8
6a: Genomics all traits (slow)	551.1	-15.4	50.7	500.4	10.9
6b: Improved intensity (slow)	659.3	-18.2	= 6a (slow)	608.7	13.0
6c: Intensity + adoption (slow)	824.1	-23.1	= 6a (slow)	773.5	16.3
6a: Genomics all traits (fast)	654.5	-11.5	77.4	577.1	8.5
6b: Improved intensity (fast)	783.1	-11.3	= 6a (fast)	705.7	10.1
6c: Intensity + adoption (fast)	978.8	-11.1	= 6a (fast)	901.4	12.7

Beef

Table 28 presents benefits, costs, NPVs, and benefit-to-cost ratios for 30-year projections of future modelling scenarios (including slow and fast implementation for genomics scenarios) for beef. Benefit to cost ratios range from 4.2:1 (scenario 4b feed intake with methane yield at 150% weighting) to 6.1:1 (scenario 6c – genomics all traits, intensity + adoption (slow)). Scenarios that can deliver increased selection intensity and adoption generate high returns on investment. However, the cost of driving additional adoption is not included in this analysis.

Under deployment of genomics for all traits, there is little economic incentive to speed up the rate of deployment of the programme.

Table 28: Benefits (economic & gross GHG trend), costs, NPVs, and benefit-to-cost ratios for 30-year projections of future modelling scenarios (including slow and fast implementation for genomics scenarios) for beef.

Future modelling scenario	Benefit (£m)		Cost (£m)	NPV (£m)	Benefit: cost ratio
	Economic (£m)	Industry-wide trend (tonnes CO2e/yr)			
1: Status quo	164.7	-5,000	-	-	-
2: Additional core traits	182.1	-5,856	-		n/a
3: Feed intake	183.3	-5,109	38.0	145.3	4.8
4a: Methane yield	184.6	-5,133	43.1	141.5	4.3
4b: Feed intake/methane yield x 150%	181.8	-4,335	= 4a	138.7	4.2
4c: Intensity + adoption	275.6	-8,045	= 4a	232.5	6.4
5: Carcase records	188.6	-4,962	= 4a	145.5	4.4
6a: Genomics all traits (slow)	161.8	-4,617	40.1	121.7	4.0
6b: Improved intensity (slow)	236.3	-6,981	= 6a (slow)	196.1	5.9
6c: Intensity + adoption (slow)	245.3	-7,254	= 6a (slow)	205.1	6.1
6a: Genomics all traits (fast)	192.2	-4,617	60.0	132.2	3.2
6b: Improved intensity (fast)	280.6	-6,981	= 6a (fast)	220.6	4.7
6c: Intensity + adoption (fast)	291.3	-7,254	= 6a (fast)	231.3	4.9

Discussion

Cost-benefit ratios, combined with associated environmental outcomes, suggest that significant economic benefits are available through implementation of an integrated national phenotype and genotype collection programme. Marginal economic benefits increase as the depth (traits and genomics) of the programme increases, for sheep. This is less pronounced for beef.

The costs incorporated into the potential national phenotype and genotype collection programme are conservative (high) and likely worst case. Costs could be reduced in several potential ways (not modelled), including:

- Through leveraging existing phenotype and genotype datasets for some breeds/traits,
- By adjusting programme scale and structure down once genomics accuracies reach adequate targets,
- By sharing resources/overheads across sheep and beef programmes, and
- By applying a more granular approach to trait by breed by herd/flock combinations.

Cost forecast sensitivity (data not shown) suggest that there is not a lot of cost saving through reducing the scale and structure because of inherent fixed costs and the cost of feed intake/methane phenotyping. Fixed costs also restrict the scale of potential cost saving realised by slower/longer implementation. As such, there is little economic incentive to speed up the rate of deployment of the programme. Further analysis is required to determine how to reduce these fixed costs and deliver efficiencies. The expectation is that the extent to which these fixed costs can be reduced will be limited, due to implicit minimum requirements for programme management and R&D.

The relevant scenarios highlight the annual volume of feed intake and methane phenotypes that would be required to meet, conservative, trait accuracy objectives. It is important to consider these phenotyping requirements in planning infrastructure needs, as the forecasts exceed the capacity of current infrastructure. Capital costs associated with additional infrastructure are not captured here. Rather, phenotypes are costed on a per animal basis. Capital costs would be included in a full-scale business plan.

Of note is that changes in environmental outcomes between scenarios do not align entirely (i.e., do not always correlate) with changes in economic outcomes. This is not unexpected given the environmental benefits realised under the range of scenarios are entirely a result of selection on indexes that are driven by economic outcomes alone and there are trade-offs (antagonisms) between positive environmental outcomes and positive economic outcomes. Other drivers of this are mentioned in the section on Potential future economic and environmental benefits from genetic improvement.

There are broader benefits from the development of a national phenotype and genotype collection programme, not considered directly in the costs here. National phenotype and genotype collection programmes can be a key tool (indirectly) for achieving outcomes reflected in Scenarios 2 and 6b/c. These sorts of programmes can be a key tool for supporting adoption and demonstrating commercial value of genetics/differences between sires, improving herd/flock linkages, and support multibreed evaluations and across breed comparisons.

Conclusion

The scale of historic and potential future economic and environmental benefits demonstrates that genetic improvement has a cornerstone role to play in driving the sustainability of the UK sheep and beef sector, including as a key tool in the response to the climate challenges the sector faces.

The future options assessment suggests that there is significant value to be gained by enhancing the genetic improvement programme for sheep and beef in the UK. Further consultation is required to clearly identify the most appropriate option. This consultation should focus on discussion with core participants in the provision of genetic evaluation services in the UK.

The national phenotype and genotype collection programme should focus heavily on building a resource to drive genetic gain for core genetic traits, as they offer significant opportunity to deliver economic and environmental benefits. This will also support adoption and demonstrate commercial value of genetics/differences between sires, improve herd/flock linkages and support multibreed evaluations and across breed comparisons to support higher selection intensity.

Decisions related to investment in the national phenotype and genotype collection programme for feed intake and methane yield should go together with an understanding of how balanced selection for economic/environmental outcomes would accrue economic and environmental benefits. Detailed approaches to manage phenotyping, considering infrastructure needs and the readiness and potential impact of implementation by different breed across the industry are also required.

Investment, supported by detailed business planning, should be made to develop a future programme that aspires to maximise the economic and environmental benefit of genetic improvement in the UK sheep and beef sector.

Appendices

Appendix 1: Historic genetic improvement in the sheep industry

The calculation of industry-weighted genetic trends for the UK sheep industry, accounting for the extent to which different breeds contribute (industry structure) based on trait genetic trends, is presented below. The industry-weighted genetic trend is used, along with trait economic weights and breed population size and type, to derive the industry-wide annual rate of economic genetic gain and to estimate the economic (NPV and annualised equivalent) and environmental (annual rate of genetic gain in GHG emissions per year, in gross emissions for all females mated and emissions intensity per kg of carcass weight terms) impact of genetic improvement.

Method

Sheep trait genetic trends are measured separately for different breeds, and those trends only capture progress in the subset of flocks that are performance recording. Genetic improvement on maternal traits is measured per ewe (traits expressed by replacements), and terminal traits per lamb born (traits expressed at sale/slaughter). To combine trends from 9 sheep breeds (for ewes and for lambs), and calculate economic and environmental impacts from genetic improvement, the following was undertaken:

1. Weight common breed types and mating combinations as either hill, crossing, or terminal.
2. Based on the composition of breeds within each breed type, estimate the proportional contribution each breed makes to every mating combination, for ewes and for rams (accounting for the proportion of each breed which is recorded and non-recorded).
3. Estimate the trait genetic trends in non-recorded flocks relative to recorded flocks.
4. Combine trait genetic trends (weighted) to calculate industry-weighted genetic trends for each trait.
5. Use economic weights and environmental coefficients for each trait, along with breed population size and type, to estimate the industry-wide annual rate of economic genetic gain and annual rate of genetic gain in GHG emissions, respectively.
6. For economic impact, calculate the annualised benefit as a payment with an equivalent net present value (NPV) to the accumulated benefits of expression over a given time (20 years).

Each of these steps are described in detail below.

Breed types and mating combinations

Ewes and rams are grouped into 3 breed types: hill, longwool/crossing, others (herein defined as crossing), and terminal (each type is composed of several different breeds). Mating combinations consist of pairings of purebred or crossbred ewes (by breed type) with rams (either by breed type OR specific breed, for Texel and Suffolk only). This produces 37 different mating combinations.

Mating combinations are classified according to the ewe breed type. Table 29 presents mating combinations comprising these 3 groups, including the number of ewes mated, and the weighting of

each pairwise combination within each breed type, based on the proportion of ewes mated (the weights are used for creating industry-weighted trends within each breed type).

Table 29: Mating combinations according to ewe and ram type, number of matings, and proportion of the matings (weight) within the relevant breed type (grouped according to ewe breed type).

Group	Ewe type	Ram type	Ewes mated	Weight (in group)
Hill	Hill (purebred)	Bred pure	2,062	58.2%
	Hill (purebred)	Longwool crossing	635	17.9%
	Hill (purebred)	Other	343	9.7%
	Hill (purebred)	Other hill	105	3.0%
	Hill (purebred)	Terminal sire	320	9.0%
	Hill x hill	Others	53	1.5%
	Hill x hill	Terminal sire	24	0.7%
Crossing	Longwool ewe (purebred)	Bred pure	277	5.0%
	Longwool ewe (purebred)	Other	46	0.8%
	Longwool ewe (purebred)	Terminal sire	60	1.1%
	Crossing (purebred)	Bred pure	48	0.9%
	Crossing (purebred)	Other	12	0.2%
	Crossing (purebred)	Terminal sire	5	0.1%
	Shortwool (purebred)	Bred pure	577	10.4%
	Shortwool (purebred)	Others	184	3.3%
	Shortwool (purebred)	Terminal sire	184	3.3%
	Longwool x Hill (mule)	Other terminal sires	345	6.2%
	Longwool x Hill (mule)	Others	501	9.0%
	Longwool x Hill (mule)	Suffolk	579	10.4%
	Longwool x Hill (mule)	Texel	1,273	22.9%
	Other crosses	Other terminal sires	193	3.5%
	Other crosses	Others	801	14.4%
	Other crosses	Suffolk	92	1.7%
	Other crosses	Texel	379	6.8%
Terminal sire	Terminal sire (purebred)	Bred pure	450	12.5%
	Terminal sire (purebred)	Other terminal sires	113	3.1%
	Terminal sire (purebred)	Others	87	2.4%
	Other terminal sire crosses	Other	670	18.6%
	Other terminal sire crosses	Other terminal sires	277	7.7%
	Other terminal sire crosses	Suffolk	191	5.3%
	Other terminal sire crosses	Texel	1,081	30.0%
	Terminal sire x (Longwool x Hill)	Other terminal sires	139	3.9%
	Terminal sire x (Longwool x Hill)	Others	133	3.7%
	Terminal sire x (Longwool x Hill)	Suffolk	60	1.7%
	Terminal sire x (Longwool x Hill)	Texel	359	9.9%
	Terminal sire x Hill	Others	15	0.4%
Terminal sire x Hill	Terminal sire	34	0.9%	

Source: Sheep Breeding in Britain 2020 ([Pollot & Boon, 2020](#)).

Genetic contributions by breed

Each mating combination in Table 29 contributes to the industry-weighted genetic trends. A calculation of the contribution (from trait genetic trends) that each individual breeds makes to every pairwise mating combination is required. Contributions are calculated based on the relative population of a breed within 5 categories: hill, longwool, crossing, shortwool, terminal sire, and other breeds. This is completed separately for ewes and rams, with each population divided into 2 groups: performance recorded and non-recorded. An estimated 20% of flocks are recorded and 80% are non-recorded, except for Terminal breeds, where 25% of flocks are recorded and 75% are non-recorded.

Table 30 describes the relative populations of 9 different breeds, according to breed type (note that here longwool, crossing, and shortwool breeds are treated as separate groups). For simplicity, these are combined into a crossing “breed type” for the rest of the analysis.

Table 30: Proportion of recorded and non-recorded ewes and rams contributing to breed type population.

Type	Breed	Ewe		Ram	
		Recorded	Non-rec.	Recorded	Non-rec.
Hill	Welsh mountain	5.2%	20.7%	4.9%	19.6%
	Scottish blackface	4.7%	18.6%	5.7%	22.6%
	Other hill	10.2%	40.7%	9.4%	37.7%
Longwool	Romney	13.6%	54.2%	20.0%	80.0%
	Other longwool	6.4%	25.8%	0.0%	0.0%
Crossing	Blueface Leicester	0.0%	0.0%	20.0%	80.0%
	Other crossing	20.0%	80.0%	0.0%	0.0%
Shortwool	Lleyn	13.2%	52.8%	12.2%	48.9%
	Easycare	4.4%	17.5%	3.3%	13.3%
	Polled Dorset	2.4%	9.7%	4.4%	17.8%
Other	Other breeds	20.0%	80.0%	20.0%	80.0%
Terminal	Charollais	2.8%	8.5%	3.7%	11.1%
	Suffolk	6.1%	18.3%	4.5%	13.6%
	Other terminals	16.1%	48.2%	16.8%	50.3%

Source: Sheep Breeding in Britain 2020 (Pollot & Boon, 2020).

