



J. Dairy Sci. TBC

<https://doi.org/10.3168/jds.2025-27532>

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A novel life cycle assessment demonstrates that targeted genetic improvement can reduce the environmental impact of beef from beef x dairy production systems in the US and the UK

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ABSTRACT

Genetic improvement has been identified as a key practice for reducing the environmental impact of live-stock systems through improved production efficiency. Beef-on-dairy (BxD) production comprises an increasingly large portion of beef supply chains and provides data collection opportunities for understanding the environmental impact of genetic improvement. Life cycle assessment (LCA) is the gold standard for measuring product-level environmental footprints and, to date, has not been applied to assess the mitigation potential of targeted genetic improvement in BxD production. The objectives of this study were to provide a framework for incorporating genetic improvement into an LCA, quantify the role of targeted genetic improvement in BxD production systems in the US and UK, and demonstrate the value of targeted genetic improvement as a key intervention for reducing the environmental impact of beef production. Life cycle assessments were completed for three BxD populations, a typical US feedlot system (US) and a premium (UK-HQ) and commodity (UK-HY) system in the UK. Each population was comprised of animals from two different genetic backgrounds: benchmark animals sired by industry average genetics, and genetically targeted animals (GT) sired by bulls from a breeding program targeting selection of traits that optimize BxD production. Within the benchmark and GT populations, animals were assigned to one of five genetic tiers, with five being the highest merit level, based on their sire's value for a BxD genetic index. Individual-level data were available for each of the growing phases, defined as weaning, rearing-milk, rearing-fed, grazing (UK-HQ only), and finishing. Average phenotypic performance in each sire tier was determined for average daily gain (ADG), days at the growing phase, feed dry matter intake (DMI) in finishing (US and UK-HY), and carcass weight.

Using these performance averages, LCA runs evaluated each combination of genetic background (benchmark and GT), population (US, UK-HQ and UK-HY), sire genetic tier (Tier 1-Tier 5) and marketing year (2024 and 2029). The life cycle impact assessment characterized sixteen environmental impact categories covering water use and quality, land use, air quality, resource use, and climate change. Across all populations and sire genetic tiers, the main processes contributing to the relevant impact categories were feed production, manure management, and, for climate change only, enteric fermentation. The finishing phase had the largest impact among all growing phases, ranging from 50-89% of impact across the relevant impact categories. Higher genetic merit (i.e., higher sire tiers) consistently led to concurrent reductions across damage categories that aggregated to lower overall environmental impact. Comparisons of benchmark Tier 3 to GT Tier 5, representing the effect of genetic improvement, resulted in reductions in overall environmental footprint of -8.7% for the US, -9.6% for the UK-HY, and -4.2% for the UK-HQ populations in the 2024 marketing year, driven in part by climate change reductions of -4.7%, -8.8%, and -4.7%, respectively. This study demonstrates that genetic improvement in commercial systems for improved production efficiency confers systemic environmental benefits that accumulate over time, underscoring the value of targeted genetic improvement as a foundational practice for improving the sustainability of livestock production.

Key words: Genetic improvement, breeding program, life cycle assessment, beef-on-dairy, environmental footprint

INTRODUCTION

Genetic improvement has played a significant role in the efficiency gains of livestock production systems for more than 100 years. As fewer animals have been needed to supply more animal protein, the environmental impact per kilogram of product produced has declined over

Received September 2, 2025.

Accepted July 8, 2026.

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The list of standard abbreviations for JDS is available at adsa.org/jds-abbreviations-26. Nonstandard abbreviations are available in the Notes.

time at the national level in countries with developed production systems (e.g., Capper, 2011; Putman et al., 2018). There remains a focus globally on reducing the environmental impact from livestock, with a particular interest in beef as it has a relatively larger potential impact compared to other animal protein sources on a per kilogram of product basis (de Vries and de Boer, 2010). Genetic improvement has not historically been considered as a key environmental intervention; however, more recently, a 2023 FAO report identified breeding programs as a promising approach to address global GHG emissions and ongoing efforts have explored the relationship between genetics and key indicators of environmental sustainability (FAO, 2023). For native beef systems in the US, the environmental impact mitigation potential of genetic selection has been estimated previously (White et al., 2015). For dairy production, a framework has been developed to estimate how genetic selection using an index affects GHG emission intensity (Amer et al., 2018), and genetic selection for feed efficiency was shown to reduce estimated GHG emission intensity of dairy production (Lucas et al., 2026). A previous LCA has shown that genetic improvement makes a material contribution to environmental impact in pigs (Thoma et al., 2024). Despite these promising initial estimates of mitigation potential, the contribution of targeted breeding programs to reducing environmental impact, including but not limited to GHG emissions, has not been verified in commercial beef-on-dairy production systems using a life cycle assessment (LCA) approach.

Life cycle assessments are considered the gold standard for environmental footprinting and have been used to footprint many livestock species (Putman et al., 2018, 2023; Rotz et al., 2024). LCA models the interconnected processes of the whole system that turns raw inputs into a product and the resulting emissions to air, water, and soil. The environmental effects of these processes are aggregated into a catalog of environmental impact categories using a standardized life cycle impact assessment (LCIA) method to generate the overall environmental footprint. For example, the ReCiPe and Product Environmental Footprint LCIA methods aggregate the effect of processes into impact categories such as acidification potential, eutrophication potential, energy use, and climate change. In turn, these impact categories roll up into the overall environmental footprint. In contrast to focusing on isolated parts of the environmental profile (e.g., only climate change impact), this holistic, process-based framework enables understanding of the tradeoffs among different environmental impact categories and among different sources of emissions. In this study, we define environmental footprint as an aggregation of multiple impact categories and distinguish it from the carbon footprint, which is synonymous with climate change impact. Al-

though LCA is routinely used for livestock environmental footprinting, a method for explicitly incorporating the impact of genetic improvement of beef-on-dairy cattle systems in an LCA has not been previously reported.

The emergence of beef-on-dairy (BxD) production systems around the world provides a unique system to study the effects of targeted genetic improvement on environmental impact of the beef supply chain due to the nature of the system and the relatively low selection pressure on traits specific to breeding a dairy cow to produce a terminal beef animal. The intensive management of BxD programs and extensive use of artificial insemination, relative to most traditional beef systems, provides the infrastructure for identification and data recording of individual animals in all growing phases. Additionally, feed composition and management practices tend to be standardized across animals, minimizing the non-genetic influence on phenotypes relevant for environmental footprints, compared to traditional extensive beef systems where pre-weaning management practices add additional variation to phenotypes that are then more difficult to appropriately model. The percentage of breedings and calvings to beef sires continues to rise globally over time (Van Doormaal, 2019; Berry, 2021; Basiel et al., 2025), accentuating the need for environmental mitigation approaches in BxD systems.

One of the first estimates of GHG emissions from BxD compared to native beef (beef-on-beef, BxB) from the finishing phase of production was published recently (Beck et al., 2025); however, the impact from before finishing and from damage categories other than climate change and the contribution of genetic improvement to reducing the environmental impact of BxD production remain unknown. Additionally, the potential of genetic improvement as an environmental intervention within BxD cattle, though noted previously by Berry (2021), has not been quantified by LCA. The objectives of this study were to (1) provide a framework for incorporating genetic improvement in an LCA, (2) quantify the environmental impact of targeted genetic improvement in BxD systems in the US and UK, and (3) demonstrate the importance of targeted genetic improvement as a key practice for reducing the environmental impact of beef production.

MATERIALS AND METHODS

An attributional LCA was conducted to quantify the expected environmental impact of genetic improvement using sire genetics from a targeted breeding program in US and UK BxD systems in 2024 and 2029 using the SimaPro software (PRé Sustainability B.V., 2024). The LCA conformed to the international standards ISO 14040 and 14044 for the principles and framework, require-

ments and guidelines for LCA (International Organization for Standardization, 2006a; b), as determined by an independent review panel who followed the ISO critical review process (International Organization for Standardization, 2014).

Systems under study

Populations and growing phases. Life cycle assessments were completed for three BxD populations, each corresponding to a different supply chain: a typical grain-finished, marbling and yield-focused, high-performance system in the United States (US), a premium, forage-finished and carcass quality-focused system in the United Kingdom (UK-HQ), and a commodity, forage-finished and high growth and yield system in the United Kingdom (UK-HY). Each of the three populations was comprised of two subpopulations with different genetic backgrounds: benchmark genetics or genetics targeted to the specific supply chain (genetically targeted, GT, sourced from the ABS Global NuEra Genetics breeding program). Benchmark animals were sired by industry average genetics and excluded GT animals. Genetically targeted animals were sired by bulls from a breeding program with two genetic lines, each tailored to specific BxD supply chain needs to optimize lifetime profitability including growth, finishing and carcass performance. One breeding line was designed for efficient growth and high-quality carcasses (NuEra T14) and sired the GT BxD animals in the US and UK-HQ populations. The other breeding line focused on efficient growth and high-yield carcasses (NuEra T15) and sired the GT BxD animals in the UK-HY population.

For the US and UK-HY populations, BxD animals progressed through four growing phases, defined by the point the animal changed diets and/or operations: weaning, rearing-milk, rearing-fed, and finishing. In the UK-HQ population, BxD animals included in this study underwent the same four phases and an additional ~180-day grazing period between the rearing-fed and finishing phases. The weaning phase included the time from birth until the calf left the dairy, rearing-milk referred to the time period animals were at the calf rearer and being fed milk replacer, rearing-fed represented the phase when animals were aggregated into larger groups at the rearer and transitioned from milk replacer to a roughage and concentrate diet, and finishing was the final growing phase where animals were fed a high concentrate diet (US) or high quality forage-based diet (UK-HQ and UK-HY) prior to harvest.

System boundary

This LCA encompassed conception of the BxD animal at the dairy farm through first processing at the packer.

The boundary included the processes for gestation of the BxD animals at the dairy, birth, initial management of the animals at the dairy, at the rearer, during pasture grazing (where applicable) and at the finisher, the production of milk replacer and feed ingredients, manure management, transport of animals and feed, and first processing of the carcasses at the packer, which entailed removal of the head, inner organs, and hide (Figure 1).