Combining the breed proportions in Table 30 with the mating combinations in Table 29, the contributions of each breed to each trait industry-weighted genetic trends for ewes and rams can be calculated (details below).

Genetic trends in recorded and non-recorded flocks

Table 31 includes trait genetic trends, by breed, for maternal and direct traits in performance recorded flocks. Trait genetic trends are based on improvement from 2015 to 2020, because 2021 records were incomplete when the data was accessed. Trends for “others” are calculated based on the average of all other breeds.

Trait genetic trends in non-recorded flocks are estimated based on the relative performance of non-recorded animals compared to recorded animals of the same breed. For Charollais, Suffolk, other terminal breeds, and polled Dorset (where recorded and non-recorded data is available), the trend in non-recorded animals is calculated at 50% of the trend in recorded animals. For all other breeds 50% was assumed.

Table 31: Genetic trends (from 2015 to 2020) by breed for maternal and direct traits, for recorded flocks.

Type	Breed	Maternal traits			Direct traits		
		Mature size	Litter Size	Maternal ability	Scan Weight	Lean weight ¹	Fat weight ¹
Hill	Welsh mountain	0.201	0.001	-0.004	0.206	-0.006	0.000
	Scottish blackface	0.149	0.007	0.018	0.180	-0.006	0.000
	Other hill	0.175	0.004	0.007	0.193	-0.006	0.000
Terminal	Charollais	0.294	0.000	0.053	0.415	0.035	-0.001
	Suffolk	0.279	0.001	0.007	0.279	0.006	0.001
	Other terminals	0.286	0.001	0.030	0.347	0.021	0.000
Crossing	Blueface Leicester	0.257	0.000	0.046	0.243	0.012	0.000
	Other crossing	0.257	0.000	0.046	0.243	0.012	0.000
Longwool	Romney	-0.049	0.001	0.029	0.005	0.012	0.000
	Other longwool	-0.049	0.001	0.029	0.005	0.012	0.000
Shortwool	Lleyln	0.218	0.007	0.057	0.251	0.012	0.000
	Easycare	0.239	0.010	0.143	0.226	0.012	0.000
	Polled Dorset	0.254	0.000	0.015	0.359	0.006	0.001
NA	Other breeds	0.193	0.002	0.037	0.227	0.012	0.000

Source: Analysis of trends provided by breed societies.

¹Lean/fat weight (both CT traits) were only available for terminal breeds and Polled Dorset. Other breed trends for lean/fat weight were estimated based on the relative performance of hill and crossing/longwool/shortwool breeds compared to terminal breeds for muscle and fat depth (trends where all breeds were available). Estimated trends affected the terminal selection index trend per lamb born, via contributions from crossbreeds.

Combining genetic trends

The mating combinations in Table 29, paired with breed proportions in Table 30 were combined with trait genetic trends from recorded flocks (Table 31) and non-recorded flocks to estimate industry-weighted genetic trend for each trait.

Industry-weighted genetic trends are calculated separately for each breed type (hill, crossing, and terminal sire), and estimated differently for maternal and direct traits. Maternal traits are based only on genetic contributions from the ewe. Direct traits are based on contributions from the ewe and ram (i.e., an average of the 2). Industry-weighted genetic trends are calculated as follows:

$$Maternal IWT_{type} = \sum_{i=1}^{H,L,T} C_i \times \left(\sum_{j=1}^{14} (Trend_r \times Ewe_{r,j} + Trend_n \times Ewe_{n,j}) \right)$$

$$Direct IWT_{type} = \sum_{i=1}^{H,L,T} C_i \times \left(\sum_{j=1}^{17} (Trend_r \times (0.5Ewe_{r,j} + 0.5Ram_{r,j}) + Trend_n \times (0.5Ewe_{n,j} + 0.5Ram_{n,j})) \right)$$

Where c represents the weighting for mating combination i , and r and n are recorded and non-recorded parameters, respectively, for trait genetic trends and the proportion of ewes and rams. Trait genetic trends multiplied by proportions of ewes/rams are summed across 14 breeds (j) in Table 29 and Table 30.

Results from the application of these equations are presented in Table 32 and Table 33, along with the equivalent industry-weighted genetic trends derived as part of the 2015 analysis²⁶ for comparison.

Table 32: Industry-weighted genetic trends (2015-2020) for maternal traits compared to 2015 analysis.

Type	2015 analysis			Current trends		
	Hill	Crossing	Terminal sire	Hill	Crossing	Terminal sire
Mature size (kg)	0.225	0.055	0.114	0.078	0.106	0.142
Litter size (lambs born)	0.003	0.001	0.001	0.001	0.001	0.001
Maternal ability (kg)	0.037	0.003	-0.003	0.006	0.017	0.019

Trait definitions: <https://signetdata.com/technical/ebvs-for-commercial-flocks/interpreting-ebvs-and-indexes/>

Table 33: Industry-weighted genetic trends (2015-2020) for direct traits compared to 2015 analysis.

Type	2015 analysis			Current trends		
	Hill	Crossing	Terminal sire	Hill	Crossing	Terminal sire
Scan weight (kg)	0.077	0.079	0.222	0.086	0.126	0.177
Lean weight (kg) ¹	0.028	0.029	0.068	-	-	0.011
Fat weight (kg) ¹	0.025	0.016	0.032	-	-	0.000

Trait definitions: <https://signetdata.com/technical/ebvs-for-commercial-flocks/interpreting-ebvs-and-indexes/>

¹ Industry-weighted trends not reported here for hill and crossing breeds, because data only available for terminal breeds and for Polled Dorset (see footnote on table 11).

Changes in industry-weighted genetic trends reflect a combination of population changes, updated economic weights, and changes to trait genetic trends by breed in the UK sheep population.

Economic impact of genetic gain

Economic benefits from genetic gain are calculated using 3 sets of economic weights (indexes) measuring the change in profit per lamb born (for hill, crossing, and terminal mated ewes), and 2 indexes measuring profit per ewe (for hill and crossing mated ewes). Economic weights are summarised in Table 34.

²⁶ AbacusBio (2015). Review of the Genetic Improvement of Beef Cattle and Sheep in the UK with Special Reference to the Potential of Genomics. Report prepared for EBLEX (AHDB).

Table 34: Economic weights for hill, crossing, and terminal economic indexes (per lamb born and per ewe).

	Hill (£)		Crossing (£)		Terminal ¹ (£)
	Per lamb	Per ewe	Per lamb	Per ewe	Per lamb
Mature size (kg)		-0.22			
Litter size (lambs born)		22.53			
Maternal ability (kg)		0.51		0.51	
Scan weight (kg)	0.51		0.51		0.51
Lean weight (kg)					4.148
Fat weight (kg)					-6.232

Source: AbacusBio (2018). Report: Trait and economic responses to selection for three breeding goals for the UK sheep industry. This report updated EVs from Conington et al. (2004) according to price changes from 2004 to 2018. EWs were adjusted to reflect prices increasing from 459p/kg in 2018 to 543p/kg for 12 months to July 2021. (Price data: <https://ahdb.org.uk/gb-deadweight-sheep-prices>)

¹ Because lean and fat weight trait have shifted from age constant to weight constant trait definitions (since 2015), scan weight was added to the terminal index to capture growth that was previously measured under the age constant lean/fat trait definitions. Lean/fat weight EWs were also adjusted to account for correlation between new weight constant traits and scan weight, and to align index units.

Selection index trends are equal to the sum of each component economic weight multiplied by the corresponding industry-weighted genetic trend. Selection index trends are compared to the 2015 analysis in the AbacusBio report (2015) Table 35²⁷.

Table 35: Selection index trends in profit per lamb and profit per ewe for hill, crossing, and terminal breeds.

	Previous analysis (2015)		Current trends	
	Per lamb born	Per ewe	Per lamb born	Per ewe
Hill	0.033	0.047	0.044	0.017
Crossing	0.034	0.01	0.065	0.009
Terminal sire	0.182	-	0.136	-

To scale up selection index trends to calculate industry-wide annual rate of economic genetic gain, selection index trends are multiplied by the number of ewes mated, which are classified by the type of ram they are mated to (Table 36). Per lamb born trends for hill, crossing, and terminal sires are multiplied by 1.01, 1.6, and 1.77 respectively, to account for the average number of lambs born per ewe (Wall et al. 2010²⁸). There is no terminal index per ewe because the assumption is that ewes are not mated to terminal rams to breed replacements.

²⁷ AbacusBio (2015). Review of the Genetic Improvement of Beef Cattle and Sheep in the UK with Special Reference to the Potential of Genomics. Report prepared for EBLEX (AHDB).

²⁸ Wall, E., et al. (2010). The potential for reducing greenhouse gas emissions for sheep and cattle in the UK using genetic selection. Commercial report by AbacusBio prepared for AHDB & Defra.

Table 36: Purebred and crossbred ewe population in 2020, according to ram mated.

	Crossbred	Purebred	Total
Hill	-	2,167	2,167
Longwool, crossing & other	2,173	2,209	4,382
Terminal sire	5,026	1,132	6,158
Total	7,193	5,508	12,707

Source: Sheep Breeding in Britain 2020 ([Pollot & Boon, 2020](#)).

Industry-wide annual rates of economic genetic gain by breed type are presented in Table 37.

Table 37: Annual rate of economic genetic gain in hill, crossing, and terminal breed types and in total.

	For lambs (£m)	For ewes (£m)
Hill	0.10	0.04
Crossing	0.45	0.04
Terminal sire	1.49	-
Total	2.11	

The industry-wide annual rate of economic genetic gain (£2.11m/year) is the marginal benefit from 1 year of improvement. Because genetic improvement is permanent and cumulative, the benefits from 1 year of improvement are expressed over many years. To account for this, genetic improvement is valued using the annualised benefit, which is derived from the NPV of 10 years of cumulative genetic improvement, followed by 10 years where the benefits from genetic improved are “locked-in”. The cumulative NPV of genetic improvement is worth £183.2m to the industry (based on 5% discount rate).

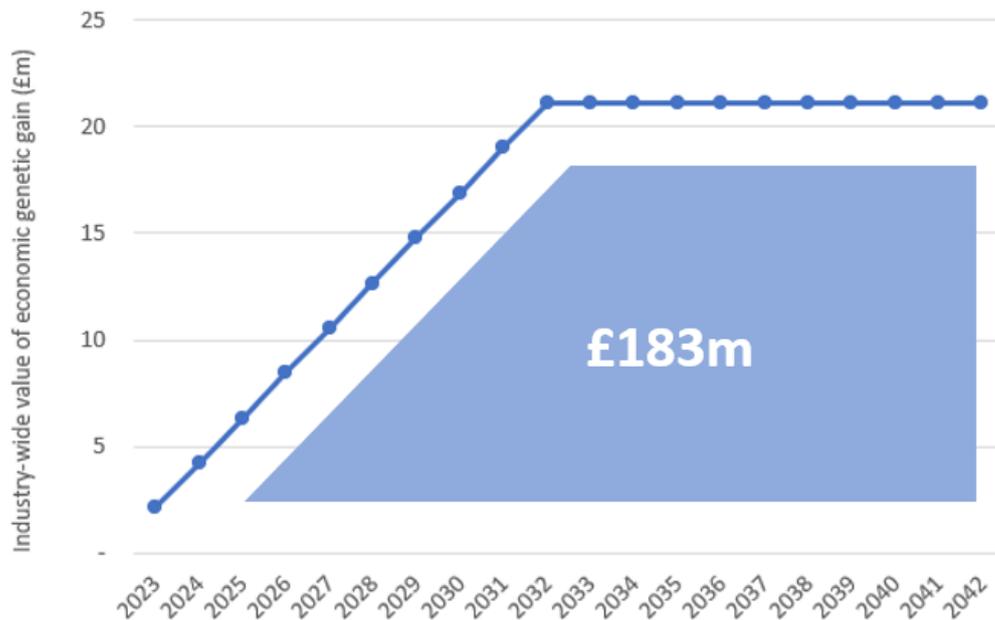


Figure 12: Industry-wide value of economic genetic gain over 20 years, based on 10 years gain at the current industry-wide annual rate of economic genetic gain, followed by 10 years where genetic gain is “locked-in”.

To calculate the annualised benefit of genetic gain, we calculate the equivalent annual payment that has the same NPV if payment is received every year for the next 20 years (applying the same discount rate). The annualised value from genetic gain is £14.7m.

Environmental impact of genetic gain

The same framework, used for economic impact modelling, was used to estimate the environmental impacts.

Environmental impacts are calculated by applying trait GHG emissions coefficients, instead of economic weights. Trait GHG emissions coefficients represent the change in emissions (annual CO₂ equivalents from enteric methane) per 1-unit increase in the trait. Like economic weights, trait GHG emissions coefficients include discount genetic expression (DGE) coefficients, meaning they account for trait expression over the course of an animal's lifetime and the contribution to progeny.

Trait GHG emissions coefficients can be reported based on the change in emissions (i.e., gross emissions) or the change in emissions per unit of meat produced per breeding female (i.e., emissions intensity). Trait GHG emission coefficients in gross and intensity terms are presented in Table 38.

Table 38: GHG coefficients (for gross emissions and emissions intensity) for hill maternal, crossing, and terminal sired animals.

Trait (units)	GHG coefficients					
	Gross (Δ CO ₂ e/ ewe/year)			Intensity (Δ CO ₂ e/ kg meat/ewe/year)		
	Hill	Crossing	Terminal	Hill ⁵	Crossing ⁵	Terminal
Mature size (kg) ¹	3.64	4.42	-	-0.33	-0.21	-
Litter size (lambs born) ¹	0.87 ²	0.60	-	-0.17 ²	-0.06	-
Maternal ability (kg) ¹	-1.01	-1.24 ³	-	-0.09	-0.11 ³	-
Scan weight (kg) ¹	-6.37	-6.48 ⁴	-4.06	-0.14	-0.30 ⁴	-0.18
Feed intake (kg) ⁶	0.56	0.50	0.22	0.02	0.02	0.01
Methane yield (kg CH ₄ /kg DM) ⁷	10.08	9.99	2.93	0.24	0.30	0.00

¹ Source: Wall, E. et al. (2010). The potential for reducing greenhouse gas emissions for sheep and cattle in the UK using genetic selection. Commercial report by AbacusBio prepared for AHDB & Defra. Refer to tables 3.4, 3.5, 3.6 (gross) and 4.2, 4.5, 4.8 (intensity).

² Litter size raised coefficients (gross = 0.77 and EI = 0.15) were adjusted to account for 89% of lambs reaching weaning.

³ Coefficients for crossing maternal ability based on hill GHG coefficients (gross = 1.01 and EI = 0.09) and adjusted to reflect differing DGE values for crossing sheep (0.677) than DGEs for hill (0.553).

⁴ Multiplied slaughter age coefficients (gross = 2.16 and EI = 0.1) by 3 to convert to scan weight (where 3 days lamb growth = ~1kg additional scan weight)

⁵ Maternal emissions intensity coefficients from Wall 2010 are based on EI for lamb product only. We adjusted these to include ewe CW, assuming EI for lamb = 25.2kg CO₂e/kg product (source: [AHDB](#)), decreased to 17.6 kg CO₂e/kg product when including an additional 8.6 kg production from cull ewes (30% replacement rate x 65kg ewe mature weight x 44% dressing percentage). The effect of this

adjustment is to reduce intensity coefficients from Wall et al. (2010)²⁹, because increases in emissions are diluted over greater levels of product, therefore reducing the effect of trait changes on EI.

⁶ Feed intake coefficients were calculated based on 23g methane per kg feed, and 25kg CO₂e per kg of methane (0.583 kg CO₂e per kg feed). DGEs applied to hill, crossing, and terminal indexes (0.96, 0.86, and 0.381, respectively) were derived from Wall et al. (2010)²⁹.

⁷ Methane yield coefficients were calculated based on changes to emissions for slaughter progeny (59% of system-wide emissions per female, or 307kg CO₂e) and for ewes (41% of system-wide emissions per female, or 199kg CO₂e). Given a fixed amount of feed, increasing methane yield (i.e., decreasing methane efficiency) will increase emissions. Terminal coefficients are based only on progeny emissions. Hill and crossing emissions come from progeny and ewe emissions. DGEs applied for progeny emissions are the same as those used for feed intake. DGEs for ewe components of hill and crossing emissions are 0.55 and 0.68 and are also derived from Wall et al. (2010)²⁹.

Trait GHG emission coefficients were used to calculate the contribution of each trait to environmental performance per breeding female and scaled up impacts across the entire industry to estimate the industry-wide annual rate of genetic gain in GHG emissions per year for all mated females, in gross emissions terms. Results are in Table 39 and Table 40.

The trend in gross emissions, per breeding female and industry-wide, is equal to a 0.1% reduction in emissions per year, relative to baseline emissions of 506kg CO₂/ewe/year³⁰, and 6,618 tonnes/year for the industry. This is driven by emissions reductions from faster growth rates (which correspond to less feed to reach the same finish weights).

²⁹ Wall, E., et al. (2010). The potential for reducing greenhouse gas emissions for sheep and cattle in the UK using genetic selection. Commercial report by AbacusBio prepared for AHDB & Defra.

³⁰ Combining emissions intensity of 25.2kg CO₂e/kg lamb meat (source: [AHDB](#)), average lamb production of 20.1kg /ewe/year (weighted average of hill, crossing, and terminal mated ewes), and a population of 12.7m ewes implies emissions per ewe of 506kg CO₂e, and 6.4m tonnes industry-wide.

Table 39: Trend in gross emissions (per trait and total) for hill, crossing, and terminal sired breeds, per ewe per year, and industry-wide impacts in tonnes per year.

	Gross (Δ CO ₂ e/ewe/year)		
	Hill	Crossing	Terminal
Mature size (kg)	0.286	0.467	-
Litter size (lambs born)	0.001	0.001	-
Maternal ability (kg)	-0.006	-0.021	-
Scan weight (kg)	-0.550	-0.815	-0.717
Rate of genetic gain in gross GHG emissions /mated female, by breed type	-0.269	-0.369	-0.717
Industry-wide rate of genetic gain in gross GHG emissions kg/mated female/year)	-0.521		
Rate of genetic gain in gross GHG emissions, by breed type	-584	-1,617	-4,418
Industry-wide rate of genetic gain in gross GHG emissions (tonnes/all mated females /year)	-6,618		

The per breed type and industry-wide annual rates of genetic gain in GHG emissions per breeding female per year in emissions intensity (per kg of product) terms are presented in Table 40. The industry-wide annual rate of genetic gain in GHG emissions intensity is -0.04 kg CO₂e/kg product mated female/year, which is equal to a 0.23% decrease in emissions per kg of product per year (based on emissions intensity of 17.6 kg CO₂e/kg product³¹).

Table 40: Trends in emissions intensity by trait, rate of genetic by breed type, and industry-wide annual rate of genetic gain in GHG emissions intensity for hill, crossing, & terminal sired ewes.

	Gross (Δ CO ₂ e/ewe/year)		
	Hill	Crossing	Terminal
Mature size (kg)	-0.053	-0.014	-
Litter size (lambs born)	-0.00015	-0.00004	-
Maternal ability (kg)	0.000	-0.001	-
Scan weight (kg)	-0.008	-0.026	-0.032
Rate of genetic gain in GHG emissions intensity, by breed type	-0.061	-0.042	-0.032
Industry-wide annual rate of genetic gain in GHG emissions intensity	-0.040		

³¹ Emissions intensity of 17.6 kg CO₂e per kg of product includes both lamb and cull ewe meat production, that is: 17.6 = 506 kg CO₂e / (20.1 kg lamb + 8.6kg cull ewe), where 25.4 = 506 kg CO₂e / 20.1 kg lamb only.

Appendix 2: Historic genetic improvement in the beef industry

The calculation of industry-weighted genetic trends for the UK beef industry, accounting for the extent to which different breeds contribute (industry structure) based on trait genetic trends, is presented below. The industry-weighted genetic trend is used, along with trait economic weights and breed population size and type, to derive the industry-wide annual rate of economic genetic gain and to estimate the economic (NPV and annualised equivalent) and environmental (annual rate of genetic gain in GHG emissions per year, in gross emissions for all females mated and emissions intensity per kg of carcass weight terms) impact of genetic improvement.

Method

Beef genetic trends are measured and reported separately for individual breeds, and those trends only capture progress in animals that are performance recording. To combine trends from 7 cattle breeds, and calculate economic and environmental impacts from genetic improvement, the following was undertaken:

1. Estimate common breed's contribution to dual-purpose and terminal index improvement.
2. Estimate trait genetic trends in non-recorded animals relative to recorded animals.
3. Combine trait genetic trends (weighted by breed) to calculate industry-weighted genetic trends for each trait.
4. Use economic weights and environmental coefficients for each trait, to estimate the industry-wide annual rate of economic genetic gain and annual rate of genetic gain in GHG emissions, respectively.
5. For economic impact, calculate the annualised benefit as a payment with an equivalent net present value (NPV) to the accumulated benefits of expression over a given time (20 years).

Each of these steps are described in detail below.

Breed weights by index and trends in non-recorded population

Economic and environmental benefits are derived using terminal and dual-purpose indexes (the dual-purpose index contains terminal and maternal traits). Industry-weighted genetic trends are calculated based on the estimated contribution from 7 different breeds to each index.

The contribution (weight) applied to the terminal breed types is based on the number calves registered with the British Cattle Movement Survey (BCMS) in 2020 and the relative proportion of each breed. For the dual-purpose breed type, the relative proportion of dams in the BCMS in 2020, was used.

We assume that 80% the population is performance recorded, the rate of genetic progress in the 20% that is not recorded is 80% of the trend in the recorded population.

Table 41: Weights for calculating industry-weighted genetic trends for terminal and dual-purpose index traits.

Breed	Index contribution	
	Terminal	Dual purpose
Angus	32%	24%
Charolais	13%	6%
Hereford	11%	12%
Limousin	32%	35%
Simmental	10%	19%
South Devon	1%	2%
Shorthorn	1%	2%

Industry-wide genetic trends

Industry-wide genetic trends are based on improvement from 2015 to 2020, because 2021 records (from breed societies and AHDB) were incomplete when the data was accessed. Industry-weighted genetic trends are calculated by combining trends from each breed according to the weights in Table 41.

Compared to the 2015 analysis¹ on the economic impact of beef genetic improvement, some traits have changed. In terminal breed types, beef value has been replaced with carcass weight and carcass conformation (carcass fat was not included, though the trends were flat). In dual purpose breed types, calving ease and weaning weight have been added. Industry-weighted genetic trends are in Table 42.

Table 42: Industry-weighted genetic trends (from 2015-2020) for terminal and dual purpose (terminal and maternal index) traits compared to 2015 trends.

Trait (units)	Genetic trend	
	2015 analysis	Current trends
Terminal index		
Carcass weight (kg)	0.810	0.502
Calving ease direct (%)	-0.003	0.025
Gestation length direct (days)	0.006	-0.026
Carcass conformation (1-45)	na	0.021
Dual purpose index		
Terminal traits		
Carcass weight (kg)	0.838	0.426
Calving ease direct (%)	-0.013	-0.004
Gestation length direct (days)	-0.035	-0.019
Carcass conformation (1-45)	na	0.016
Maternal traits		
Mature cow weight (kg)	1.919	0.679
Calving interval (days)	0.065	-0.022
Age at first calving (days)	-0.001	-0.411
Longevity (years)	0.009	0.000
Calving ease maternal (%)	na	0.022
Maternal weaning weight (KG)	na	0.216

Source: Analysis of trends provided by breed societies.

Trait definitions: <https://irp-cdn.multiscreensite.com/17b79915/files/uploaded/BREEDPLAN%20-%20The%20Traits%20Explained.pdf>

Economic impact of genetic gain

Economic impacts are derived using terminal and dual-purpose indexes. Selection index trends (which measure profit per female mated) are equal to the sum of each index's component economic weight multiplied by the corresponding industry-weighted genetic trend. Economic weights measure the change in system-wide profit associated with a 1-unit increase in each trait (Table 43).

Table 43: Economic weights for terminal and maternal traits.

Trait (units)	EW (£)
Terminal traits (Terminal & Dual-purpose index)	
Carcase weight (kg)	1.78
Calving ease direct (%)	6.86
Gestation length direct (days)	-3.27
Carcase conformation (1-45)	6.19
Maternal traits (Dual-purpose index only)	
Mature cow weight (kg)	-1.63
Calving interval (days)	-1.75
Age at first calving (days)	-0.55
Longevity (years)	21.32
Calving ease maternal (%)	3.31
Maternal weaning weight (KG)	0.8

Source: Maternal & terminal breeding objectives for the UK beef industry, 2018 (AbacusBio report prepared for SRUC)

The industry-wide annual rates of economic genetic gain for terminal and dual-purpose indexes are calculated by scaling up selection index trends to account for the 1.48m³² beef cows in the UK (Table 44). We assume that 63% of breeding females are mated on the terminal index, and 37% are mated on the dual-purpose index (Todd et al. 2011)³³.

³² www.gov.uk/government/statistical-data-sets/structure-of-the-livestock-industry-in-england-at-december

³³ Todd D.L., et al. (2011). Gene flow in a national cross-breeding beef population. *Animal*. 5(12):1874-86. doi: 10.1017/S1751731111001017. PMID: 22440463.

Table 44: Selection index trends in profit female mated and industry-wide annual rate of economic genetic gain on terminal and dual-purpose indexes.

	Selection index trend (£ per female mated)	Industry-wide annual rate of gain (£m)
Terminal	1.27	0.70
Dual purpose		
<i>Terminal</i>	0.89	0.83
<i>Maternal</i>	-0.60	-0.56
Total dual purpose	0.29	0.27

Ten years of cumulative genetic improvement in both indexes (at industry-wide annual rates of economic genetic gain of £0.7m and £0.27m for terminal and dual purpose matings, respectively) followed by 10 years where the benefits from genetic improvement are “locked-in” has a total NPV of £84m, and an annualised benefit of £6.8m (Table 45).

Table 45: Net present value and annualised benefits for terminal index and dual purpose index improvement.