Allocation

The impact from processes creating multiple outputs or co-products was allocated according to the hierarchy of preferred allocation methods outlined in the ISO 14040/44 standards (International Organization for Standardization, 2006b; a). The multi-output processes that required allocation were gestation, which resulted in both milk production and the BxD calf, and harvest of the BxD animal, which resulted in the carcass, including hide, meat and bone meal. Allocation for gestation was performed based on energy content using the Agrifootprint energy library (Blonk et al., 2022). For harvest, economic allocation was used to distribute the impact among the co-products.

Life cycle inventory

Animal phenotypes. Animal phenotypes for growth performance in each growing phase, carcass weight, and mortality were sourced from primary, individual-level records (Table 1). In and out weights and associated dates from each growing phase (all three populations) and finishing feed intake data (US and UK-HY) were from primary, individual-level records collected in commercial settings where GT and benchmark animals were co-mingled and managed together. After quality filtering, mean phenotype values for out weights of each growing phase, days at each growing phase, dry matter intake at finishing, and carcass weight were adjusted to minimize non-genetic effects, and the resulting adjusted mean phenotypes were used to calculate average daily gain (ADG) within each growing phase, genetic level, and population. Quality filtering and phenotype adjustment procedures are detailed below.

Quality filtering. For each trait (out weights for each growing phase, days at each growing phase, dry matter intake at finishing, and carcass weight), within each sex (steers and heifers), growing phase (weaning, rearing-milk, rearing-fed, finishing), and population (US, UK-HY, UK-HQ), outliers falling outside three standard deviations of the mean were removed. To correct for management and temporal effects, contemporary groups were assigned by concatenating the operation name, year, and season the animal entered that operation (US

and UK-HQ) or operation name, year, and half year the animal entered that operation (UK-HY). Contemporary groups comprised of single animals were removed.

The UK-HY population was smaller than the UK-HQ and US populations and so contemporary groups were formed using operation-year-half_year (where the two levels of half_year are the first and second halves of the year) instead of operation-year-season (where the four levels of season are winter, spring, fall, and summer). Using operation-year-half_year allowed for more animals per contemporary group in the UK-HY population, and thus fewer animals removed during subsequent quality filtering to remove singleton contemporary groups.

Adjusting phenotypes to correct for non-genetic effects. Following quality filtering, linear models were fitted separately for each trait (Table 2) using the linear modeling (*lm*) function in the R statistical software (R Core Team, 2024) for each trait within each growing phase and population to correct for non-genetic effects. Each trait was modeled as a variable dependent on genetic background (GT and benchmark), sex (steer and heifer), contemporary group, and, for the

US population, dam breed (Holstein and Holstein-Jersey cross). Dam breed was the same across BxD animals in both UK populations (Holstein), so it was excluded from the UK population models. For out weight, age in days was included as a covariate. For days at the growing phase, in weight was included as a covariate.

Post-hoc comparisons were performed using the *emmeans* package (Lenth, 2025) in R to calculate least squared means of performance traits for GT and benchmark animals and corresponding 95% confidence intervals. Adjusted mean phenotypes for out weights at each growing phase and days at each growing phase were used to calculate ADG as: $ADG = (\text{out weight of growing phase} - \text{out weight of previous growing phase}) / \text{days at growing phase}$. These values and finishing DMI values (US and UK-HY) were used as LCA model inputs.

Feed characteristics. Within each growing phase in each population, animals were fed approximately the same diet. Feed composition and nutritional values were based on feed analysis reports where available and provided by a nutritionist when primary data were unavailable. Based on the ingredients listed in the feed composition, life cy-

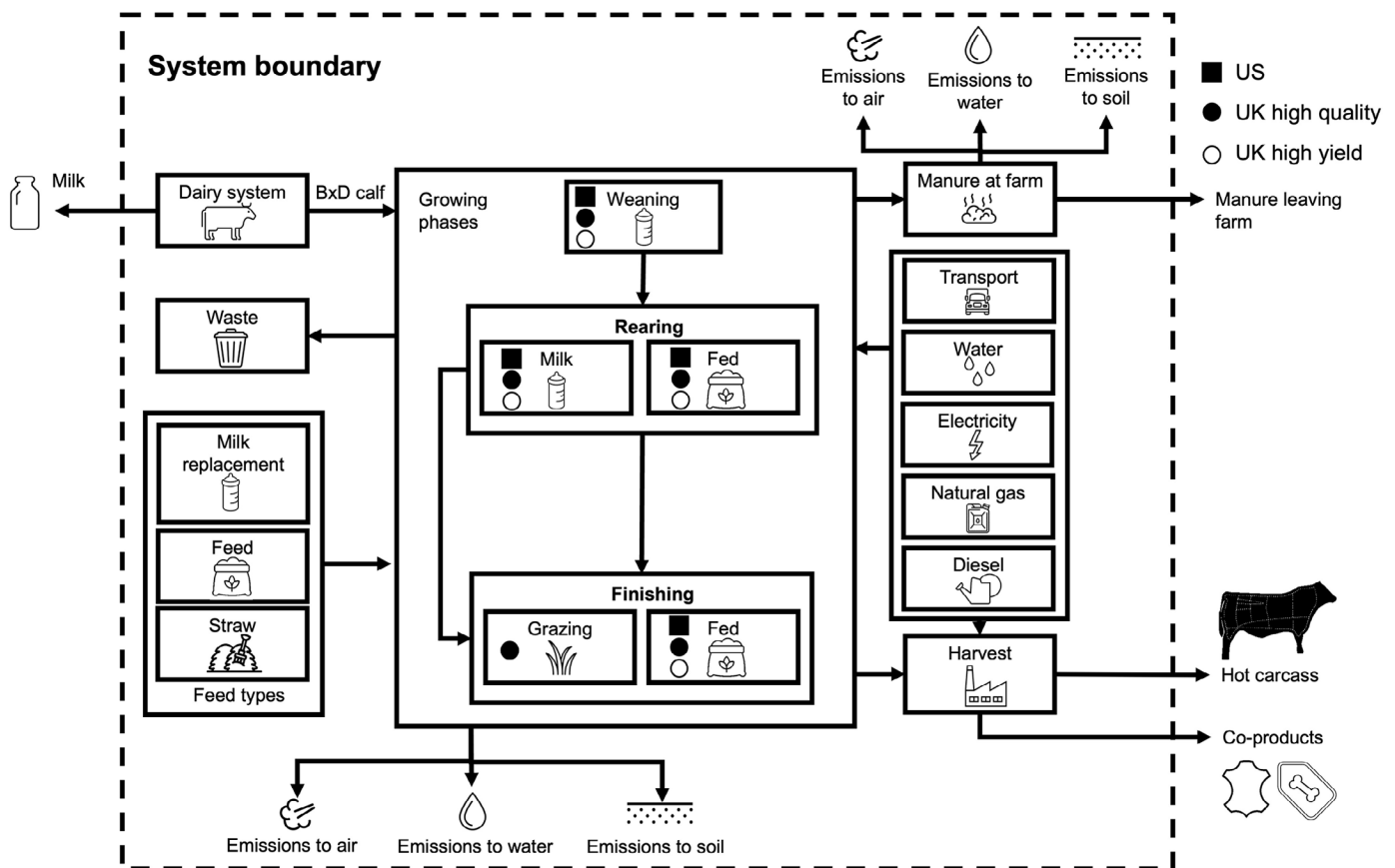


Figure 1. System boundary of the BxD production systems in the US, UK-high quality (UK-HQ), and UK-high yield (UK-HY). Each box represents a process, and within each process there are inputs from and outputs to the environment, which are not all visualized in this diagram. Diagram courtesy of PRé Sustainability.

Table 1. Count of animals in each population, within each genetic background, after quality filtering.

Population	No. animals		
	Genetically targeted	Benchmark	Total
US	1,775	1,410	3,185
UK high quality	3,749	6,465	10,214
UK high yield	860	2,272	3,132

cle inventory data for feed ingredients were sourced from the Agrifootprint 6.3 (Blonk et al., 2022) and Ecoinvent 3.10 (FitzGerald D. et al., 2023) databases. Specifically, milk replacer at weaning and in the rearing-milk phases were sourced from Agrifootprint (Blonk et al., 2022) for all three populations. The ration fed at the rearing-fed phase, and the US finishing ration was a typical ration for the animal class and growing phase as provided by a nutritionist. For UK-HQ, animals were grazed on rye grass during the grazing phase. Ration ingredients composition and feed analysis reports were available for the finishing diets in the two UK populations. Feed ingredient LCIA data from the rearing-fed, grazing, and finishing phases were sourced from Agrifootprint and Ecoinvent.

Manure management and climate zone characteristics. For the UK-HQ and UK-HY populations, wheat straw was used for deep bedding in the weaning, rearing-milk, rearing-fed, and finishing phases. Manure in these housed phases was scraped with the bedding from the pens and stored in piles for a period longer than one month prior to application to nearby croplands for growing animal feed. For the grazing phase in the UK-HQ population, manure was deposited on pasture. For climate change impact calculations from manure management, IPCC emission factors for a cool temperate, and moist climate were used, as animals in the dataset were raised in this climatic region in the UK.

In the US, manure at the weaning and rearing phases was deposited in deep bedding of wheat straw. At both

the dairy and the rearer, bedding mixed with manure was scraped between batches of animals, stored for longer than a month, and applied to surrounding cropland for growing feed. At the finishing phase, manure was scraped on a weekly basis and aggregated in windrows that were intensively composted. The animals in the US dataset were primarily in a temperate and dry climate throughout their lives, so this climatic zone was used for IPCC emission factor selection in calculating climate change impact from manure management.

Functional unit

Per the Global Roundtable for Sustainable Beef Carbon Footprint guidelines, all impact values were expressed per one kilogram of carcass weight after first processing (Global Roundtable for Sustainable Beef, 2022).