	Net present value (£m)	Annualised benefit (£m)
Terminal	60.54	4.86
Dual purpose	23.70	1.90
Total	84.24	6.76

Figure 13 shows 10 years of genetic improvement, followed by 10 years where genetic gain is “locked-in”, where the total area under both curves is equal to the total NPV of £84m. The slope during first 10 years is equal to the combined industry-wide annual rates of economic genetic gain from terminal and dual-purpose matings (£0.97m/year).

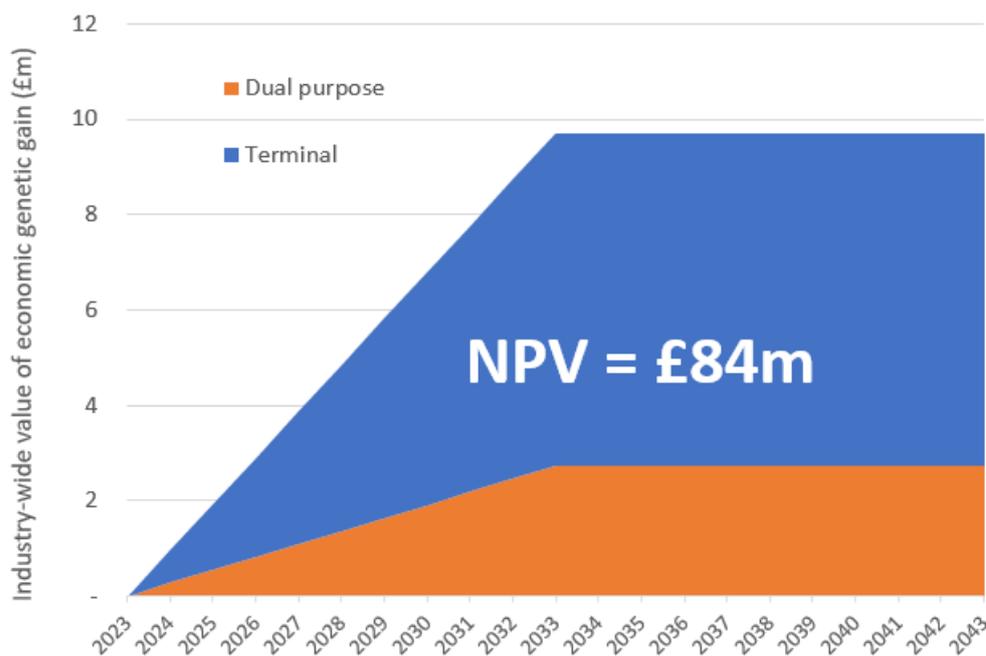


Figure 13: Industry-wide value of economic genetic gain over 20 years for matings on terminal and dual-purpose indexes, based on 10 years gain at the current industry-wide annual rate of economic genetic gain, followed by 10 years where genetic gain is “locked-in”.

Environmental impact of genetic gain

The same framework, used for economic impact modelling, was used to estimate the environmental impacts.

Environmental impacts are calculated by applying trait GHG emissions coefficients, instead of economic weights. Trait GHG emissions coefficients represent the change in emissions (annual CO2 equivalents from enteric methane) per 1-unit increase in the trait. Like economic weights, trait GHG emissions coefficients include discount genetic expression (DGE) coefficients, meaning they account for trait expression over the course of an animal’s lifetime and the contribution to progeny.

Trait GHG emissions coefficients can be reported based on the change in emissions (i.e., gross emissions) or the change in emissions per unit of meat produced per breeding female (i.e., emissions intensity). Trait GHG emission coefficients in gross and intensity terms are presented in Table 46.

Table 46: GHG coefficients for gross emissions and emissions intensity for terminal and maternal traits.

Trait (units)	GHG coefficients	
	Gross (Δ CO ₂ e/ cow/year)	Intensity (Δ CO ₂ e/ kg meat/cow/year)
Carcase weight (kg) ¹	-5.27 (T) & -8.34 (DP)	-0.04 (T) & -0.07 (DP)
Mature cow weight (kg) ¹	0.95	0.01
Calving interval (days) ¹	-5.77	0.01
Age at first calving (days) ¹	-0.54	0.002
Longevity (years)	-26.83 ²	-0.11 ³
Maternal weaning weight (kg) ¹	-5.76	-0.05
Feed intake (kg) ⁴	0.45 (T) & 0.39 (DP)	0.002 (T & DP)
Methane yield (kg CH ₄ /kg DM) ⁵	90.04 (T) & 50.98 (DP)	0.471 (T) & 0.267 (DP)

¹ Source: Wall, E. et al. (2010). The potential for reducing greenhouse gas emissions for sheep and cattle in the UK using genetic selection. Commercial report by AbacusBio prepared for AHDB & Defra. Refer to tables 3.8 & 3.9 (gross) and 4.11 & 4.14 (intensity).

² Longevity gross GHG coefficient based on reduction in feed required for replacements as longevity increases, where base replacement requirement is 1,512kgs (0.245 replacement rate x 6,173kgs feed per replacement). A 1-year increase in longevity reduces the replacement rate, and reduces the feed required by 362kg. Assuming 23g methane per kg feed, and 25kg CO₂e per kg of methane, this equates to a 190kg reduction in CO₂e, and is multiplied by the DGE for replacements (0.141, Wall et al. 2010).

³ Longevity emissions intensity GHG coefficient is based on deviation from base EI of 23.4 (source: [AHDB](#)) associated with a 190kg CO₂e decrease in emissions, and a 1.71kg decrease in product from less cull cow meat (given a 5% change in replacement rate and a 315kg cull cow carcass).

⁴ Feed intake coefficients were calculated based on 23g methane per kg feed, and 25kg CO₂e per kg of methane (0.583 kg CO₂e per kg feed). DGEs applied to terminal and dual-purpose indexes (slaughter trait, 0.77, and annual cow trait, 0.68) were derived from Wall et al. (2010). Intensity coefficients are based on deviation from base EI of 23.4 and have the same DGEs applied.

⁵ Methane yield coefficients were calculated based on changes to emissions for slaughter progeny (61% of system-wide emissions per female, or 2713kg CO₂e) and for cows (39% of system-wide emissions per female, or 1756kg CO₂e). Given a fixed amount of feed, increasing methane yield (i.e., decreasing methane efficiency) will increase emissions. The terminal gross coefficient is based only on progeny emissions. The dual-purpose gross coefficient is equal to the terminal coefficient plus a coefficient that captures changes to cow emissions. DGEs applied are the same as those used for feed intake. Intensity coefficients are based on deviation from base EI of 23.4 and have the same DGEs applied.

The industry-wide rate of genetic gain in gross GHG emissions of -5,000 tonnes/ year (Table 47). This represents a 0.08% decrease in industry-wide gross emissions per year (based on industry-wide emissions of 6.6m tonnes³⁴).

³⁴ 6.6m tonnes is based on system wide emissions of 4,469 kg CO₂e/mated female/year, and a population of 1.48m cow, where the system-wide emissions per cow is calculated from EI of 23.4 kg CO₂e per kg product (source: [AHDB](#)) and assuming 191kg product per female (source: Wall, E., et al. (2010). The potential for reducing greenhouse gas emissions for sheep and cattle in the UK using genetic selection. Commercial report by AbacusBio prepared for AHDB & Defra.

The industry-wide annual rate of genetic gain in GHG emissions intensity is -0.03 kg CO₂e/ kg product/ year (Table 48), equal to a 0.13% decrease in emissions per kg of product per year (based on emissions intensity of 23.4 kg CO₂e/kg product).

Table 47: Rate of genetic gain in gross GHG emissions per mated female and industry-wide annual rate of genetic gain in gross GHG emissions for terminal and dual-purpose mated females

	Terminal	Dual purpose
Carcase weight (kg)	-2.648	-3.556
Mature cow weight (kg)	-	0.645
Calving interval (days)	-	0.125
Age at first calving (days)	-	0.222
Longevity (years)	-	0.005
Maternal weaning weight (KG)	-	-1.247
Rate of genetic gain in gross GHG emissions /mated female, by index	-2.648	-3.807
Rate of genetic gain in gross GHG emissions /mated female¹	-3.378	
Industry-wide rate of genetic gain in gross GHG emissions, by index	-1,450	-3,550
Industry-wide rate of genetic gain in gross GHG emissions¹	-5,000	

¹ 63% of 1.48 females mated on dual-purpose index.

Table 48: Rates of genetic gain in GHG emissions intensity for terminal and dual-purpose mated females.

	Terminal	Dual purpose
Carcase weight (kg)	-0.020	-0.030
Mature cow weight (kg)		0.007
Calving interval (days)		0.000
Age at first calving (days)		-0.001
Longevity (years)		0.000
Maternal weaning weight (KG)		-0.011
Industry-wide rate of genetic gain in GHG emissions intensity, by index	-0.020	-0.035
Industry-wide rate of genetic gain in GHG emissions intensity¹	-0.029	

¹ 63% of 1.48 females mated on dual-purpose index.

Appendix 3: Future modelling framework

Selection index modelling – incorporating new traits

In selection index modelling, the future scenarios incorporated two new traits, feed intake and methane yield, in all indexes. The feed intake trait was incorporated using economic weights calculated from previous work³⁵³⁶. The economic weight for methane yield is harder to estimate, as it can be tied to a nominal carbon price per tonne, and this may not reflect the level emphasis required to make meaningful progress in this trait when in a selection index with other traits. Future scenarios instead incorporated methane yield with the economic weight required to give this trait approximately 20% of the index variance. This was calculated by increasing the theoretical full index variance by 20%, then dividing this through by the variance of the methane yield trait from literature, to find the economic weight required.

Geneflow model methodology

The geneflow model works by initialising a historic trend in the progeny (calves or lambs born each year), with the merit at “year 0” set to 0 as a reference point. The merit of the dams can then be calculated as a weighted average of past progeny merit, where the weightings are determined by the age distribution of dams used. This assumes no selection on an index is occurring within the dams. The merit of sires used is calculated using the same method, but with the addition of a selection differential to reflect that the sires used each year will be selected from the top $x\%$ of the progeny in previous cohorts. The selection differentials are calculated as the product of the index standard deviation, the average accuracy, and the selection intensity, which is a function of the proportion selected. In each model the index standard deviations and accuracies are derived from the selection index theory framework.

Once the merit of sires and dams has been established, the merit of progeny from year 1 onwards is set as the average merit of the sires and dams in year 1, creating a recursive model from this point which captures the lags and flows of genetic improvement. Future changes to indexes or key industry parameters are modified from either year 1 on, or in cases such as incorporating genomics, after a set number of years to reflect the reality that these changes may require lead in time for implementation.

Environmental impact calculations

The economic and environmental impacts from each of the future modelling scenarios were estimated based on the selection index trends from the geneflow model. In the selection index modelling, each scenario tested provides a set of expected responses in each index trait, based on the information sources available. These component trait responses were standardised to the response in each trait

³⁵ AbacusBio (2018). Trait and economic responses to selection for three breeding goals for the UK sheep industry. Report prepared for Defra: Genetic trends from industry breeding goals.

³⁶ AbacusBio (2018). Maternal and Terminal breeding objectives for the UK beef industry. Report prepared for SRUC.

per 1 unit increase in the index, then divided through by the economic weights to get the expected change in the trait units. These changes were then multiplied by the trait GHG emission coefficients to find the expected change in GHG emissions for a 1 unit increase in index. This figure could then be multiplied by the selection index trend to produce the annual rate of genetic gain in GHG emissions for each future modelling scenario.

UK sheep parameters

Selection index

The full genetic parameters used in the selection index modelling are available in Supplementary material 1: Inputs for future modelling (Excel file).

Geneflow

The industry parameters used in the sheep geneflow modelling are shown in Table 49, while the age structure of hill, crossing, and terminal sires and dams is presented in Table 50.

Table 49: Industry parameters used in the sheep geneflow modelling.

Sheep gene flow parameters			
Breeding ewe population	12,706,500		
Discount factor	5%		
Lambs per ewe	1.2		
	Terminal	Hill	Crossing
Proportion of population (including crossbreds)	48%	17%	34%
Proportion performance recording	25%	20%	20%
Historic trend and ewe merit base year - historic ram superiority estimated to fit trend			
Economic index trends	Terminal	Hill	Crossing
Profit per lamb born (£)	0.24	0.106	0.130
Profit per breeding ewe (£)		0.043	0.019
Current ram superiority per lamb born index	1.42	0.71	0.85
Current ram superiority per breeding ewe index		0.29	0.12
Ewe merit base year, per lamb born index	2.79	0.84	1.17
Ewe merit base year, per breeding ewe index		0.23	0.17
Index SD* current per lamb born	4.55	1.33	1.33
Index SD* current per breeding ewe		3.69	0.64
Average ram accuracy current per lamb born	0.30	0.61	0.61
Average ram accuracy current per ewe mated		0.20	0.30
Ram selection intensity current per lamb born	1.06	0.88	1.05
Ram selection intensity current per ewe mated		0.39	0.65
Ram selection proportion current per lamb born	35%	45%	35%
Ram selection proportion current per ewe mated		77%	60%

*Full index SD from selection index theory

Table 50: Age structure of hill, crossing, and terminal sires and dams.

Age	Terminal		Hill		Crossing	
	Sires	Dams	Sires	Dams	Sires	Dams
1	28.5%	2.0%	10.3%	0.6%	11.7%	3.1%
2	32.0%	28.5%	31.0%	25.4%	34.6%	27.0%
3	19.6%	25.1%	26.0%	26.0%	26.4%	23.5%
4	9.7%	19.0%	17.4%	24.1%	12.5%	19.4%
5	4.8%	12.4%	6.8%	14.9%	9.3%	13.8%
6	2.6%	7.2%	4.2%	5.9%	3.3%	7.9%
7	2.8%	5.8%	4.3%	3.2%	2.2%	5.1%

UK beef parameters

Selection index

The full genetic parameters used in the selection index modelling are available in Supplementary material 1: Inputs for future modelling (Excel file).

Geneflow

The industry parameters used in the beef geneflow modelling are shown in Table 51, while the age structure of dams, natural service and artificial insemination sires presented in Table 52.

Table 51: Industry parameters used in the beef gene flow modelling.

Beef gene flow parameters				
Breeding cow population	1,480,000			
Discount factor	5%			
	Terminal		Dual purpose	
Current proportion of herds performance recording	80%		80%	
Proportion of genetic trend in non-recording herds	80%		80%	
Performance lag in non-recording herds	-10		-10	
Percentage of cows mated on dual purpose index	63%			
AI usage in recording herds	10%			
AI usage in non-recording herds	5%			
	Terminal		Dual purpose	
Index SD* current	54.96		49.82	
Current trend in recording breeding cows	1.33		0.31	
Trend as a % of SD	2.4%		0.6%	
	Terminal		Dual purpose	
Average accuracies	Recording	Non-recording	Recording	Non-recording
AI bulls current	0.93	0.93	0.86	0.86
NS bulls current	0.64	0.64	0.72	0.72
Terminal				
	Recording	Non-recording	Recording	Non-recording
Selection proportions	prop selected	prop selected	selection differential	selection differential
AI bulls current	0.65	0.76	29.17	20.71
NS bulls current	0.85	0.91	9.65	6.28
Dual purpose				
	Recording	Non-recording	Recording	Non-recording
	prop selected	prop selected	selection differential	selection differential
AI bulls current	0.92	0.93	6.89	6.23
NS bulls current	0.99	0.99	0.96	0.96

*Full index SD from selection index

Table 52: Age structure of dams, natural service and artificial insemination sires.

Proportion of ages at birth of their calves	Dams	NS sires	AI sires
2	24%	9.6%	0.7%
3	20%	35.7%	8.7%
4	18%	21.4%	12.2%
5	15%	12.5%	11.4%
6	10%	10.3%	13.6%
7	6%	6.6%	15.0%
8	4%	2.7%	11.0%
9	2%	0.7%	9.2%
10	1%	0.0%	5.2%
>10	0%	0.5%	13.1%

Future modelling scenarios

The future modelling scenarios were designed to investigate the economic and environmental impact where the following levers are available:

- Modifications to traits and selection indexes
 - These flow through into increased index standard deviations, which affects sire selection differentials
- Changes to performance recording strategies
 - The number or type of records per trait affects sire selection differentials through changes in accuracy
 - Changes in proportions of recording flocks/herds will change the number of impacts in the calculation of benefits
- Changes to key industry parameters
 - Increasing the selection differentials for sires by improving selection proportions
 - Modifying age distributions e.g., more use of younger sires with genomic selection
 - Proportion of AI usage in the beef model

The set of scenarios tested were built up in a stepwise fashion (with an exception for a scenario testing increasing the emphasis on feed intake and methane yield), with detailed descriptions of the scenarios provided below.

The ‘additional core traits’ scenario reflects the change that in the historic modelling, not all traits present in the full index formulations had trends and contributed to the industry-wide genetic trends reported. In the *status quo* model, only the traits that contributed to the historical modelling industry-weighted genetic trends had economic weights in the selection index modelling to avoid over inflation of the index standard deviations for the *status quo*. In the additional core traits scenario, the economic weights for all base index traits are included and estimates for the number of progeny records were updated to include records for a wider range of traits compared to the *status quo*.

The feed efficiency trait scenario included the addition of a feed intake trait to all indexes across both sheep and beef. The trait modelled was residual feed intake for sheep, and total feed intake for beef,

as these traits had economic weights calculated for the UK industries in previous work, where these weights were -£0.95/unit for RFI in sheep, and -£82.29/unit for beef. It was modelled that feed intake would be included as an industry trait from a genomic evaluation, with a genomic selection accuracy of 0.33 for RFI in sheep and 0.49 for total feed intake in beef.

The scenario modelling the incorporation of a methane yield trait to all indexes across sheep and beef used heritabilities and phenotypic variance estimates from literature and added methane yield alongside feed intake from the previous scenario. The trait was added at an economic weight derived to give methane yield around 20% emphasis within each index, using the method described earlier in this appendix. These economic weights were -£9.49 for Maternal sheep, -£11.71 for Terminal sheep, -£32.16 for Dual Purpose beef and -£30.94 for Terminal beef. As per feed intake, the methane yield trait was modelled as an industry trait from a genomic evaluation, with a genomic selection accuracy set at 0.23 and 0.32 for Maternal and Terminal sheep respectively, and 0.32 for both beef indexes.

The next scenario, 'increased weighting on feed efficiency and methane yield by 50%', used the same parameters as the methane yield scenario described above. However, the economic weights for feed intake and methane yield in all indexes were multiplied by 1.5. This scenario aimed to look at whether increasing the emphasis of these traits within the index would lead to a significant increase in the environmental benefits and was the only scenario that sat outside the stepwise approach to building up the future modelling.

Once methane yield had been added to all indexes, a scenario was run looking at the impact of improving the sire selection proportions in the geneflow model by 25% with these new indexes incorporating the new traits. This scenario used the parameterisation where methane yield was set to have around 20% emphasis, and all sire selection proportions were improved by 25% from base levels across sheep and beef. Improved selection proportions increase the selection differentials, which are a product of index accuracy, the index standard deviation and the selection intensity, where the selection intensity is calculated from the selection proportions. Increasing this selection differential increases the genetic trend by boosting the merit of sires

The improvements in selection proportions were followed up with an 'improved adoption' scenario where the proportion of the population in performance recording flocks or herds within the geneflow model were increased to 50% for sheep (from 20-25%) and to 90% in beef (from 80%). Increasing the proportion of performance recording flocks or herds increases the number of impacted by the industry-industry-weighted genetic trend for recorded flocks/herds, compared to non-recording which only receive a proportion of the trend achieved in those recording flocks/herds.

In the beef selection index modelling, carcass conformation and fat scores are the profit traits included in the Terminal and Dual-purpose indexes. However, these tend to be predicted from ultrasound muscle and fat depth records rather than having direct carcass records available on progeny of sires for selection. The 'include carcass records' scenario (for beef only) assessed the impact of directly including carcass fat and conformation records as information sources within the beef selection index modelling, for the indexes that incorporate feed intake and methane yield traits.

The final future modelling scenarios tested were three scenarios that built on full scale implementation of genomic predictions across both industries. Genomic predictions were added as information sources for all index profit traits, alongside the existing information sources (traditional progeny records included in previous scenarios) including carcass fat and conformation records for beef. The genomic prediction accuracies for each trait were set to align with the number of records that would realistically be available in a reference population after 5 years (based on WP3 modelling) for a representative breed for each index. The accuracies used are provided in Supplementary material 1: Inputs for future modelling (Excel file). In the first of the three industry genomics scenarios, the selection proportions and proportions of performance recording flocks/herds remained the same as the *status quo* scenario, in the second scenario the sire selection proportions were improved by 25%, and in the third scenario the proportion of performance recording flocks/herds in was increased to model improved adoption.

Drivers of beef environmental outcomes

A detailed analysis was conducted to understand the underlying drivers of the environmental outcomes observed in beef future modelling. This commentary on this analysis is presented below.

- Scenario 2, compared to 1, adds more traits of economic and environmental importance. This increases the standard deviation of the selection index, resulting in increased variation and increased selection differentials for sires at the same selection proportions.
- Progression from scenario 2 to 3 to 4 sees lower heritability/accuracy traits added to the index (FI/MY). For these traits, relatively high economic weights were used, which generates economic benefits that overcome the effect of these lower heritability/accuracy on the standard deviation of the index (breakeven). In contrast, these lower heritability/accuracy traits contribute relatively less to GHG outcomes, compared to other index traits such as growth, so this causes a different outcome (diverges from the direction of economic outcomes) in terms of GHG impacts for these scenarios.
- Scenario 4b emphasises FI/MY, and results in slightly lower economic gains and amplifies the negative impact on GHG outcomes.
- Scenario 5 produces more favourable economic outcomes, driven largely by improvements in fat reduction, which doesn't contribute to improving GHG outcomes because fat has no impact on GHG outcomes (explains why it is worse than 3 and 4a in terms of GHG)
- Scenario 6a, relative to 3/4a, spreads the emphasis out across the traits, and further pulls emphasis away from growth, reducing the GHG outcomes realised by core index traits.

Appendix 4: Tertiary performance indicators

Table 53 presents an assessment of the measurability, relevance, and influence that AHDB/Defra have, for a range of tertiary indicator metrics.

Table 53: Tertiary Performance Indicators.

Driver	Indicator Metric/s	Measurability	Relevance to Primary Metric	AHDB/Defra Influence
Genetic variation	Inbreeding coefficient statistics of new calf cohorts	Moderate	Moderate	High
Genetic variation	Selection index & breeding value standard deviations	High	Very High	High
Accuracy of selection	Average accuracy of breeding values (pre-mating) for key traits	High	Very High	High
Accuracy of selection	Numbers of genotypes and phenotypes submitted annually	Very High	High	Very High
Selection intensity	Calf/lamb registration statistics from top ranked sires	High	High	High
Generation interval	Calf/lamb registration statistics by sire age	High	High	High
Adoption/participation	Numbers or % of herds/flocks submitting genotypes & phenotypes	Very High	Very High	Very High
Adoption/participation	Calf/lamb registration statistics - % of calves/lambs registered by herds/flocks that meet prescribed standards (e.g. genotypes & phenotypes).	High	High	High
Breed numbers and diversity	Number of breeds undertaking genetic evaluation	Very High	Moderate	High
Breed sizes	Calf/lamb registrations by breed	Very High	Low	Moderate
Livestock prices	Livestock price statistics	High	Moderate	Low
Costs	Cost of production obtained from industry benchmarking datasets	Moderate	Moderate	Low
Livestock productivity	Productivity benchmarks obtained from industry benchmarking	Low	Moderate	Moderate
Market requirements & incentives	Product specifications/schedules for key markets and applicable premiums. Details of broader supplier and supply chain requirements	Low	Moderate	Moderate
Social license requirements & incentives	Implementation of new (non-economic) breeding traits	Very High	Low	Very High

Appendix 5: Industry consultation – structured interviews

Background

This project wanted to gain industry views on what genetic improvement tools and services should look like in ten years' time, and likely beyond that. Concern has been raised for several decades about the low pick up of modern genetic improvement tools by bull and ram breeders, and the consequent low penetration into the commercial farm market. Penetration rate has generally remained static for these decades, with a small core of committed performance recording enthusiasts aligned with academic experts. Therefore, genetic gain has not been as fast as it could have been and its penetration across commercial farms is considered to have been low.

This is in great contrast to the dairy, pig & poultry sectors which have embraced modern tools and have documented dramatic changes in animal productivity from doing so. As well, some ram and bull breeders have moved to use services offered from other countries which makes access to data for UK breeding beef herds and sheep flocks difficult. This is of particular concern with the advent of genomic technologies because these have been shown to deliver increased rates of genetic gain when calibrated for local populations.

This project is looking to define a vision for the future of beef & sheep genetics that will deliver greater genetic gain, through systems that can increase rates of genetic gain and simultaneously increase penetration of improved genetics in commercial beef & sheep farms across the UK.

In order to address the issue of uptake, the project aims to solicit views from a cross-section of industry users and key opinion formers who are impacted by genetics, from genetic product and service providers through the supply chain to retailers as representatives of consumer demand. This report summarises the responses gathered from interviews of 35 people and draws some conclusions from these. Those interviewed are listed at the end of the report, along with the questions put to them.

Development of interview questions

A necessary part of assessing industry need was to hear from people in industry. For the scope of this information gathering, it was decided the best return for effort would come from targeted interviews across a range of "user types". Since genetic decisions impact on farmers, the supply chains they supply and their service providers (e.g., vets, farm consultants), people from the following sub-groups were interviewed (number of interviews in brackets, total of 35);

- Commercial breeding companies (5)
- Levy Boards (4)
- Beef & sheep farmers (5)
- Livestock specialists (7)
- Food service/retailers (8)
- Breed Society (6)

NB: Participants with expertise, or known to have strong views, were sought out. Thus, this was not intended to be a representative sample, rather a means of challenging the project team's thinking and raising relevant questions.