Impact assessment

Life cycle impact assessment was conducted according to the Product Environmental Footprint (PEF) method 3.1 (European Commission, 2021) as detailed in Supplemental Table 1. The flows of materials, energy, and emissions from the LCIA were multiplied by characterization factors to aggregate the flows into sixteen impact categories. For example, methane and nitrous oxide emissions calculated using the IPCC Tier 2 method were converted to carbon dioxide equivalents by multiplying the amount of each greenhouse gas by its respective global warming potential value, a type of characterization factor. Specifically, the global warming potential values over a 100-year time horizon defined in the IPCC Sixth Assessment Report were used as characterization factors for climate change impact. This allowed summing of methane and nitrous oxide using the same units to calculate the total climate change impact. Units of characterized results

Table 2. Models used for adjusting phenotypes to remove non-genetic effects

Trait	Model
Out weight (for each growing phase)	Out weight ~ genetic level ¹ + age in days when out weight was measured + sex + (dam breed ²) + contemporary group ³
Days at growing phase (for each growing phase)	Days at growing phase ~ genetic level ¹ + in weight + age in days at start of growing phase + sex + (dam breed ²) + contemporary group ³
Average daily dry matter intake (DMI, finishing only for US and UK- high yield populations)	DMI ~ genetic level ¹ + in weight + age in days at start of trial + days on trial + sex + (dam breed ²) + finisher contemporary group ³
Carcass weight	Carcass weight ~ genetic level ¹ + sex + harvest age in days + (dam breed ²) + finisher contemporary group ³

¹For reference population phenotypes, genetic level refers to genetic background (either benchmark or genetically targeted). For phenotypes across different sire tiers, genetic level refers to the sire tier.

²Dam breed was included in the model only for the US population.

³Contemporary groups were assigned by concatenating operation name, year, and season that the animal entered that operation (US and UK high quality); or operation name, year, and half year that the animal entered that operation (UK high yield).

were calculated and consolidated into the following impact categories:

1. Climate Change
2. Water Scarcity
3. Land Use
4. Acidification
5. Marine Eutrophication
6. Terrestrial Eutrophication
7. Aquatic Freshwater Eutrophication
8. Resource Use, Energy Carriers
9. Eco-toxicity, Freshwater
10. Particulate Matter Respiratory Inorganics
11. Resource Use, Mineral
12. Ozone depletion
13. Human toxicity, cancer
14. Human toxicity, non-cancer
15. Ionizing radiation, human health
16. Photochemical ozone formation, human health

Impact values were normalized and weighted according to their relative importance as defined by PEF 3.1 (Supplemental Table 1). The normalized, weighted impact values were then ranked in descending order, and the impact categories that collectively contributed to the top 80% of overall impact were considered the most relevant categories, per the PEF 3.1 method. Within each of the relevant categories, the impact was further split out by the contribution from each growing phase and from each of the following processes: gestation, enteric fermentation, processing at the packer, manure management, feed production, transportation, and other processes, which included bedding and water intake. A contribution analysis was conducted to identify the top growing phases and processes affecting the relevant impact categories.

Framework to account for genetic merit in an LCA

A series of LCIA runs were conducted to collectively capture the range in environmental impact of BxD animals corresponding to the variation in the genetic merit of their sires, as marketed in 2024, and the projected variation in sire genetic merit expected to be marketed in 2029 based on current genetic trends. For each population, the range in sire genetic merit was divided into five tiers based on sire genetic index values, calculated using a proprietary index developed for the breeding program, within the benchmark animals and separately within the GT animals. The LCIA was then repeated for each sire genetic tier, including the progeny of the sires in that tier, within the benchmark and GT populations, for each marketing year. The series of LCIA runs resulted in an environmental footprint profile for each sire tier, genetic

background, population and marketing year. The method to account for genetic merit in an LCA is detailed below and diagrammed in Figure 2.

Defining progeny key performance indicators. Progeny key performance indicators (KPIs) were determined from the reference population contribution analysis and defined as the progeny traits affected by genetics that most influenced differences in environmental impact, which were finishing ADG, days in the finishing phase, and finishing DMI (for the US and UK-HY populations only, as no DMI measurements were available for UK-HQ animals). These KPIs were used as the input values for the LCIA runs.

Steps 1-3. Fitting regression models to calculate progeny KPI given a sire genetic merit tier. Within each of the three populations, the same procedure was performed to quantify the rate of improvement, split the range into genetic merit tiers, and calculate the corresponding progeny KPIs across the genetic merit range. Benchmark and GT animals were combined into one dataset, then split into five sire genetic merit tiers based on their sire's genetic index value (Step 1 in Figure 2). Each population (US, UK-HQ and UK-HY) had a slightly different index, but all indices focused on improving growth, feed efficiency, and carcass performance (weight and yield). Sire tier cutoffs were equally spaced and centered around the mean index value, for that population, such that Tier 3 corresponded to average genetic merit, Tier 1 had the lowest genetic merit, and Tier 5 had the highest genetic merit. Tier 1 and 5 also included sires that were respectively lower or higher than the sire tier index thresholds.

For each sire tier, mean progeny KPIs were calculated and adjusted for non-genetic effects using the same models for adjusting phenotypes in the reference population, where genetic level referred to sire tier instead of genetic background (Step 2 in Figure 2, models listed in Table 2). Specifically, for ADG, least-squares means were first calculated for each sire tier for in and out weights and days at the finishing phase. Then, ADG was calculated using the adjusted in and out weights and days ($ADG = (\text{out weight} - \text{in weight})/\text{days}$). For DMI, least-squares means for DMI were estimated for each sire tier and adjusted for non-genetic effects. Because UK-HQ lacked feed intake data, DMI least-squares means were not calculated for this population, and DMI values from the reference population were used in the calculation. The resulting progeny KPIs (ADG and DMI) were then regressed on sire tier to generate a prediction model for each KPI to predict progeny KPI given a sire tier (Step 3 in Figure 2). The same procedure was performed within each of the three populations. Although the range in genetic merit was different between the benchmark and GT animals, the relationship between progeny KPI and sire

genetic merit was expected to be the same. Consequently, for steps 1-3, benchmark and GT animals were combined into one dataset to fit the prediction equations for progeny KPI, given sire genetic merit level, to maximize the reference dataset used for this prediction.

Steps 4-6. Setting sire tiers based on index trends and calculating progeny KPIs for each sire tier. To determine the rate of increase in average sire index value over time, a linear model was fit for the genetic index trend for benchmark sires and separately for GT sires. The index trend was then used to predict the average index for benchmark and GT sires in marketing year 2029, assuming a linear improvement in the genetic index (Step 4 in Figure 2). For each genetic background (benchmark and GT) within each year (2024 and 2029), the five sire tiers were recentered around the mean index value using the same method as in Step 1. Benchmark and GT sire tiers were set separately within each population because past genetic selection using the index resulted in the tiers in the GT population spanning a range in index values that was shifted to the right compared to the benchmark population. The regression models fit in Step 3 were then used to calculate average

daily gain (all populations) and DMI (US and UK-HY) for each sire tier in each marketing year.

Because animals were in commercial operations, their harvest dates were largely dependent on cattle market prices or other management considerations rather than solely on reaching an ideal harvest weight or finish. Consequently, days at finishing and, in turn, finishing weight phenotypes would be expected to be influenced at some level by factors beyond their genetic potential for growth and efficiency. To minimize this non-genetic, market-driven variation, finishing out weight was standardized within each population: the average finishing out weight between benchmark and GT animals in the reference population was calculated and used as the finishing out weight for all runs. The number of days in the finishing phase was then back-calculated using the projected ADG, finishing out weight, and finishing in weight: $\text{days at finishing} = (\text{finishing end weight} - \text{finishing in weight}) / \text{ADG}$, where finishing in weight values were not changed from reference population values. For example, in the US population, finishing in weights were assumed to be the same across the five sire tiers within the benchmark population (275 kg for all five benchmark sire tiers) and