Project members developed a series of questions in the following steps:

1. Discussion of the needs specific to the type of questions to be asked.
2. CIEL then drafted a set of questions for feedback from other project members.
3. Other project members added questions and advised on desired changes to wording.
4. A draft set of questions were then used with three interviewees as a pilot.
5. This led to Question 16 being split into 2 parts (16a & 16b).

It was initially considered desirable to have structured questions that would mainly be used to facilitate quantification of answers. However, the final set of questions comprised more open questions without constraints on how they be answered. This was felt to be better at gaining feedback on industry views than a constrained set of questions that might not allow interviewees to answer in the way they thought best. This made the assessment of responses a longer process, but it is considered more value was gained because of this.

All interviews were carried out using video calls. Questions put to the interviewees are detailed in an attached file derived from the PowerPoint slides used to put the questions to those interviewed. Facilitation focused on helping the interviewee(s) answer a question but was generally very light touch.

The interviewees

A sample size of 35 was aimed for, but since not all people initially contacted were available to be interviewed, more were approached (50) to obtain the 35 sought. Interviews took between 1 and 2 hours per interviewee. One interview was conducted with 4 people representing the entity being interviewed (this was the longest interview), which did not complete. The last few questions were answered for this entity by email after being sent the questions.

A list of the people interviewed is provided at the end of this document. Given the business priorities of the people targeted, this was very successful, capturing over 90% of those targeted.

In order to reduce assessment bias to a minimum, the names of those interviewed were removed along with any descriptors which would easily identify them. Responses from the interviews were captured by notes directly entered into a spreadsheet, or handwritten notes added to that spreadsheet later. The anonymised data has been saved as a spreadsheet and attached with this document to the message sent to the project team.

Findings

The numbers of the following sections are the question numbers. Questions where response data would directly identify interviewees was anonymised and not assessed.

1. *What industry do you currently represent /work in? Beef /sheep /both?*

Livestock type	Number of interviewees
Beef	31
Sheep	24
Beef & Sheep	19

Note: Total is greater than 35 because those classing themselves as “beef & sheep” were counted in the respective totals for beef and for sheep.

2. *What is your job title or role description?*

This information is detailed in an appended table at the end of this document together with the names of companies that interviewees work for.

3. *How long have you personally been involved in this industry?*

Anonymised data has been adjusted to represent this as 10-year wide bands up to 30 plus years, plus one band for 5 years or less. This banded approach was used both to anonymise the data and to remove the strong influence of several people who had been in industry for many years.

Analysis of the banded data showed an average of 20 years in the industry, (s.d. = 8.5), ranging from 2 to 63 years, in the original data. The median for unbanded data was 23 years.

4. *What are likely to be your biggest business challenges in the next 5-10 years?*

Responses were aggregated and counts done of similar issues. Net Zero (Carbon) and environmental impact received the most hits (33) followed by loss of subsidies (14), efficiency & profitability (9), staff recruitment (7) with 6 hits for each of challenges to red meat consumption, sustainability and the need for increased uptake of genetics technology (KE). So in order of magnitude for importance the three biggest issues were;

- Environment > Subsidies > Efficiency/profitability

5. *Do you believe improved genetics can help address these challenges or deliver value for your business in other areas?*

The overwhelming answer to this was yes, as would be expected when the majority of people interviewed are working directly to improve genetics. So, genetics is one of the tools to use to address key issues. Of the issues mentioned, there were 7 references to Greenhouse Gas

emissions and Net Zero, and 5 related to the need for good KE support to increase uptake of genetics from modern improvement programmes. Another related theme was the need for management and feeding to change to best suit improved genetics.

6. How well do current beef & sheep genetic information services suit industry needs? Please rate on a scale of 1 (Not very well) to 5 (Very well)

The average score here was 2.63 (s.d. = 0.96) with a range from 1 to 4.5. These statistics show that the assessment of whether current services meet the needs of industry resulted in a wide range of figures. Clearly separating responses into those for sheep and beef was not possible as a significant number of interviewees made reference to both sheep and beef. Removing those that were just for sheep or just for beef, produced similar results for beef (average=2.58) and sheep (2.72).

7. Of the services you know of, which best deliver for industry?

Interestingly, ICBF (Irish Cattle Breeders Federation) received the highest hit rate (13), closely followed by Signet (11). These were followed by SIL (6 for Sheep Improvement Ltd, the New Zealand System), Innovis (4) and then 3 hits each for AHDB (dairy, beef & lamb), Texels, SRUC and USA/Canada.

It is telling that companies outside the UK receive high recognition here, with ICBF topping the list. References to ICBF are frequent in responses to later questions, reflecting the high profile it has gained in industry. However, one interviewee made the point that there had been massive investment into ICBF which overcame much resistance, drove uptake and fuelled development.

8. What is the most important role for a service providing genetic information to industry? (Select all that apply and rank according to most important)

This table lists frequency of hits. Most interviewees were comfortable listing options but not ranking them.

Option		Freq
A	Providing genetic benchmarks aligned with farm KPIs	10
B	Defining the best breeding objectives	5
C	Characterise genetic variation & allow industry to select what is best for them	8
D	Identifying elite animals	11
E	Translating genetic information into practical ratings of worth	18
F	Identifying who has the best genetics	3

G	Supporting traceability	1
H	Using a common language that everyone understands	18
I	Being very engaged with Industry	12
J	Providing a single unbiased estimate of genetic merit for industry	16

There is a common theme here related to the challenges uptake has from use of jargon and technical information. A common language across all breeds and all animal types is wanted. Better systems for rating animals on their worth are sought and these should be better linked to on farm outcomes. There is strong support for having a system which provides unbiased and independent benchmarks for the UK.

9. For genetic information to be useful in your business, genetic services should....

(i) Focus on? (Please detail and rank three things)

Repeating the previous question, the dominant issue was use of plain English (23 hits) followed by a desire to have merit linked directly to farm KPIs to make them more relevant to farmers (12 hits). The next most desired items (8 hits each) were bringing more traits into consideration to better describe whole genetic merit, and to pull things together into a measure of “sustainability”. The next ideas (4 or 5 hits) were making things relevant to wider industry, having evaluations across breeds (breaking down siloes), and support for collecting more performance data.

(ii) Create extra value for you by? (Please detail and rank three things)

The leading idea by far (19 hits) was addressing the issues of complexity, duplication and over-complication which led to confusion. These are key issues we know about, so it was good to see such strong support for action to address them.

The following two ideas reinforced this as reducing techno-speak (9 hits) and reducing the amount of information put in front of farmers (6 hits). Another way of saying we not only want a common language, but it must be in plain English.

The next highest were breaking down the siloes separating breeds (5 hits) and reducing the amount of competition in a greatly fragmented industry to allow more focus to go on delivering genetic gain. Several interviewees made the point that competition between a few large genetics businesses worked because their scale allowed investment in richer and deeper performance data sets (and in genomics – Mark Young), and this created a real incentive for innovation. One respondent considered a problem was KE push when we needed KE pull from end-users.

(iii) Create extra value for you by? (Please detail and rank three things)

Generally, the answers to this question were not so clear cut on what was wanted by many people, with a wide range of ideas and none that stood out as strongly as for other questions.

Continuing the theme of making information more directly relevant to farmers and easy to use, there was a request for visual depiction of information, not just numbers. A good suggestion was a tiered system for data, so that those who needed to, could delve into the detail, but for the average user some simple metrics were wanted, tied directly to on-farm outcomes.

Once again, the need for KE support was made.

(iv) Create extra value for you by? (Please detail and rank three things)

The strongest theme here reiterated that of other questions – the need for metrics linking merit to on-farm outcomes. The next most common issues were including more traits to best define whole flock or herd merit (maternal traits important here) but to keep things simple, possibly a tough challenge. Sharing data was considered “a given” in a system that gave the owner of the data simple tools to control access to that data.

KE would be helped by case studies and the point was made that farmers learn well from other farmers.

10. To what extent do you think industry is hampered by having a number of different genetics services and lack of common language that everyone understands?

Answers here were a little surprising. A strong statement was made about avoiding having “all our eggs in one basket” i.e. having different systems or breeder groups with different objectives was seen as providing useful competition yet they also saw value in generating across industry benchmarks and conducting across industry evaluations.

In trying to reconcile this with previous ideas about competition and fragmentation, one could conclude that the UK needs a small number of breeds for different livestock types, with each of these being run by companies or co-operative farmer membership where all involved shared a common objective. Such can be the case with regard to genetic improvement, where different companies try different things, but where a common data system allows benchmarks to be estimated across industry.

Ideas seem to be coalescing around a common data system, to allow industry benchmarking, and scope for different large scale breed groups to conduct their own selection programmes to deliver differentiated products for farmers. Adopting pig/poultry model would see farmers aligning themselves with a genetics provider, and that provider using all tools available to achieve rapid genetic gain, using case studies to illustrate how the new genotypes perform. One interviewee suggested we lose the focus on merit of individuals and watch where populations were, and were going to, then commit to buying from these breeder groups or companies.

11. Is there a need to merge existing services? If so, which?

Surprisingly, more people said No to this question, yet there was a strong call for great change. This might be linked to the need for aggregated data being used for across industry evaluations, but allowing breeder groups to chart their own direction. It looks like this is most efficiently dealt with by having large scale breeding populations (larger than is the current norm) to deliver rapid genetic gain, and aggregated data for benchmarking and for maintaining data security on behalf of industry.

Some argued for investing where most change was occurring now i.e. don't try to be fair to all players and focus on those most likely to deliver good outcomes. ICBF establishment was cited as an example of how this happened, and how it brought industry with them.

12. Thinking about what an ideal service might look like, what would attract more people & businesses to make good use of genetic information?

- Keep it simple – use a common language, have tools that allow a farmer to input details about their farm and the flock/herd performance, to find genetics suited to that farm.
- Commercial farm data feeds into the evaluation.
- Link to farm outcomes, ideally business KPIs
- Pull industry data together and conduct across population evaluations to generate benchmarks. This needs an independent custodian to hold the data securely for industry good. Governance of this is a critical issue to ensure there isn't perceived bias.
- Such an information system needs to be tiered, scaled, flexible and modular to best suit users and to enable it to evolve to suit industry needs.
- Invest in growing richer, wider, deeper datasets, and make access to information
- KE was seen as a critical need, both for skilled specialists and good case studies that farmers can relate to.
- Financial incentives for using high merit stock was mentioned – this is what ICBF did to bring farmers to the table.
- Lastly, invest in the winners because we need rapid change and we will lose time trying to be fair.

13. If you are not using genetic information in your business currently, what are your reasons and/or barriers to doing so?

- Almost all interviewees use genetic information routinely, with those that did not being further away in the supply chain. Some used this question to address issues that inhibited wider usage of the services and tools. These were
 - Hard to link genetic info to farm outcomes
 - Many in industry think genetics is not as important as nutrition and health. That may be because it is hard to see what improved genetics delivers, particularly when it delivers small incremental gains. By contrast, nutrition and health status can change and the effects are seen quickly.
- Meat processors say they want more, good genetic data to help in their procurement of superior carcass animals.

- The main problem for wider industry is that too few ram and bull breeders, use the modern genetics tool available. Retrospectively it was not possible to interpret whether this related to buyers not asking for figures of breeders not using them.

14. How else could genetic information help your business?

- Health traits and environmental impact were top of this list (7 hits)
- Resilience/longevity and productivity came in 2nd (4 hits)
- Eating quality (3 hits)
- Feed conversion efficiency (2 hits).

It was considered that greater use of commercial farm data would lend more credibility to evaluations and that genomics needed to be brought to the table. Making information more visual would help and bringing in animal soundness assessments would address the concern that animals with good figures can be unsound.

15. To make genetic information more useful to you, what (additional – outside genetic merit) information could have value for you?

Top of the list was abattoir data (16 hits), followed by Health (10), GHG/Environment (10), Eating quality (8) and maternal traits (7).

Benchmarks came up time and again in the responses, measures of connectedness, and having an industry standard for performance measures.

One interviewee stated we needed to stop being focused on merit for individuals and define genetic progress in terms of change in populations, following the lead of the poultry and pig industries.

16 (i) Where do you want to use genetic information in your business (or role)?

Option		Freq
A	On the farm (or site of work), not in the office	22
B	In the office	22
C	In business meetings with clients	21
D	In meetings with my specialist support service providers (e.g. vets, genetics companies or breeders, nutritionists, management consultants)	25
E	In an app on my phone	17
F	In an internet browser application on my home or work computer	19

Some of the respondents were these specialists, implying they want to use this with their clients. Overall though, all options were selected to a high degree with no selections receiving only a few hits.

16 (ii) How do you want it presented to you? Tick all that apply

Option		Freq
A	In a system that allows me to filter and reorder data on different criteria	16
B	As summaries produced by third party specialists and sent to me	7
C	As formatted tables and graphs	6
D	As data tables I can sort and filter myself	6
E	As simple dashboards to show me high level comparisons for different family lines, flock/herds, farms, businesses	26

Clear favourites here with dashboards to show high level metrics (benchmarks), combined with tools that allow users to interrogate the data and sort and sift in different ways.

17. What is the most compelling reason for you to share data from your business? Rank in order of priority the top 5 reasons you would share data.