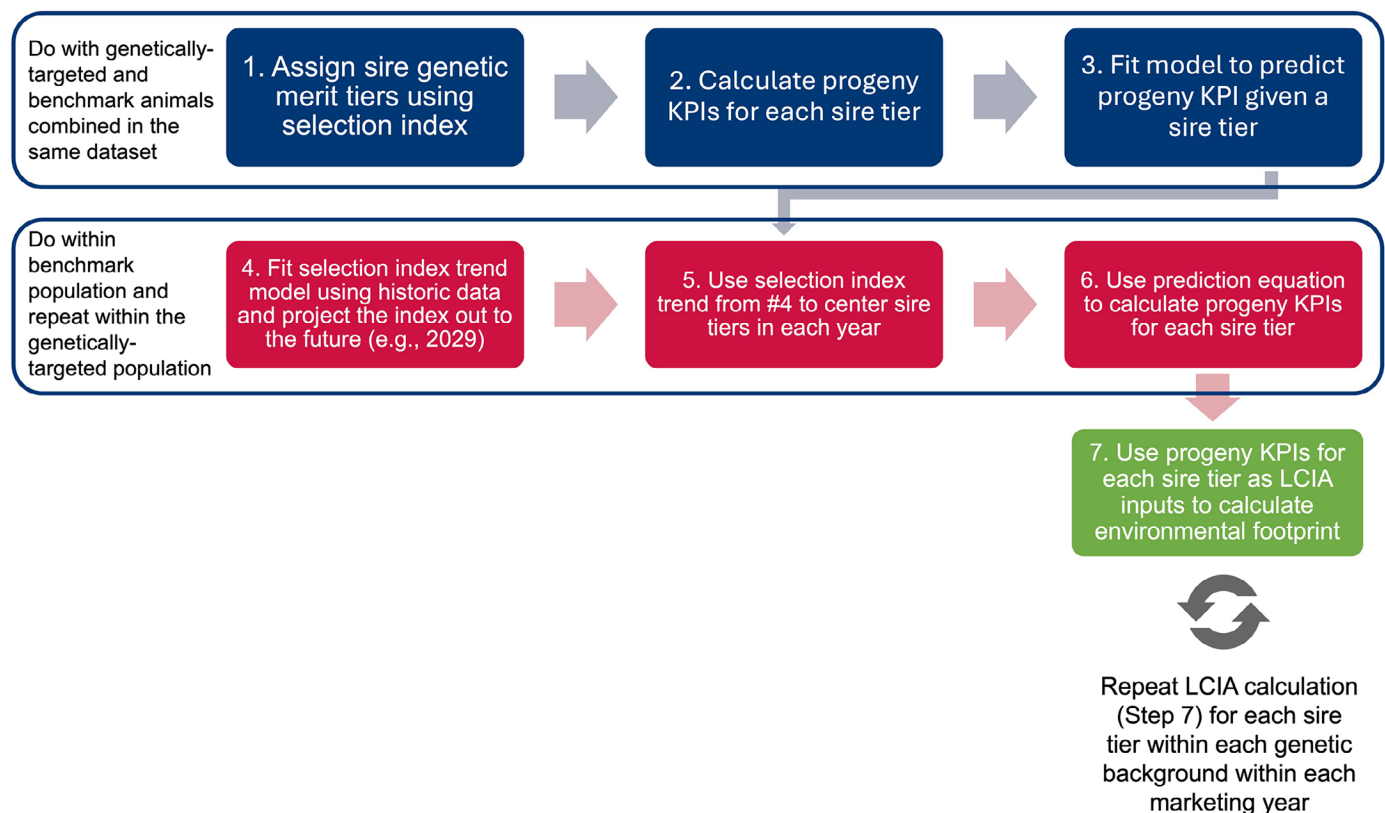


Figure 2. Framework to incorporate genetic merit into a life cycle assessment by first calculating progeny KPI profiles for each genetic merit level (sire tier within benchmark or genetically targeted animals) using prediction models fitted in a reference population, and using the resulting KPIs in LCA runs encompassing the range in genetic merit.

likewise in the GT population (287 kg for all five GT sire tiers) in both 2024 and 2029. Although it is possible that finishing out weights could change in the future, the same value was used to enable a fair comparison of environmental impact across the different timepoints, such that differences in impact were driven by overall performance rather than growing a larger animal.

Step 7. Using progeny KPIs for each sire tier to calculate environmental footprint. The resulting progeny KPIs (finishing ADG, days at finishing, and finishing DMI for US and UK-HY,) for each of the five tiers were then used in LCA runs to calculate the environmental footprint for each of the five tiers, in each marketing year, in each genetic background and in each population. All other inputs remained at reference population values.

Significance testing for differences in climate change impact between sire tiers

Testing was performed to determine the significance of the difference in climate change impact between sire tiers when accounting for the variation in the progeny KPIs (finishing ADG and finishing DMI) used as LCA inputs. Pairwise comparisons selected for significance testing reflected practical assumptions about dairy farmer decision-making when selecting BxD genetics. Dairy farmers that currently use average industry genetics (benchmark) may switch to average targeted genetics or to the best available genetics in a given marketing year. Accordingly, the pairwise comparisons highlighted were benchmark Tier 3 and GT Tier 3 in 2024, GT Tier 3 and GT Tier 5 in 2024, benchmark Tier 3 and GT Tier 3 in 2029, and GT Tier 3 and GT Tier 5 in 2029.

To generate distributions of climate change impact given the uncertainty around the progeny KPIs, Monte Carlo sampling was performed by randomly sampling from the distributions of DMI and ADG, then re-calculating climate change impact in SimaPro. The DMI and ADG distributions were assumed to be normally distributed and defined using the mean and standard deviation calculated for each sire tier using the reference population data. Each iteration of sampling and recalculation was executed 500 times. In R, the resulting coefficient of variation (CV) was monitored over the iterations to determine at what iteration the CV stabilized. The Mann-Whitney U test was then performed to test for the significance of the difference in the distributions of climate change impact between two sire tiers, where the distributions were created from the iterations required to reach a stable CV.

Assumptions and limitations

The effect of non-genetic factors such as management practices, variation in diet, and market prices that influence timing of animal harvest contributed to variation in progeny performance beyond the effect of genetic differences. To minimize the impact from these non-genetic effects, a large sample size across three years (animals harvested in 2021-2024) and various operations was used, and progeny performance data were corrected for these non-genetic factors, as described above. For the LCIA runs, progeny performance data were also standardized to a common harvest weight across sire tiers, genetic backgrounds, and marketing years within each population to isolate the effect of genetics.

RESULTS

Adjusted phenotypes for progeny performance traits from birth to harvest used as LCA inputs are summarized in Table 3. Higher genetic merit, whether due to higher sire tier or later marketing year, was associated with faster ADG, fewer days to harvest, and, for the US and UK-HY populations, decreased DMI. These genetic-driven performance improvements manifested as lower environmental footprint.

Identification of the most relevant impact categories from the reference population

As illustrated in Figure 3, climate change, particulate matter, acidification, and terrestrial eutrophication contributed to the top 80% portion of the environmental footprint for all three reference populations and were considered relevant impact categories (Table 4-Table 6). In addition to this shared core group of categories, marine eutrophication was a relevant category for UK-HQ and UK-HY, land use and fossil fuel resource use were relevant for UK-HY, and freshwater ecotoxicity and water use were relevant for the US. The same categories were identified as relevant in the tiered populations (Figure 4). Impact values from the other categories comprising the remaining 20% of the footprint were listed in Supplemental Table 2.

Contribution from growing phases

The finishing phase had the largest impact among all growing phases, ranging from 50-89% of impact across relevant environmental impact categories, marketing years, sire genetic merit tiers, and populations (Figure 5, Supplemental Figure 1), because animals were the largest at this growing phase and remained at the finishing phase for the longest period of their lives. The combi-

nation of high energy requirements and duration of the finishing period resulted in greater feed intake driving a larger feed production impact as well as more manure excreted compared to other growing phases. For the UK-HQ population, the grazing period was the second largest contributor for acidification, climate change, marine and terrestrial eutrophication, and particulate matter, followed by the rearing-milk and rearing-fed phases (Figure 5a, Supplemental Figure 1a). Rearing-milk and rearing-fed were respectively the second and third largest contributors in the UK-HY population (Figure 5b, Supplemental Figure 1b) and the third and second largest contributors in the US population (Figure 5c, Supplemental Figure 1c). The notable contribution of the rearing-milk phase across impact categories in all three populations was driven primarily by the production of milk replacer.

Process contribution

Across all populations and sire genetic merit tiers, the main processes contributing to the relevant environmental impact categories were feed production, manure management, and, for climate change only, enteric fermentation (Figure 6, Supplemental Figure 2). Feed production was the leading contributor to freshwater ecotoxicity (60-71% across populations, sire tiers, and marketing years), land use (82-89%), fossil fuel use (70-87%), and water use (82-95%). Manure management was the largest contributor to acidification (52-79%) and particulate matter (56-81%), followed by feed production for both impact categories (17-38% for acidification and 14-33% for particulate matter). Feed production and manure manage-

ment collectively contributed to the majority of marine (87-94%) and terrestrial (91-95%) eutrophication across sire tiers and marketing years in all three populations. Feed production and manure management were equal or larger contributors to climate change impact (31-43% and 23-43%, respectively) relative to enteric fermentation (15-32%), depending on the population.

In the grazing period specific to the UK-HQ population, the processes driving environmental impact differed from the other growing phases. Since animals were grazed, feed production was not a relevant source for any impact category during this growing phase. Manure management was the main source of environmental impact for eutrophication, acidification, and particulate matter during the grazing phase. Unlike in other growing phases, enteric fermentation was the top contributor to climate change in the grazing period (56%) followed by manure management (40%) because relative to the rearing and finishing phases, the digestibility of feed (rye grass in pasture) was lower, animals were expending additional energy to roam and graze, and ADG was slower. Collectively, these three factors in turn increased enteric fermentation and manure management emissions (Figure 6).

Impact categories relevant for all populations: Climate change, particulate matter, acidification, and eutrophication. Emissions of carbon dioxide, methane, and nitrous oxide were the primary drivers of climate change impact across the sub-processes. Climate change impact from manure management was driven by manure methane and nitrous oxide emissions (Supplemental Figure 3). For feed production, the main influencer of climate

Table 3. Adjusted phenotypes for progeny performance traits in marketing year 2024, averaged across the benchmark and genetically targeted populations

Growing phase	Trait ¹	Population		
		UK high quality	UK high yield	US
Weaning	In weight (kg)	36	34	42
	Duration (days)	23	31	1
	ADG (kg/day)	0.65	0.65	0.68
Rearing-milk	In weight (kg)	55	65	43
	Duration (days)	47	42	70
	ADG (kg/day)	0.83	1.00	0.56
Rearing-fed	In weight (kg)	94	108	82
	Duration (days)	47	51	168
	ADG (kg/day)	0.83	1.00	1.34
Grazing	In weight (kg)	132	NA	NA
	Duration (days)	180	NA	NA
	ADG (kg/day)	0.48	NA	NA
Finishing	In weight (kg)	219	158	281
	Duration (days)	370	343	240
	ADG (kg/day)	0.88	1.19	1.38
Harvest	Out weight (kg)	544	563	612
	Carcass weight (kg)	316	313	401

¹Average daily gain (ADG) values calculated from the weights and durations listed in the table may not exactly match due to differences in rounding.

change impact was emissions from the production and application of fertilizers for growing feed. Enteric methane emissions drove the climate change impact from enteric fermentation. For transportation, climate change impact was most strongly affected by the burning of fossil fuels when trucking animals between operations. Transport distance and animal weight influenced the transportation impact: longer distances and heavier animals increased the emissions from transport.

In the finishing phase, across all populations, and the grazing phase in the UK-HQ population, manure management and feed production were the leading processes contributing to particulate matter, acidification potential, and terrestrial and marine eutrophication. Ammonia that volatilized from manure was a precursor for particulate matter formation. Particulates released into the air during the production and application of fertilizer for growing feed also contributed to particulate matter formation. Ammonia from manure and ammonia and nitrogen oxides from fertilizer production and application could leach into the soil and water, contributing to the terrestrial and marine eutrophication potential. Fertilizer application for

the production of wheat straw used for bedding in rearing also contributed to terrestrial and marine eutrophication potential in the UK populations.

Other impact categories that were relevant to some but not all populations. Water usage and water ecotoxicity were also identified as relevant impact categories for the US population. Water usage was primarily from the irrigation of crops for feed production, and water ecotoxicity was influenced by crop protection products used during feed production. Land use for growing crops for feed was identified as a relevant impact category for UK-HY. Fossil fuels usage from transporting animals between operations was identified as a relevant impact category for UK-HY, but not in other populations because other impact categories (e.g., climate change, particulate matter, acidification, eutrophication) had proportionally larger contributions to the environmental footprint.

Effect of genetic merit on estimated environmental impact

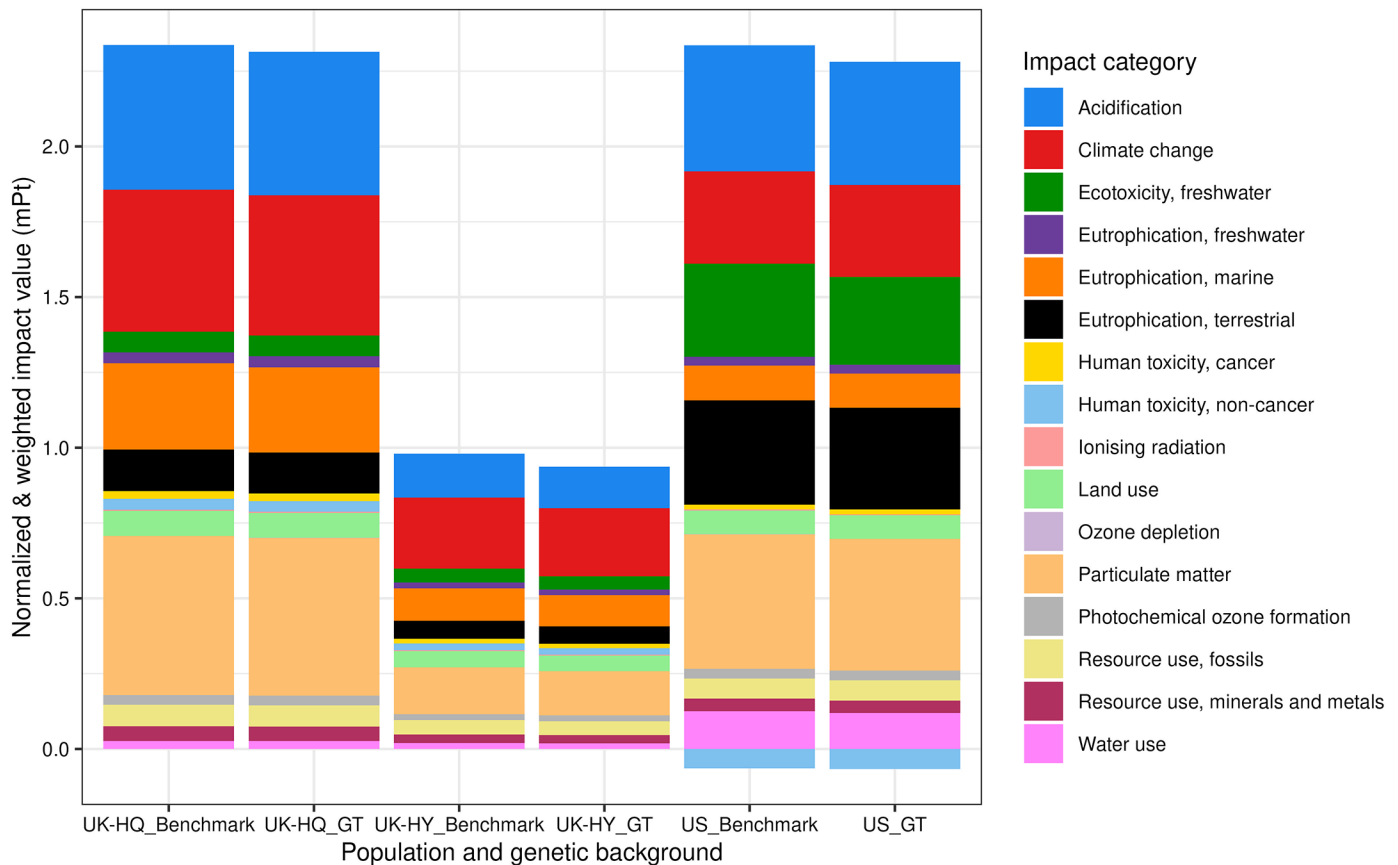


Figure 3. Contribution of each impact category to the environmental footprint of the UK high-quality (HQ), UK high-yield (HY), and US benchmark and genetically targeted (GT) reference populations, normalized and weighted to millipoints (mPt) per the PEF 3.1 method.

Lai and Cleveland: LCA FOR GENETIC IMPROVEMENT IN BEEF-ON-DAIRY

Table 4. Environmental impact profiles for relevant categories in 2024 and 2029 for industry average animals (benchmark – Tier 3) and high genetic merit animals (genetically targeted – Tier 5) in the UK high quality population expressed per kg of carcass weight

Year	Impact category ¹	Unit	Benchmark-Tier 3	Genetically targeted-Tier 5
2024	Acidification	mol H ⁺ eq	0.440	0.423
2024	Climate change	kg CO ₂ eq	17.4	16.6
2024	Eutrophication, marine	kg N eq	0.193	0.185
2024	Eutrophication, terrestrial	mol N eq	0.676	0.644
2024	Particulate matter	disease incidence	3.59e-06	3.45e-06
2029	Acidification	mol H ⁺ eq	0.439	0.420
2029	Climate change	kg CO ₂ eq	17.4	16.5
2029	Eutrophication, marine	kg N eq	0.192	0.184
2029	Eutrophication, terrestrial	mol N eq	0.674	0.639
2029	Particulate matter	disease incidence	3.58e-06	3.43e-06

¹Values for additional impact categories, including those that were not defined as relevant, are listed in Supplementary Table 2.

Estimated environmental benefits from genetic-driven performance improvements. Higher genetic merit (i.e., higher sire merit tiers) consistently led to lower environmental impact by influencing progeny performance in slightly different ways among the three populations. Genetic merit predominantly affected ADG, DMI, and finishing in weight which, in turn, influenced environmental impact. In all three populations, higher genetic merit yielded larger ADG. Dry matter intake and finishing in weight followed different trends across the three populations, but the combined effect of faster growth with less feed over the finishing period yielded lower environmental impact for higher genetic merit animals. Impact values across sire genetic tiers, populations, marketing years, and impact categories that were relevant to at least one population are shown in Supplemental Figures 1 and 2, and Supplemental table 2.

For the UK-HQ population, environmental benefits resulting from higher genetic merit were driven primarily by greater ADG leading to fewer days to harvest. In weights were similar between benchmark and GT animals (GT was 1 kg heavier than benchmark), and since no feed intake data were available, the reduction in impact from higher genetic merit was driven solely by greater ADG. Anecdotal results from feed trials would suggest that that GT animals were more feed efficient than benchmark animals, however no feed intake data were available for the animals in this study to evaluate this possibility.

In the UK-HY population, reductions in environmental impact from higher genetic merit sires were driven not only by greater ADG, but also lower DMI, which was captured in feed intake trial data. In weights were similar between benchmark and GT animals, so the fewer days to harvest was driven solely by faster ADG. The reduction

Table 5. Environmental impact profiles for relevant categories in 2024 and 2029 for industry average animals (benchmark – Tier 3) and high genetic merit animals (genetically targeted – Tier 5) in the UK high yield population expressed per kg of carcass weight

Year	Impact category ¹	Unit	Benchmark-Tier 3	Genetically targeted-Tier 5
2024	Acidification	mol H ⁺ eq	0.134	0.117
2024	Climate change	kg CO ₂ eq	8.51	7.76
2024	Eutrophication, marine	kg N eq	0.0697	0.0637
2024	Eutrophication, terrestrial	mol N eq	0.288	0.260
2024	Land use	Soil quality index point	549	509
2024	Particulate matter	disease incidence	1.06e-06	9.26e-07
2024	Resource use, fossils	MJ	36.1	33.6
2029	Acidification	mol H ⁺ eq	0.134	0.114
2029	Climate change	kg CO ₂ eq	8.50	7.62
2029	Eutrophication, marine	kg N eq	0.0696	0.0628
2029	Eutrophication, terrestrial	mol N eq	0.288	0.255
2029	Land use	Soil quality index point	549	503
2029	Particulate matter	disease incidence	1.06e-06	9.00e-07
2029	Resource use, fossils	MJ	36.1	33.2

¹Values for additional impact categories, including those that were not defined as relevant, are listed in Supplementary Table 2.

Table 6. Environmental impact profiles for relevant categories in 2024 and 2029 for industry average animals (benchmark – Tier 3) and high genetic merit animals (genetically targeted – Tier 5) in the US population expressed per kg of carcass weight

Year	Impact category ¹	Unit	Benchmark-Tier 3	Genetically targeted-Tier 5
2024	Acidification	mol H ⁺ eq	0.400	0.360
2024	Climate change	kg CO ₂ eq	11.3	10.7
2024	Ecotoxicity, freshwater	CTUe	1840	1640
2024	Eutrophication, terrestrial	mol N eq	1.76	1.59
2024	Particulate matter	disease incidence	3.14e-06	2.84e-06
2024	Water use	m3 deprivation	16.9	15.4
2029	Acidification	mol H ⁺ eq	0.398	0.349
2029	Climate change	kg CO ₂ eq	11.2	10.5
2029	Ecotoxicity, freshwater	CTUe	1830	1600
2029	Eutrophication, terrestrial	mol N eq	1.75	1.54
2029	Particulate matter	disease incidence	3.12e-06	2.75e-06
2029	Water use	m3 deprivation	16.9	15.1

¹Values for additional impact categories, including those that were not defined as relevant, are listed in Supplemental Table 2.

in feed requirements to reach the same harvest weight, resulting from higher genetic merit, translated to lower impact from feed production, enteric emissions, and manure management.