Option		Freq
A	Uptake of, or engagement with, genetic improvement tools	15
B	Gaining value through sharing data	15
C	Sharing value when sharing data	9
D	Contributing data from your business to help drive genetic improvement for UK beef or sheep?	22
E	Contribute to industry benchmarks	14
F	Compare your data or information to industry benchmarks	15
G	Support research and development	15
H	To provide consumer traceability	6
I	Gain extra levels of service from specialists like veterinarians, feed companies or genetics suppliers	9

J	Any other reason(s)	3
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The most popular choices here relate to sharing data to provide better information for genetic improvement. So, there was a strong altruistic theme here. As such, they seem to reflect the value that would accrue with the farmer, their breeder, or major genetics companies who know about the value that good across-population connections give to searching for high merit animals.

18. Under what conditions would you share data from your business?

Option		Freq
A	Only where I controlled who had access	14
B	Only where someone representing my interests, controlled access e.g. a breed society of industry representative body	10
C	Only where security met minimum standards to maximise data integrity and prevent unapproved access	17

Key issues are security and being able to control access to data.

19. What would most stop you sharing your data?

Option		Freq
A	Extra work needed to collate check & upload data	18
B	Lack of reasonable security for my data	12
C	Lack of being able to control access of others to my data	13
D	No obvious benefit being returned to me	19

Surprisingly given the answers to the previous question, security was not the main issue here. It was more about whether benefits would come from doing this, or the effort required to prepare data for export.

20. What other data is there that you want to use, to produce relevant genetic information for industry and for you?

For traits, these were;

- Health (18)
- Carcase data (14)

- Maternal traits (11)
- GHG, Net Zero and environmental impact (8)
- Eating quality (7)
- Feed efficiency (5)
- DNA parentage (5)

Other streams included – retailer data, wool quality, feed and management system used to test the animals under, labour use per stock unit, lamb & calf survival.

21. Further comments about the provision of genetic information for UK sheep and beef, use of such information, or issues to address in reviewing industry need.

- Need to bring in commercial farm data into evaluations
- KE is critically important to effect change – we must increase uptake. We will need extra advisers to do this. However, we must not forget that farmers learn best from other farmers.
- Data integrity is very important with a centralised data system performing regular QA audits highly desirable.
- Systems need to be easy to use and based on a common language. Farm relevance is critically important.
- A national data system needed to operate across all 4 nations within the UK.
- Data sharing would be the default setting.
- We need to do more to demystify genetics – the goal is livestock improvement, genetics is simply the underlying mechanism we exploit.
- Breed societies have a disproportionate influence on UK genetics.
- There was unease about the narrow base of genetic expertise within the UK, with the perception that this was mostly located at SRUC and AHDB. (*This issue encapsulates two separate issues. 1. Reduced funding for skilled specialists that are easy to access. 2. The merit in having genetics services centralised – Mark Young*).
- We cannot afford to be fair to everyone. We need to back winners to develop a new system that is not constrained by the current business model. ICBF have some learnings here – they backed a few numerically superior breeds to develop a system that all breeds can use.
- We must learn from the livestock industries who are exploiting genetics to its fullest potential.

We must not stifle competition, but a more effective model would be to have a lot fewer breeding populations, of much larger size, and focus the measuring of performance and DNA testing on these populations. Farmers would buy bulls or rams from these populations, in most likelihood, without looking at the figures for individual animals.

Criticism of current delivery model

Of note was trenchant criticism from two interviewees of the current model for delivering genetic gain based on consistently low penetration of modern tools, particularly for sheep, while a majority of motivated beef breeders have opted for systems run from overseas. They state that this has been the case for more than 20 years. Responses from these and some other interviewees stated that having many breeds inhibits genetic change and that these breed structures, along with the current model for genetic services, must significantly change.

The two interviewees that were most critical challenged project members to look at livestock types that are making much better use of genetic tools to improve animal production and health, such as poultry, pigs and dairy cattle, and learn from them. They argued that we should not continue to invest in models that have not been working for many years.

List of people interviewed

The list of people interviewed is provided below (Table 54). Responses were anonymised before examination & interpretation.

Table 54: List of people interviewed

Company	Person/people	Position
Aberdeen Angus Society	Robert Gilchrist	Breed Development Manager
ABP	Liz Ford	Agricultural Projects Manager
AFBI	Steven Morrison	Head of Livestock Production Science
AgriSearch	Jason Rankin	General Manager
AHDB/Livestock Information Services	Ray Keatinge	Product Manager - Innovation Lead
Charolais Cattle Society	Ben Harman	British Charolais Council, Pedigree beef farmer, Chair NBA Beef Pedigree Group
Cogent	Boomer Birch	Beef Programme Manager
Dalehead Foods	Liz Rees, Bethany Rogers, Megan Watkins	Lamb Supply Chain Manager
Dawn/Dunbia	Sarah Haire	Head of Agriculture
Dovecote Park	Kate Sutton	Cattle Procurement Manager
Exlana	Peter Baber	Director & Breeder
Farmer	Adam Quinney	Commercial Farmer
Farmer	Gary Gray	Farm Manager
Farmer	Ben Wilson	Farm Manager
Genus	Mark Smith	Europe, Middle East & Africa Beef Director
HCC /Meat Promotion Wales	John Richards	Industry Development & Relations Manager
Independent consultant	Fiona Lovatt	Veterinary Consultant
Independent consultant	Kate Phillips	Independent Sheep Consultant
Independent consultant	Liz Genever	Sheep and beef Consultant
Independent consultant	Maurice Bichard	Practical Animal Breeding & Genetics Expert
Innovis	Dewi Jones	CEO & founder
Kepak	Julie Finch	Agriculture Governance and Compliance Manager
KTN	David Telford	Head of Agri-foods
Limousin Cattle Society	Alison Glasgow	Technical Manager
McDonalds	Harriet Wilson	Head of Agriculture - Sustainable Sourcing
National Beef Association	Neil Shand	CEO
National Sheep Association	Phil Stocker, Sean Riches	CEO, ram breeder
QMS	Bruce McConachie	Head of Industry Development
SAC	Daniel Stout	Agriculture Consultant
SAC	Mary Young	Ruminant nutritionist SAC, Beef specialist
Semex	Phil Halhead	Beef Genetics Consultant
Stabiliser Cattle Company	Seth Wareing	Business Manager
Tesco	Elin Havard, Jack Davis	Elin - Agriculture Advisor Beef, R&D and Reporting Jack - Agri Advisor Lamb & Future Farmer Foundation
Texel Sheep Society	John Yates, Ed Smith, Paul Phillips, Peter Mitchell, Steve Smith, Ian Murray	CEO, Projects Manager & breed society representatives
Waitrose	Jake Pickering	Senior Agriculture Manager

Appendix 6: Genetic improvement programme assessment framework

The objective of work package 2 was to identify the most appropriate industry genetic improvement infrastructure for the UK sheep and beef sector, through a process of industry consultation, and a quantitative assessment of the potential options available against a set of key criteria, arriving at the most preferred/highest scoring option.

A framework was devised by determining the core components (*value drivers* or *ease of implementation drivers*) of a genetic improvement programme necessary to achieve a *desired outcome*. A list of underpinning *key criteria* was then established for each the *driver*.

For example, a *desired outcome* of a genetic improvement programme is to generate a high rate of genetic improvement for the whole industry. This relies on a high level of participation and adoption by the industry. In this instance, the *driver* which is going to deliver *value* to users of a genetic improvement system is the *potential to maximise user adoption and participation*. But there are many ways in which user adoption and participation can be encouraged, such as offering relevant tools and services to users, and maintaining a simple and easy-to-use system through standardisation, open access, and appropriate interfaces. Each of these underpinning components are *key criteria*.

The framework was developed to assess what is necessary to deliver value to end-users (*value drivers*) versus what is essential to consider when establishing and/or maintaining a new genetic improvement programme (*ease of implementation drivers*). The framework features four categories of value drivers and four ease of implementation drivers. The agreed drivers, desired outcomes, and criteria are summarised in the following section.

Framework components - Drivers, desired outcomes, and criteria

Value drivers

Driver: Potential to maximise user adoption and participation

Desired outcome: User adoption and participation ensures benefits of genetic progress accumulate across as much of the industry as possible, maximising impact and industry value. Participation also supports increased volumes of phenotypic/genotypic data to underpin breeding value (BV) accuracy and rates of genetic progress.

Criteria:

1. Standardisation to support understandability for users, particularly commercial users.
2. Open access that is independent from breed society membership and registration.
3. Enables genomic evaluation of commercial animals, including crossbreds.
4. Provides access to tools and indexes that align with the needs of UK users.
5. Easy to align and deliver industry extension/adoption support to users and industry.

6. Customisable interfaces and reporting to support flexible delivery of information to users.

Driver: Providing data pipelines, data ownership/control and ease of R&D alignment to maximise value from collected data

Desired outcome: Faster rates of genetic progress are contingent on data and continuing R&D effort. Breeding value accuracy and the relevance of breeding value information (to commercial outcomes) requires significant volumes of high quality phenotypic and genotypic data for traits that are commercially relevant. Data pipelines must be conducive to ease of collection and submission of data and leveraging industry/commercial datasets. Maximisation of the value of this data requires accessibility for R&D providers and a phenotype and genotype collection programme structure that supports complementary R&D effort.

Criteria:

1. Relatively standardised platform/phenotype and genotype collection programmes that supports cost effective development of supporting R&D programmes and industry reference herds/flocks etc.
2. Flexible database that can upload, store, and integrate data from multiple sources and formats.
3. Centralised data repository that minimises duplication and can pull from other databases in advance to each analysis, but which is also able to be accessed for R&D and KE and open to a range of R&D providers.
4. Supports an industry-good approach to trait and index development, investment prioritisation, resource allocation etc.

Driver: Enabling control over platform development, service delivery and innovation

Desired outcome: Rates of genetic progress and industry impact/value can be enhanced by the availability of a contemporary and well-maintained genetic evaluation platform. Timely implementation of enhancements and optimized data collection and implementation of new traits with minimal resource bottlenecks supports maintenance of a state-of-the-art evaluation service. Investment priorities must be aligned to UK stakeholder requirements and reflect industry-good outcomes.

Criteria:

1. Traits and indexes customisable to UK requirements, underpinned by UK data etc. and with potential to support across breed evaluations.
2. UK stakeholders control the ongoing development of the infrastructure and services to align with industry requirements.
3. Ownership and management are conducive to timely implementation of enhancements (no resource bottlenecks or competing priorities).
4. Service delivery can be matched to UK user requirements.

5. Model can support an appropriate governance structure to create transparency and alignment with industry needs.
6. Clear data privacy, usage, and storage rules to protect data and minimise competition.

Driver: Integrating/aligning with other platforms

Desired outcome: Infrastructure platform needs to be internationally credible and able to link/align with other international platforms to support benchmarking against international animals, sharing/pooling of data with international collaborators and importation of international animals (particularly overseas sires). Capacity to link with other national/industry databases - e.g., processor data and livestock movement databases - can complement genetic evaluation and further leverage its value/impact. Platform also needs to be able to align with UK farm management platforms to support on-farm collection of phenotypic data, and link breeding/genetics to on-farm activities and outcomes.

Criteria:

1. Platform can support linkage to other international platforms for benchmarking, data sharing and integration of international animal evaluations.
2. Platform can link and integrate with other major national/industry databases (genetic and non-genetic data at an animal level) to increase data volumes and support additional applications of genetic data.
3. Platform can integrate with farm management software to support ease of data collection and link genetics to on-farm outcomes.
4. Data platform is auditable and subject to appropriate quality controls to support use for QA and industry integrity applications e.g., breed/sire verification for branding claims.

Ease of implementation drivers

Driver: Taking a short time to establish

Desired outcome: The time taken to establish the system must be manageable, making use of existing infrastructure, data pipelines and data where appropriate.

Criteria:

1. Ability to leverage existing infrastructure and data to expedite development.
2. Timeframe to develop and implement a minimum viable evaluation.
3. Compatibility of minimum viable product with current industry and stakeholder requirements.

Driver: Minimising ongoing resource and investment requirements

Desired outcome: The extent to which the system can utilise third parties and third-party investment for key functions, or share infrastructure costs with other users (e.g., international), maximising the

value of AHDB/Govt support. A state-of-the-art genetic improvement system requires infrastructure investments, user support and R&D that need to be part of a sustainable service delivery model.

Criteria:

1. Requirement for ongoing investment into infrastructure and infrastructure maintenance, versus use of independent third-party infrastructure.
2. Model is flexible and can engage multiple providers to support maintenance, development, and service delivery.
3. Capacity to leverage contributions from external parties (non-AHDB/Gov) for extension, user support and basic R&D.

Driver: Minimising strategic, technical, and political complexity

Desired outcome: The extent to which the expected transition from the current state to the future state is achievable and does not pose major risk to timely/successful implementation. Key factors are the availability of UK resources/expertise and leadership and the level of reliance on stakeholder support/participation.

Criteria:

1. Level of delivery risk for AHDB/Gov associated with leadership and coordination of key components of national genetic improvement programme (infrastructure, service delivery, user support, adoption, R&D etc).
2. Level of stakeholder cooperation and support required to establish minimum viable product and secure user support/participation.
3. Level of risk that model establishment could fail due to high reliance on support from current key stakeholders and the level of disruption to their current business model.
4. Suitability of the platform for engaging commercial farmers and broader industry in delivery and governance of the scheme.