In the US population, higher genetic merit was associated with heavier finishing in weight, in addition to greater ADG and a slight increase in average daily DMI. The increase in DMI with increasing genetic merit was offset by a heavier finishing in weight and a greater ADG,

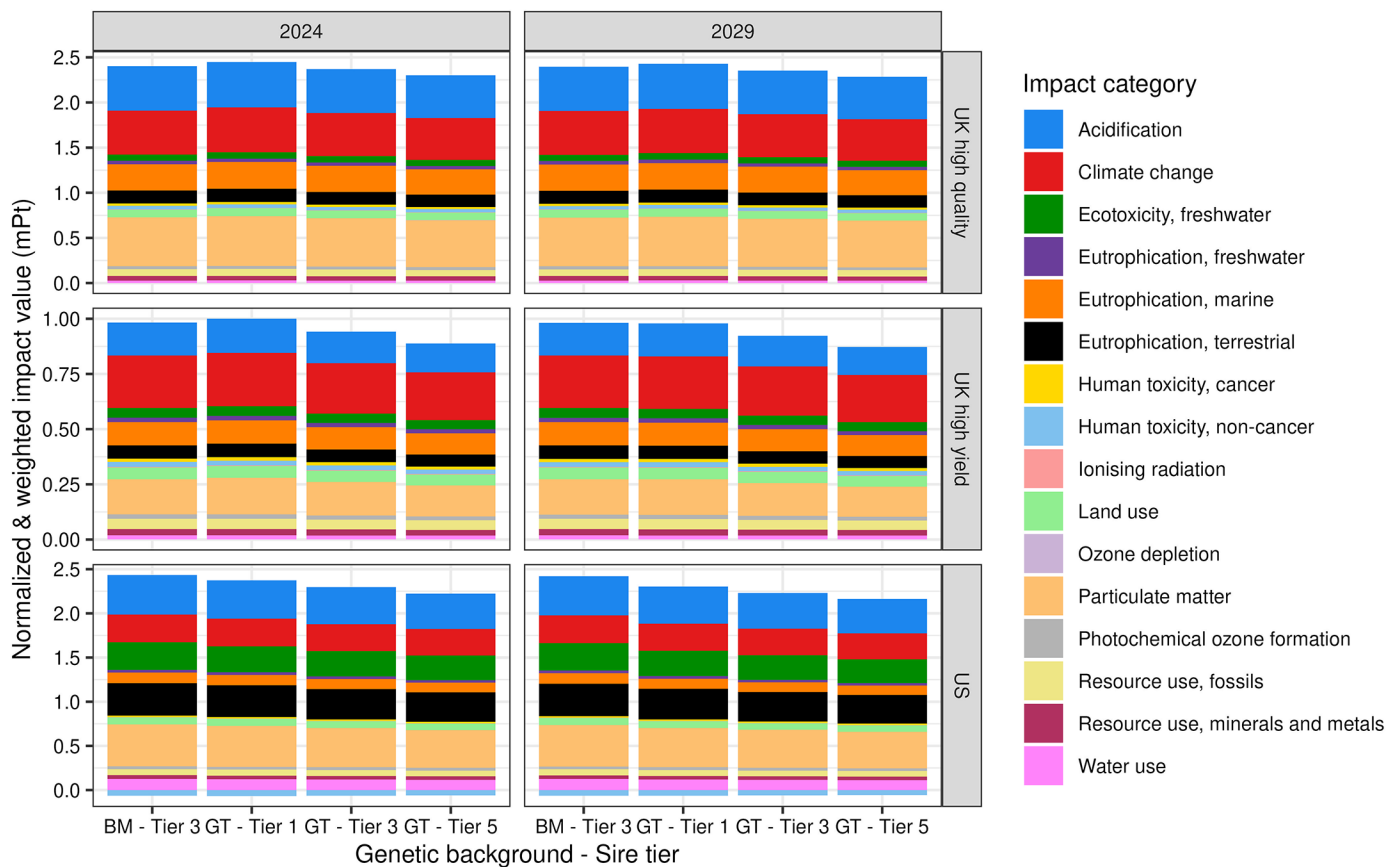


Figure 4. Contribution of each impact category to the environmental footprint across sire tiers of benchmark (BM) and genetically targeted (GT) animals within the UK high-quality, UK high-yield, and US populations, normalized and weighted to millipoints (mPt) per the PEF 3.1 method.

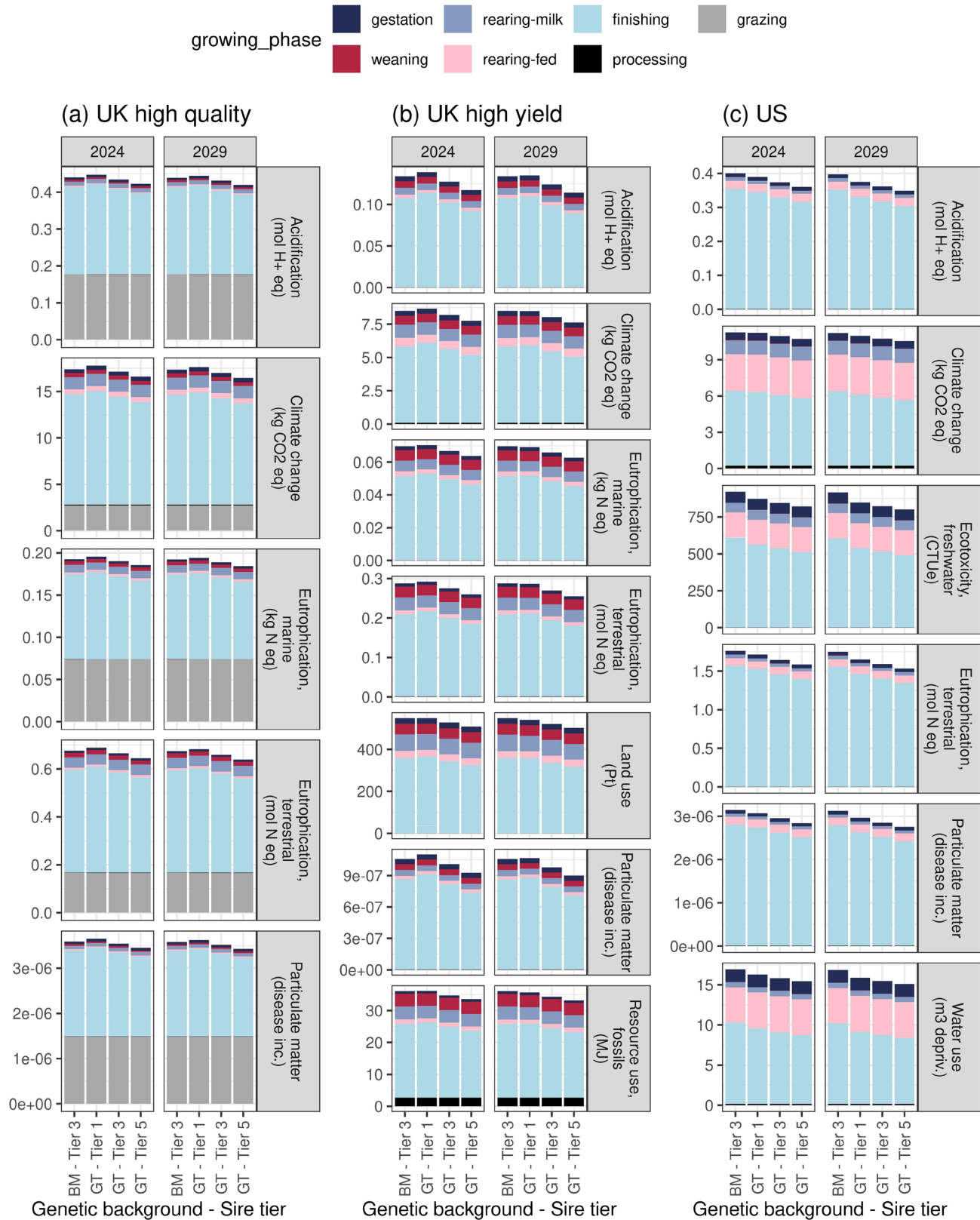


Figure 5. Contribution to each relevant environmental impact category from each growing phase in marketing years 2024 and 2029 for benchmark (BM) and genetically targeted (GT) animals in the (a) the UK high quality, (b), UK high yield, and (c) US populations, split out by sire tier. Benchmark Tier 3 represents industry average genetics.