Driver: Offering sustainability and a high likelihood of generating funding opportunities to support operations

Desired outcome: Costs of delivering genetic evaluation services can be recovered via user charges. The system must put users as key beneficiaries, these users must be easily identified, and transparent charges applied. Expected costs need to be competitive with current charges and international platforms.

Criteria:

1. The model incorporates clearly defined end-users with the capacity to apply charges for service delivery.
2. User charges can be transparent and minimises duplication/overlap with other related charges and services (e.g., breed society fees).

3. Users paying for the service are the key beneficiaries.
4. Funding model can support flexibility with investment prioritisation (need to direct investment where it is most needed).

Framework for weighting and scoring

A weighting method was applied to the above descriptive framework, that allowed a level of importance to be assigned to each of the 8 drivers. Subsequently, a scoring system was developed to rank genetic improvement programme options based on their ability to deliver on the drivers, from the perspective of stakeholders.

External stakeholder input was sought, along with input from the project team, to weight the value drivers and implementation drivers out of 100 (the four drivers in each category sum to 100). This was achieved by circulating a questionnaire to 29 contacts from which 16 complete responses were received. The results of the questionnaire inform the relative weighting or importance of the drivers. See Supplementary material 4: Stakeholder questionnaire for weighting of criteria and scoring of options (Word & Excel file) for a full account of how stakeholders were engaged.

A second questionnaire was developed for respondents to score each genetic improvement programme option (see section: Options for the) and was circulated to the same contacts as previously See Supplementary material 4: Stakeholder questionnaire for weighting of criteria and scoring of options (Word & Excel file) for a full account of how stakeholders were engaged. The genetic improvement programmes were scored out of 10 for their potential to meet each driver. By not disclosing the results of the weighting questionnaire, respondents were unaware of the average relative importance of each driver, allowing the genetic improvement programme options to be scored in an unbiased way.

The mean scores for each driver were then multiplied by the weighting factor for the driver, from the first questionnaire. This was completed for each of the options presented. The total ranking scores for value drivers and ease of implementation drivers were then scaled to a 5-point scale and plotted in a value-ease matrix of four quadrants. The top right quadrant contains programmes that were evaluated as both high ease and high value, whilst the corresponding bottom left quadrant displayed low ease and low value genetic improvement programmes.

Questionnaire results – All stakeholders

The results of the weighting questionnaire collected from 10 respondents are summarised in Table 55, by mean score and standard deviation. There is a clear points-based advantage for genetic improvement programmes which score higher in criteria that maximise user adoption and participation. There is also a smaller deviation in the scores associated with data pipeline provision and local control.

Table 55: The relative importance (weighting) of value drivers and implementation drivers for a genetic improvement programme based on aggregated questionnaire responses (n = 10)

Value Drivers	Mean	SD
Maximising user adoption and participation	34.4	11.2
Providing data pipelines, data ownership/control and ease of R&D alignment to maximise value from collected data	25.7	4.8
Enabling local control over platform development, service delivery and innovation	20.7	5.5
Integrating/aligning with other platforms	19.2	10.5
Implementation Drivers	Mean	SD
Taking a short time to establish	22.2	4.8
Minimising ongoing resource and investment requirements	28.1	6.3
Minimising strategic, technical and political complexity	26.1	8.4
Offering sustainability and a high likelihood of generating funding	23.6	8.2

The results from the option scoring questionnaire are presented below in Table 56 as mean scores (out of 10) from 10 respondents. The results show that as the genetic improvement programme/infrastructure becomes more comprehensive and less fragmented, the expectation is to see potentially higher user adoption and participation, value from data, local control over service delivery and innovation, and integration with other platforms. In terms of implementation, as the genetic improvement system becomes more cohesive, the expectation is that there will be less political, technical, and strategic complexity and higher sustainability. Conversely, respondents anticipate that the more cohesive programmes will take a longer time to establish and with higher ongoing resource/investment needs.

Table 56: Mean scores (n = 16) for 4 genetic improvement programme options when scored out of 10 against value drivers and ease of implementation drivers.

Value Drivers	A ¹	B ²	C ³	D ⁴
Maximising user adoption and participation	4.4	6.3	7.6	8.5
Providing data pipelines, data ownership/control and ease of R&D alignment to maximise value from collected data	4.1	6.2	7.8	8.9
Enabling local control over platform development, service delivery and innovation	4.4	5.7	7.7	8.2
Integrating/aligning with other platforms	3.8	5.7	7.3	8.9
Implementation Drivers	A ¹	B ²	C ³	D ⁴
Taking a short time to establish	7.9	6.6	4.4	3.1
Minimising ongoing resource and investment requirements	6.8	5.9	5.1	4.5
Minimising strategic, technical and political complexity	5.9	6.1	5.6	4.8
Offering sustainability and a high likelihood of generating funding	4.1	5.6	7.1	7.6

¹Status Quo supported by RD&E

²National genetic improvement infrastructure - existing platform

³National genetic improvement infrastructure - UK platform

⁴Full national genetic improvement programme & integrated infrastructure

The scaled and weighted scores are summarised in Table 57 below. Once weighted, the trade-off between the value drivers and ease of implementation drivers is apparent, but the relative differences between the options is smaller for the ease of implementation.

Table 57: Final adjusted scores for 4 potential genetic improvement programmes as assessed by a stakeholder questionnaire (n=16).

Value Drivers	A¹	B²	C³	D⁴
Maximising user adoption and participation	1.5	2.2	2.6	2.9
Providing data pipelines, data ownership/control and ease of R&D alignment to maximise value from collected data	1.1	1.6	2.0	2.3
Enabling local control over platform development, service delivery and innovation	0.9	1.2	1.6	1.7
Integrating/aligning with other platforms	0.7	1.1	1.4	1.7
Total	4.2	6.0	7.6	8.6
Implementation Drivers	A¹	B²	C³	D⁴
Taking a short time to establish	1.8	1.5	1.0	0.7
Minimising ongoing resource and investment requirements	1.9	1.7	1.4	1.3
Minimising strategic, technical and political complexity	1.5	1.6	1.5	1.3
Offering sustainability and a high likelihood of generating funding	1.0	1.3	1.7	1.8
Total	6.2	6.0	5.5	5.0

¹Status Quo supported by RD&E

²National genetic improvement infrastructure - existing platform

³National genetic improvement infrastructure - UK platform

⁴Full national genetic improvement programme & integrated infrastructure

Results are presented graphically in Figure 14, which is discussed in the main body of the report. The figure highlights programmes that were scored as being easy to implement (low to high from bottom to top) and/or offer high value to the industry (low to high from left to right).

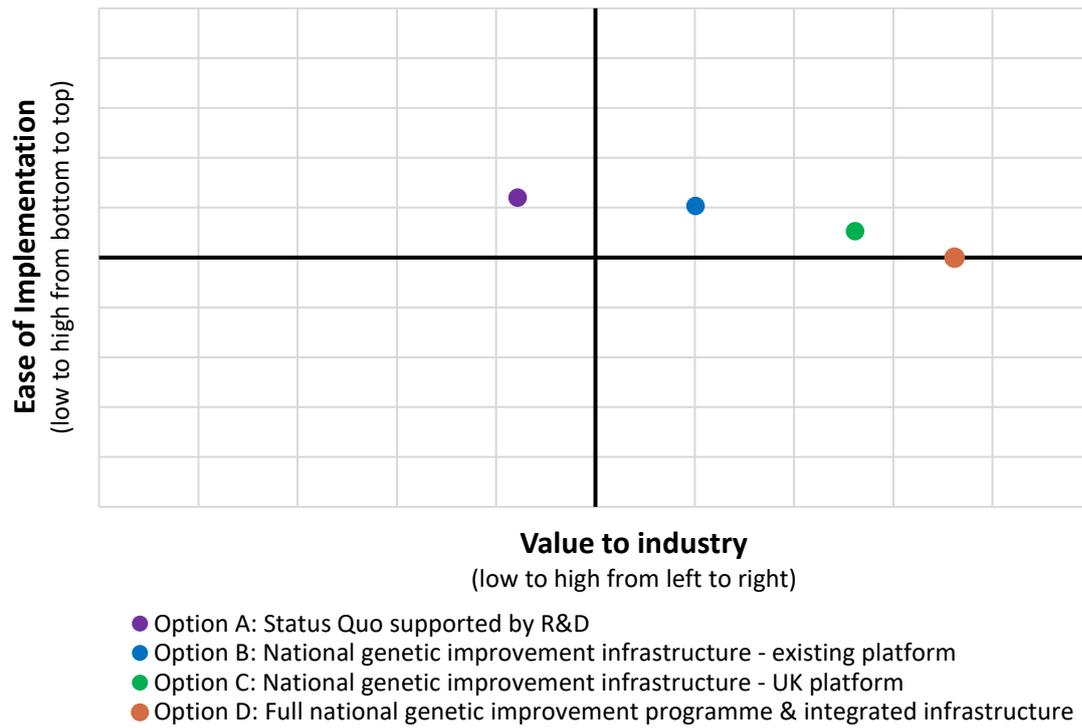


Figure 14: Value ease matrix for 4 potential genetic improvement programmes, as assessed by stakeholders.

Questionnaire results – project team

Results in the previous section were summarised for all questionnaire respondents. In Figure 15 below, results are presented for the project team only. Key differences in scoring when contrasted to Figure 14 include the perception that Option A offers less value than what all stakeholders scored. Furthermore, Options B, C, and D were considered slightly more challenging to implement compared with stakeholder scoring. In terms of value, team members scored Option B lower than stakeholders. Consequently, Option A was considered low value but easy to implement; Options B and C were moderate to high value and moderately easy to implement; and Option D was high value but slightly difficult to implement.

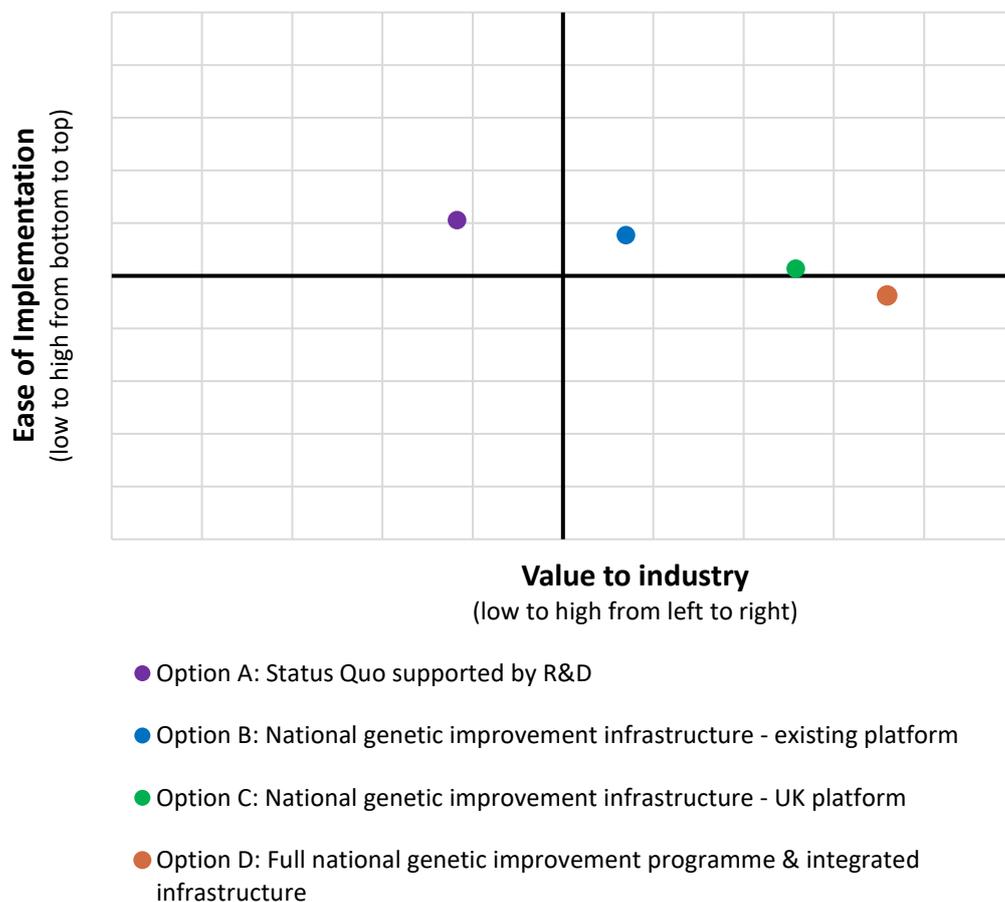


Figure 15: Value ease matrix for 4 potential genetic improvement programmes, as assessed by 10 consortia members.

Supplementary material

Supplementary material 1: Inputs for future modelling (Excel file)

Supplementary material 2: International genetic improvement programmes (Excel file)

Supplementary material 3: Responses from structured interviews (Excel file)

Supplementary material 4: Stakeholder questionnaire for weighting of criteria and scoring of options (Word & Excel file)

Supplementary material 5: Potential national phenotype and genotype collection programme costing model (Excel file)