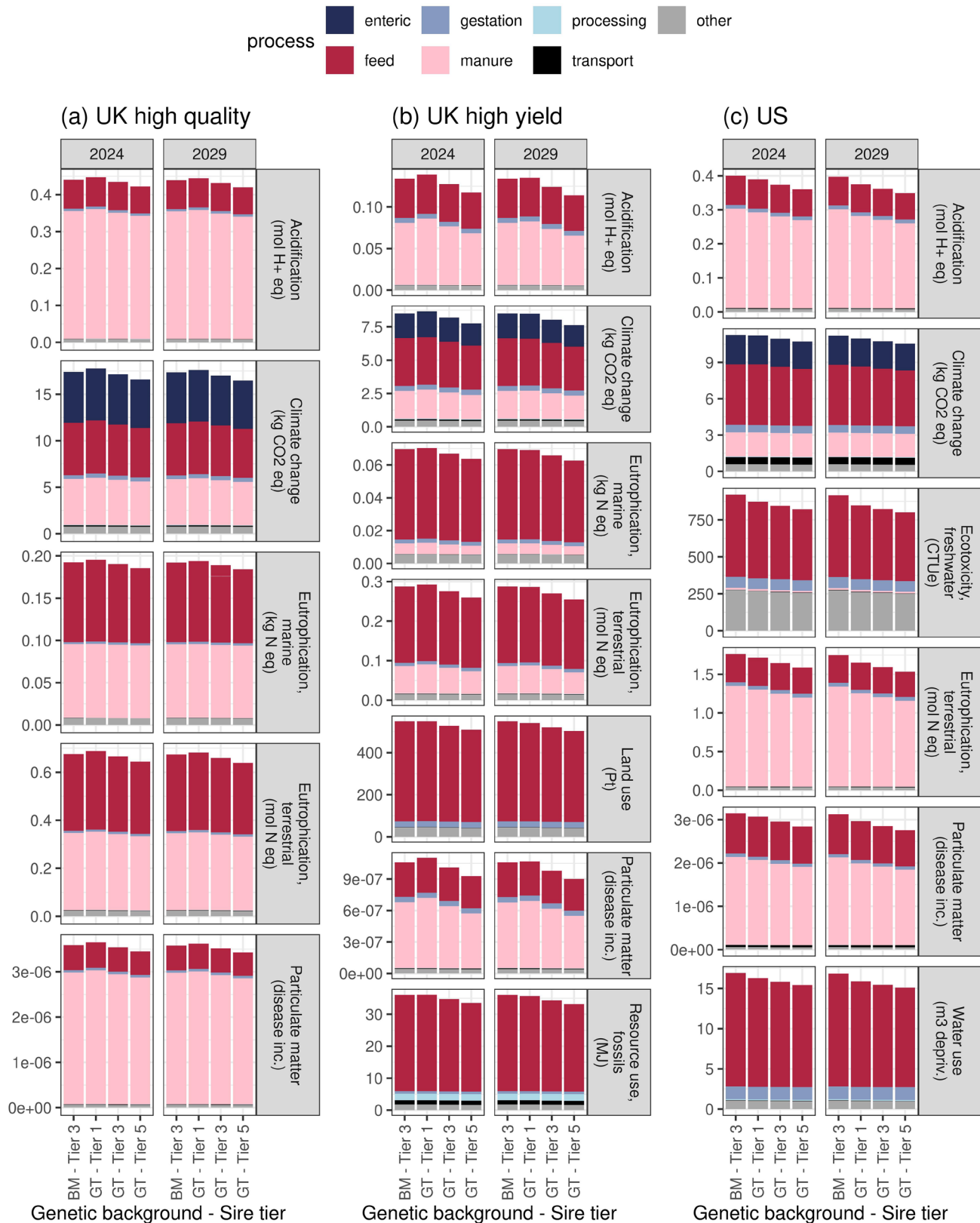


Figure 6. Contribution to each relevant environmental impact category from different sources in marketing years 2024 and 2029 for benchmark (BM) and genetically targeted (GT) animals in the (a) the UK high quality, (b), UK high yield, and (c) US populations, split out by sire tier. Benchmark Tier 3 represents industry average genetics.

leading to fewer days at finishing. Consequently, the total feed consumed over the finishing phase decreased with increasing genetic merit, leading to lower impact from enteric emissions and manure excreted.

Although genetic merit had varying effects on progeny KPIs across the three populations, in each population higher genetic merit led to lower environmental impact resulting from systemic efficiency improvements. Additionally, genetic merit was positively correlated with growth rate and DMI throughout the finishing phase, leading to fewer days to harvest. Consequently, animals in higher sire genetic merit tiers had fewer days to produce enteric emissions, excrete manure, and consume feed which, in turn, led to lower environmental impact, whether due to higher sire tier, targeted genetic background, or genetic improvement over time.

Temporal change in estimated environmental footprint. From 2024 to 2029, average genetic merit (represented by Tier 3) in both the benchmark and GT populations was predicted to improve in all three populations. Average genetic merit in the GT population was predicted to improve more quickly than that of the benchmark population due to targeted genetic improvement. As the result of differing genetic trends, the difference in environmental impact between benchmark and GT animals was predicted to increase from 2024 to 2029. Using climate change impact in the US population as an example, the difference between benchmark Tier 3 and GT Tier 3 was $-0.30 \text{ kg CO}_2\text{e/kg CW}$ in 2024 and was projected to increase to $-0.46 \text{ kg CO}_2\text{e/kg CW}$ in 2029. A similar temporal trend of an increasing reduction in impact of GT animals relative to benchmark was observed across all impact categories in all three populations (Figure 5, Figure 6, Supplemental Figure 1, Supplemental Figure 2). There was a difference in climate change impact between GT Tier 3 and benchmark T3 in 2024, in all three populations (UK-HQ $p = 0.0038$, UK-HY $p = 0.0035$, US $p = 0.0015$), with stronger evidence for a difference in the 2029 projection due to the increased separation in genetic merit and resulting climate change impact (UK-HQ $p = 0.0012$, UK-HY $p = 2.54\text{E-}81$, US $p = 3.07\text{E-}18$) using the Mann-Whitney U test.

As a result of the genetic merit improving more quickly in the GT population, the overlap in the range of environmental impact values covered by the five sire tiers in the benchmark compared to the GT population was projected to shrink over time. Using climate change in the US as an example, the range in climate change from the benchmark and GT sire tiers overlapped by $0.22 \text{ kg CO}_2\text{e/kg CW}$ in 2024 and was projected to overlap by $0.02 \text{ kg CO}_2\text{e/kg CW}$ by 2029. The same trend of increasing separation between benchmark and GT from 2024 to 2029 was observed in all impact categories in all three populations (Figure 5, Figure 6, Supplemental

Figure 1, Supplemental Figure 2), albeit at a slower rate of separation in the UK populations (for climate change, 0.95 to $0.83 \text{ kg CO}_2\text{e/kg CW}$ in UK-HQ and 0.60 to $0.44 \text{ kg CO}_2\text{e/kg CW}$ for UK-HY).

Industry example: Switching from benchmark to highest merit targeted genetics. In a commercial situation a dairy producer may decide to invest in genetic improvement of BxD animals and switch from using industry average genetics to high-indexing targeted genetics. This comparison corresponds to substituting benchmark Tier 3 genetics with GT Tier 5 genetics. In marketing year 2024, switching from benchmark Tier 3 to GT Tier 5 genetics in the US population resulted in a slightly greater DMI, which was offset by the greater ADG driving improved feed efficiency (decreased in FCR) and fewer days to finish. Evaluating this switch in all three populations, these improvements in progeny performance translated to a 3.7-12.5% reduction in impact, depending on the impact category and population (Table 4, Table 5, and Table 6), amounting to a 4.2-8.7% overall environmental footprint reduction (Figure 4). These reductions were projected to grow by 2029 to 4.1-14.9% across populations and relevant impact categories, amounting to a 4.7-11.2% overall environmental footprint reduction (Figure 4). Using climate change as an example, the impact from GT Tier 5 relative to the average benchmark genetic level (Tier 3) was 4.7% lower ($-0.82 \text{ kg CO}_2\text{e/kg CW}$) for the UK-HQ population (Table 4), 8.8% lower ($-0.75 \text{ kg CO}_2\text{e/kg CW}$) for the UK-HY population (Table 5), and 4.7% lower ($-0.53 \text{ kg CO}_2\text{e/kg CW}$) for the US population (Table 6). In the 2029 marketing year, the reduction in climate change impact of GT Tier 5 relative to benchmark Tier 3 was predicted to grow to 5.4% ($-0.90 \text{ kg CO}_2\text{e/kg CW}$) for UK-HQ (Table 4), 10.4% ($-0.88 \text{ kg CO}_2\text{e/kg CW}$) for UK-HY (Table 5), and 6.0% ($-0.67 \text{ kg CO}_2\text{e/kg CW}$) for US (Table 6) due to expected faster genetic improvement and, in turn, faster reduction in climate change impact in the GT population relative to the benchmark population. When accounting for the variation in DMI and ADG at finishing, differences in climate change impact between benchmark Tier 3 vs. GT Tier 5 were observed using the Mann-Whitney U test ($p < 0.05$) for all three populations in both marketing years.

DISCUSSION

We present a novel framework to incorporate genetic improvement in bovine LCAs and apply our approach to estimate the environmental footprint for BxD production across sixteen impact categories. This study evaluated the environmental impact of targeted genetic improvement from three BxD production systems in the US and UK, in two marketing years, using a LCA approach. Because the variation in environment and management

strongly influences performance in cattle production, we developed a framework to minimize this variation and isolate the effect of genetic improvement by adjusting progeny phenotypes for non-genetic effects and using them as inputs into the LCA model. We created sire genetic tiers and used the adjusted phenotypes for each tier to capture environmental footprint across a range in genetic merit. Additionally, we projected the genetic trend of the benchmark and GT sires and used the relationship between the sire tier and progeny performance observed in commercial data to predict future environmental footprint. In each of the three populations, the GT animals had 4.2-8.7% lower environmental impact than benchmark animals in 2024, and the reduction increased to 4.7-11.2% in 2029. Although the performance of both the benchmark and GT populations was projected to improve based on genetic trends, traits like feed efficiency and growth were predicted to improve more quickly in the GT animals, accelerating the reduction in environmental impact relative to benchmark animals. In the present study, comparisons were made relative to the benchmark population in the same year; however, the base year could be reset to any tier in any year to adjust the comparisons for different baselines. The acceleration of the GT genetic trend was attributed to directed selection for growth and efficiency traits in the designed BxD breeding program evaluated in this study. The genetic index used here contains a unique blend of traits that would differ from index selection used in other breeding programs and would, thus, also uniquely affect environmental impact. While the resulting impact described here is only applicable to the breeding program studied, the proposed framework can be applied in future LCAs to assess environmental impact from genetic improvement in other populations.

Although to date no BxD LCAs accounting for genetic improvement have been published, previous environmental footprinting studies have incorporated genetic improvement into calculations for selected impact categories for BxB and dairy production. For BxB production, White et al. (2015) modeled how different genetic, reproductive, and nutrition management methods would affect the environmental impact of the cow-calf sector, demonstrating that selecting higher-indexing natural service or AI sires could reduce land use, water use, and GHG emissions by ~11%. Amer et al. proposed a method for estimating how greenhouse gas emission intensity changes when employing genetic selection, using the genetic trends in the Irish dairy herd as an initial example (Amer et al., 2018) and applying this framework to Irish beef cattle (Quinton et al., 2018) and dairy cattle in New Zealand (Zhang et al., 2019). More recently, another study showed through simulations that dairy animals in the top 25% of genetic merit, as defined

by a specific selection index, had lower enteric methane nitrogenous, phosphorous, and total degradable volatile solids emissions compared to the bottom 25% of the herd (Weigel et al., 2025). Focusing on one trait and one impact category, a carbon footprinting study estimated that selection on residual feed intake could reduce lifetime GHG emissions from dairy cattle by 2.42-7.31% (Lucas et al., 2026). These studies demonstrate that regardless of the production system or type of genetic improvement, genetic improvement for improved production efficiency consistently delivers environmental benefits.

Using a more comprehensive approach, LCAs using standardized LCIA frameworks accounting for genetic merit have been reported for pig production. In an LCA for swine production, Thoma et al. (2024) demonstrated that genetically targeted pigs had an estimated 7-8% lower environmental effect across impact categories. One key methodology difference between Thoma et al. and the present study was handling of phenotypes. Phenotype adjustment was not necessary for their pig production system because, unlike cattle, the environment and management are relatively consistent across batches of pigs, which typically spend their life indoors. Additionally, the main sources of emissions from that study were feed production and manure management. Because pigs are monogastric, enteric emissions were not a significant source of total emissions. Reductions in manure excretion were the primary driver of climate change impact reduction, as most of the carbon footprint from swine is the result of manure management practices. Despite the difference in methodology in preparing performance phenotypes as LCA inputs and the difference in the primary sources of emissions, these studies concluded that genetic improvement through a targeted breeding program for improved efficiency conferred systematic environmental benefits that can be quantified in partial environmental effect calculations and in an LCA.

Previous reports for BxD environmental footprinting have focused on climate change impact, and previous BxB LCAs characterized other impact categories using different units, preventing comparison of other impact categories. Beck et al. (2025) calculated that the carbon footprints for calf-fed (i.e., entered the feedyard directly from the rearer) BxD animals from the finishing phase in the US was 5.84 kg CO₂e/kg CW. This value was similar to the values calculated in the present study of 5.6-6.2 kg CO₂e/kg CW, depending on sire tier, from the finishing phase of the US population in 2024 (Figure 5c, Supplemental Figure 1c). Due to the allocation of much of the dairy dam's impacts to the dairy sector, the BxD footprints reported by Beck et al. (2025) and the present study were, unsurprisingly, lower than BxB carbon footprints that they and others estimated, an effect observed previously in beef from dairy herds (i.e., straightbred

dairy, not BxD) (de Vries and de Boer, 2010; Gerber et al., 2015). Beck et al. (2025) found that when considering only the direct emissions from BxD and BxB cattle, BxD cattle had a 3.8 or 11.7% greater carbon footprint compared to BxB cattle when yearling-fed (i.e., entered a grazing stocker system before entering the finishing phase) and calf-fed, respectively, but when dam emissions were allocated, the carbon footprint of BxD steers was 51% lower than that of BxB steers. Similarly, in the present BxD LCA, only the impact from the dairy dam during gestation was included in the environmental footprint; the rest of the impact would be allocated to milk production. In contrast, BxB LCAs allocate all the impact from the beef dams and sires to beef production (Stackhouse-Lawson et al., 2012; Rotz et al., 2019; Putman et al., 2023). This allocation method resulted in climate change impact from partial LCAs from cradle to gate of 21.3 ± 2.3 kg CO₂e/kg CW (Rotz et al., 2019) and 21.0 kg CO₂e/kg CW (Putman et al., 2023) for conventional US beef systems. The FAO included post-farm emissions in their emission intensity estimates, resulting in 26.00 kg CO₂e/kg CW in grassland systems and 14.83 kg CO₂e/kg CW in mixed systems in the US (from GLEAM 3 using 2015 base year, FAO, 2022). Putnam et al. also reported a full life cycle climate change impact from cradle to grave (birth to consumption) of 42.7 kg CO₂ e/kg of consumed beef (2023). The climate change impact from a Northern European beef production system has similarly been reported as 20.4 kg CO₂e/kg CW (FAO, 2022). Although the environmental footprint to grow BxD animals from birth to harvest may be similar or slightly higher than that of BxB animals, co-producing milk and a terminal calf from the same dairy dam dilutes the environmental impact across the beef and dairy sectors, resulting in a lower footprint of BxD production.

To a lesser extent than dam allocation, the differences in production phases between BxD and BxB also contributed to the difference in environmental footprint. While BxB animals are typically grazed for most of their lives, BxD animals are usually intensively managed without access to pasture, except for the short grazing period in the UK-HQ system. Accordingly, the enteric fermentation footprint comprised a relatively larger portion of the overall carbon footprint in BxB production compared to BxD, whereas the BxD overall carbon footprint is more heavily influenced by feed production and manure management, especially in the US and UK-HY populations. Notably, the finishing phase comprised the largest portion of the BxD environmental footprint, which contrasts with BxB systems, where the finishing phase is a relatively small contributor (Putman et al., 2023). Therefore, improvements to efficiency and growth in the finishing phase for BxD production have the largest environmental mitigation potential. Given the historic lack of genetic

improvement for what is essentially a dairy by-product, this is a particularly important result as it provides a more specific target for improving BxD production to reduce environmental impact.

These comparisons should be interpreted with caution, as the systems are modeled using different methodological choices, and the data sources and data granularity across the studies varies. Additionally, although the carbon footprint for BxD production calculated in the present study was lower than previously reported BxB carbon footprints, this reduction could have tradeoffs in other impact categories. However, these previous studies either used different units for impact categories or did not report on other impact categories, precluding meaningful comparison.

While these environmental impact assessments follow current best practice, opportunities remain to more precisely quantify climate change and other impact categories affected by reactive nitrogen by measuring instead of estimating emissions and nitrogenous compounds from enteric fermentation and manure management. In this and many LCAs, emissions from enteric fermentation and manure management were estimated from body weight and ADG, with some adjustment for feed digestibility for enteric fermentation emissions using IPCC equations. This assumes that all animals within and across sire tiers have the same enteric methane and manure nitrous oxide emission factor given the same diet. However, there is a growing body of evidence that contradicts this assumption and indicates there can be wide variation in nitrogen excretion rates (Bougouin et al., 2022) and methane emission factors among animals fed the same diet also vary, particularly as the digestibility of the diet increases (Vargas et al., 2025). Additionally, nitrogenous emissions to air, water, and soil from manure management are key contributors to multiple impact categories in addition to climate change, including acidification, smog formation, and eutrophication. Measuring rather than estimating enteric emissions and manure nitrogenous compounds can capture this variation in enteric methane and manure emission factors within and across sire tiers and any significant deviations from the IPCC values.

The environmental benefits resulting from genetic improvement targeted for feed efficiency and growth are smaller than the enteric methane mitigation potential that has been reported for other interventions, such as feed additives, as recently reviewed by Kelly and Kebreab (2023). However, genetic improvement differs from other interventions, including feed additives, in three key ways: (1) the performance improvements from genetic improvement are cumulative and permanent, (2) genetic improvement for feed efficiency and growth confers benefits for a variety of environmental impact categories in addition to climate change impact, and (3) genetic im-

provement creates a more profitable animal for producers using a technology with which producers and regulatory bodies are already familiar. For these reasons, genetic improvement is a promising strategy for improving the sustainability of livestock production. Although there is currently a strong focus on reducing enteric emissions to lower climate change impact, manure management and feed production remain the largest contributors of impact for all other environmental impact categories for BxD production. Consequently, these sources cannot be deprioritized below enteric fermentation when developing strategies to mitigate the environmental impact livestock production systems.

CONCLUSION

We present the first LCA to quantify the environmental benefits of genetic improvement targeted for improved feed efficiency and growth in BxD systems in the US and UK, yielding a 4.2-8.7% reduction in overall environmental footprint across systems in 2024. Using an LCA approach enabled contextualizing the effect of genetic improvement on various processes within sixteen different impact categories encompassing water quality and usage, air quality, land use, resource scarcity, and climate change. Relative to enteric methane emissions, feed production and manure management are similarly large or larger contributors to not only climate change, but also to other impact categories including eutrophication, acidification, and particulate matter formation. As BxD production continues to grow in the face of increasingly stringent environmental expectations, the demand for high-performing, low environmental impact BxD animals will continue to rise. When paired with proper management, targeted genetics meets the needs of producers while providing meaningful environmental benefits in addition to climate change mitigation that retailers and other downstream supply chain stakeholders value. In short, targeted genetic improvement is incremental but instrumental for mitigating the environmental impact of animal protein production.

Supplemental Material

Supplemental tables and figures can be found at Mendele Data at DOI: 10.17632/3x6jbdpxt2.1

NOTES

Funding information

This study was supported by Innovate UK, part of UK Research and Innovation, under the project titled “Climate Smart Beef Genetics - Innovative approaches to

the reduce environmental impact of the UK beef supply chain” (reference number 10045515) and ABS Global.

Acknowledgements

We gratefully acknowledge the team of Analysts at PRé Sustainability (Amersfoort, Netherlands) who developed the LCA model to generate the results presented; Amanda Bushell, Sarah Frank, Clay Moyer, Chad Robertson, Allegra Palmer, Garth Boyd, and Matt Sutton-Vermeulon from The Context Network LLC (since acquired by Kearney, Chicago, IL, USA) for project management assistance; the four ISO panelists who provided invaluable feedback during the critical review process; Dr. Ziqing Weng, Dr. Johnna Granville, Dr. Alex Brown, Dr. Irene Breider, Fern Pearston, Rhys Roberts, Dr. Lydia Hardie, Jinmei Liu, Dr. Melanie Hess, Grant Sardella, and Dr. Tonya Amen from the ABS Product Development team (DeForest, WI, USA), who provided technical assistance; and Dr. Tim Bodine, the nutritionist at Northwest Research and Nutrition, LLC (Pasco, WA, USA) who provided the ration composition and nutritional values for growing phases with missing feed data.

Ethics statement

Ethical approval was not necessary because the data used in this study was repurposed from data collected in the past.

Conflict of interest statement

The authors EL and MAC are employed by ABS Global, which is the company that funded part of this research.

Nonstandard abbreviations used: BXB = BEEF-ON-BEEF; BXD = beef-on-dairy; CW = carcass weight; GT = genetically targeted; KPI = key performance indicators; LCA = life cycle assessment; LCIA = life cycle impact assessment; PEF = Product Environmental Footprint; UK-HQ = United Kingdom, high quality; UK-HY = United Kingdom, high yield; US = United States

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